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F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (CHEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C).//0.21:115:28//HOMO SAPIENS (HUMAN).//P24821

F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F 5.2 IN CHROMOSOME III.//1.7e-25:139:48//CAENORHABDITIS ELEGANS.//Q09232

F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PROTEIN DP5).//0.14:65:41//HOMO SAPIENS (HUMAN).//000198

F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//8.1e-108:192:98//MUS MUSCULUS (MOUSE).//P17427

F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPONSON TN4556.//0.046:176:31//STREPTOMYCES FRADIAE.//P20186

F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//1.4e-07:245:25//RATTUS NORVEGICUS (RAT).//P41777

F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN.//1.0:12:66//SIMIAN VIRUS 5 (STRAIN W3) (SV5).//P07577

F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR I(A)3).//1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P01094

F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP).//0.99:38:31//HAEMOPHILUS INFLUENZAE.//P43709

F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C1B 9.04 IN CHROMOSOME I.//5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429

F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-CCR2 INTERGENIC REGION.//6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN.//0.68:34:47//THERMOPROTEUSTENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19302

F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F 6.10 IN CHROMOSOME III.//7.9e-19:179:34//CAENORHABDITIS ELEGANS.//Q21986

F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.6e-17:37:75//HOMO SAPIENS (HUMAN).//P39188

F-NT2RP3002146//CUTICLE COLLAGEN 40.//0.00034:90:37//CAENORHABDITIS ELEGANS.//P34804

F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO P RECURSOR (ALLELE S).//0.011:166:28//HOMO SAPIENS (HUMAN).//P10163

F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 50

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HOMOLOG (GTP-BINDING PROTEIN GST1-HS).//4.8e-11:60:53//HOMO SAPIENS (HUMAN).//P15170

F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TF IID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.028:191:29//HOMO SAPIENS (HUMAN).//000268

F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//2.3e-131:223:91//MUS MUSCULUS (MOUSE).//Q02614

F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP).//1.0:65:33//LACTOBACILLUS CASEI.//P55153

F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY!!!!//2.4e-26:114:62//HOMO SAPIENS (HUMAN).//P39194

F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MST84D.//0.25:31:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645

F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.069:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT).//P04102

F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MICROFIBRIL PROTEIN) (AMF).//0.0079:187:24//GALLUS GALLUS (CHICKEN).//P55080

F-NT2RP3002255//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.6e-10:168:34//MUS MUSCULUS (MOUSE).//P05143

F-NT2RP3002273//SCD6 PROTEIN.//1.5e-11:160:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45978

F-NT2RP3002276//PROBABLE E4 PROTEIN.//0.91:54:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06922

F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C4D7.04C IN CHROMOSOME I.//1.7e-42:191:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014171

F-NT2RP3002304

F-NT2RP3002330//NNP-1 PROTEIN.//0.52:140:18//MUS MUSCULUS (MOUSE).//P56183

F-NT2RP3002343//5E5 ANTIGEN.//0.0056:189:30//RATTUS NORVEGICUS (RAT).//Q63003

F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.15) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) MITOCHONDRIAL PRECURSOR.//1.0e-66:196:68//HOMO SAPIENS (HUMAN).//P13995

F-NT2RP3002352//PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROENDOCRINE-DLG) (NE-DLG).//0.79:173:27//HOMO SAPIENS (HUMAN).//Q92796

F-NT2RP3002377//PUTATIVE HELICASE YGR271W.//1.0e-56:216:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53327

F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6.//1.4e-19:136:31//SACCHAROMYCES CEREVISIAE (BAK

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ER'S YEAST). //P53091
 F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C)
 (EBNA-4B). //0.74:107:36//EPSTEIN-BARR VIRUS (STRAI
 N B95-8) (HUMAN HERPESVIRUS 4). //P03204
 F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT). //5.6e-06:
 57:42//AGROBACTERIUM TUMEFACIENS. //P50018
 F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B1
 0.04 IN CHROMOSOME I. //0.00032:52:48//SCHIZOSACCHA
 ROMYCES POMBE (FISSION YEAST). //Q10438
 F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FR 10
 E2-JEN1 INTERGENIC REGION. //9.4e-42:209:42//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //P36007
 F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GP
 M1-MCR1 INTERGENIC REGION. //7.7e-32:162:37//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //P36059
 F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-
 ASSOCIATED PROTEIN C2G11.03C. //2.1e-45:241:43//SCH
 IZOSACCHAROMYCES POMBE (FISSION YEAST). //Q09805
 F-NT2RP3002545
 F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C 20
 3.4 IN CHROMOSOME III. //2.8e-41:161:52//CAENORHABD
 ITIS ELEGANS. //Q10010
 F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180. //0.
 56:130:24//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PR
 V). //P33479
 F-NT2RP3002587
 F-NT2RP3002590
 F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECUR
 SOR (PDI) (EC 5.3.4.1) (THIOREDOXIN- RELATED GLYCOP
 ROTEIN 1). //0.00091:111:28//SACCHAROMYCES CEREVISI 30
 AE (BAKER'S YEAST). //P17967
 F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BL
 AB 3' REGION. //1.0:65:40//STREPTOMYCES CACA01. //P33
 654
 F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093. //2.4e-1
 7:101:44//SYNECHOCYSTIS SP. (STRAIN PCC 6803). //P5
 0027
 F-NT2RP3002631//METALLOTHIONEIN-1B (MT-1B). //0.09
 2:36:33//HOMO SAPIENS (HUMAN). //P07438
 F-NT2RP3002650//DUALIN. //3.0e-21:184:37//GALLUS GA 40
 LLUS (CHICKEN). //Q90830
 F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECU
 RSOR. //0.00016:223:33//HOMO SAPIENS (HUMAN). //P081
 23
 F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A. //0.16:
 72:31//CAENORHABDITI SELEGANS. //P37165
 F-NT2RP3002663//OXYSEROL-BINDING PROTEIN. //5.4e-2
 3:168:41//HOMO SAPIENS (HUMAN). //P22059
 F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN S
 K01-RPL44A INTERGENIC REGION. //6.0e-38:203:43//SACC 50

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BAROMYCES CEREVISIAE (BAKER'S YEAST). //P53893
 F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHA
 IN 4L (EC 1.6.5.3). //0.25:63:31//ARTEMIA SALINA (B
 RINE SHRIMP). //P19049
 F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LE
 F3-IAP2 INTERGENIC REGION. //0.029:60:36//AUTOGRAPH
 A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).
 //P41469
 F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF1B. //5.3e-
 61:130:88//MUS MUSCULUS (MOUSE). //Q60575
 F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENO
 PROTEIN (MCS). //7.4e-05:109:33//MUS MUSCULUS (MOUS
 E). //P15265
 F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICAS
 E DDX10 (DEAH BOX PROTEIN 10). //0.77:70:32//HOMO S
 APIENS (HUMAN). //Q13206
 F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.
 07 IN CHROMOSOME I. //6.7e-11:66:40//SCHIZOSACCHARO
 MYCES POMBE (FISSION YEAST). //Q14056
 F-NT2RP3002770//COLLAGEN ALPHA 1(IX) CHAIN (FRACME
 NT). //0.33:87:34//MUS MUSCULUS (MOUSE). //Q05722
 F-NT2RP3002785//LETHAL(2) DENTICLELESS PROTEIN (DTL
 83 PROTEIN). //9.7e-36:187:39//DROSOPHILA MELANOGAS
 TER (FRUIT FLY). //Q24371
 F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/5.6e-08:41:73//HOMO SAPIENS (HUMAN). //P3918
 8
 F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTR
 Y !!!!!/0.0034:35:65//HOMO SAPIENS (HUMAN). //P3919
 3
 F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CE
 NTROMERE PROTEIN B) (CENP-B). //3.2e-17:148:37//MUS
 MUSCULUS (MOUSE). //P27790
 F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GS
 H1-CHS6 INTERGENIC REGION. //1.7e-05:95:31//SACCHAR
 OMYCES CEREVISIAE (BAKER'S YEAST). //P42951
 F-NT2RP3002869//TRYPSIN INHIBITOR II (BDTI-II). //0.
 97:23:39//BRYONIA DIOICA (RED BRYONY). //P11968
 F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECUR
 SOR (CLONE PRP33). //0.00017:140:31//RATTUS NORVEGI
 CUS (RAT). //P04474
 F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTR
 Y !!!!!/2.5e-06:55:60//HOMO SAPIENS (HUMAN). //P391
 94
 F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BI
 NDING PROTEIN) (BBP). //4.6e-08:129:38//HOMO SAPIEN
 S (HUMAN). //Q13625
 F-NT2RP3002911//HYPOTHETICAL PROTEIN C18. //0.99:2
 6:50//SWINEPOX VIRUS (STRAIN KASZA) (SPV). //P32217
 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEI

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N. //1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q04652
 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN). //0.55:116:27//DROSOPHILA MELANOGASTER (FRUIT FLY). //P33450
 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BL TR-SPO11IC INTERGENIC REGION. //0.87:67:37//BACILLUS SUBTILIS. //P54445
 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID--COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4). //6.7e-56:189:59//HOMO SAPIENS (HUMAN). //060488
 F-NT2RP3002972//HYPOTHETICAL 73.0 KD PROTEIN IN CL A4-MID1 INTERGENIC REGION. //0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P48566
 F-NT2RP3002978//PROBABLE E5 PROTEIN. //0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51. //P26553
 F-NT2RP3002985//METALLOTHIONEIN (MT). //0.0031:49:42//PLEURONECTES PLATESSA (PLAICE). //P07216
 F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (NOTCH PROTEIN). //1.0:111:29//MUS MUSCULUS (MOUSE). //Q01705
 F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A 4.1 IN CHROMOSOME III. //0.96:112:25//CAENORHABDITIS ELEGANS. //P41879
 F-NT2RP3003032
 F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F 8.06C IN CHROMOSOME I PRECURSOR. //9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10254
 F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN). //3.7e-25:167:34//HOMO SAPIENS (HUMAN). //P16157
 F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.1) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT). //0.074:82:39//SULFOLOBUS SOLFATARICUS. //033780
 F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP). //0.0085:128:30//HOMO SAPIENS (HUMAN). //P50552
 F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT). //0.028:165:31//VULPES VULPES (RED FOX). //P53353
 F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)). //1.0e-14:243:25//ESCHERICHIA COLI. //P02981
 F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40. //7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32583
 F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65). //0.024:61:42//GALLUS GALLUS (CHICKEN). //P46936
 F-NT2RP3003138//KINESIN-LIKE PROTEIN KIF4. //1.1e-1

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18:151:93//MUS MUSCULUS (MOUSE). //P33174
 F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1. //1.0:70:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q92337
 F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (HMFG) (BREAST EPITHELIAL ANTIGEN BA46) (MFGM). //2.0e-12:121:37//HOMO SAPIENS (HUMAN). //Q08431
 F-NT2RP3003150
 F-NT2RP3003157//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1). //4.0e-79:260:54//HOMO SAPIENS (HUMAN). //P51522
 F-NT2RP3003185//TROPOMYOSIN. //0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q02088
 F-NT2RP3003193//ZINC FINGER PROTEIN 135. //7.2e-91:239:65//HOMO SAPIENS (HUMAN). //P52742
 F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SI PU-PBPC INTERGENIC REGION. //1.3e-07:117:34//BACILLUS SUBTILIS. //P42966
 F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME I. //9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10149
 F-NT2RP3003204//RAS-LIKE PROTEIN RASB. //0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //P32252
 F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION. //0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38190
 F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40. //0.019:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32583
 F-NT2RP3003230//CORONIN-LIKE PROTEIN P57. //8.3e-74:183:73//BOS TAURUS (BOVINE). //Q92176
 F-NT2RP3003242//STANNIOCALCIN PRECURSOR. //1.4e-21:127:37//HOMO SAPIENS (HUMAN). //P52823
 F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR. //3.1e-51:198:52//MUS MUSCULUS (MOUSE). //P15533
 F-NT2RP3003264//E6 PROTEIN. //1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48. //Q80920
 F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION. //8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38344
 F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDNM). //8.0e-108:226:88//MUS MUSCULUS (MOUSE). //P39054
 F-NT2RP3003290//BIOH PROTEIN. //0.0055:107:30//ESCHERICHIA COLI. //P13001
 F-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-). //1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //064948
 F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOL

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OG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547
 F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.
 //0.18:225:26//ACANTHAMOEBA CASTELLANII (AMOEBA)./
 /P05659
 F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PO
 (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.
 0014:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME
 TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052).//8.8e-1
 8:94:43//MUS MUSCULUS (MOUSE).//Q62191
 F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAA0176 (FRA
 GMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q1
 4681
 F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICD
 C-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA
 COLI.//P75991
 F-NT2RP3003346//!!!! ALU SUBFAMILY SB2 WARNING ENT
 RY !!!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN).//P39
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 F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D
 7.2 IN CHROMOSOME III.//3.7e-10:118:33//CAENORHABD
 ITIS ELEGANS.//P30641
 F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.
 //1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP3003384
 F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS
 MUSCULUS (MOUSE).//Q60649
 F-NT2RP3003403
 F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOM
 O SAPIENS (HUMAN).//015370
 F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//
 BOVINE PAPILLOMAVIRUSTYPE 2.//P11300
 F-NT2RP3003427//HOLOTRICIN 3 PRECURSOR.//0.012:36:
 41//HOLOTRICIA DIOMPHALIA.//Q25055
 F-NT2RP3003433
 F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VM
 A7-RPS25A INTERGENIC REGION.//0.0042:110:40//SACCH
 AROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
 F-NT2RP3003490
 F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10)
 (PROTEIN GROES) (HEAT SHOCK 10 KD PROTEIN).//0.99:
 49:34//LEPTOSPIRA INTERROGANS.//P35472
 F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SAC
 CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURS
 OR.//0.0026:175:30//HOMO SAPIENS (HUMAN).//P29400
 F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT)./
 /0.19:21:47//BOS TAURUS (BOVINE).//P20072
 F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN ME
 T30-PIG2 INTERGENIC REGION.//7.3e-27:159:43//SACCH

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AROMYCES CEREVISIAE (BAKER'S YEAST).//P40529
 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.
 7.48).//1.0:99:30//TURNIP YELLOW MOSAIC VIRUS.//P1
 0358
 F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.
 //0.33:128:32//CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTR
 Y !!!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN).//P391
 95
 10 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-
 54:114:94//CANIS FAMILIARIS (DOG).//P24409
 F-NT2RP3003621//COAGULATION FACTOR XII PRECURSOR
 (EC 3.4.21.38) (HAGEMANFACTOR) (HAF).//2.0e-15:89:
 40//HOMO SAPIENS (HUMAN).//P00748
 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84D
 D.//0.99:22:50//DROSOPHILA MELANOGASTER (FRUIT FL
 Y).//Q01645
 F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.
 30:111:25//BRACHYDANIORERIO (ZEBRAFISH) (ZEBRA DAN
 IO).//Q90267
 F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RP
 L14B-GPA1 INTERGENIC REGION.//1.1e-20:127:37//SACC
 HAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.
 34:52:34//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROP
 EAN WHITE SHRIMP).//P81060
 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRE
 CURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7)./
 /8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209
 30 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FA
 B1-PES4 INTERGENIC REGION.//4.3e-25:159:40//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMC
 -17.//0.067:63:31//GALLUS GALLUS (CHICKEN).//P0231
 4
 F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:
 27//RATTUS NORVEGICUS (RAT).//P35446
 F-NT2RP3003716//SLIT PROTEIN PRECURSOR.//1.3e-12:1
 50:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P2401
 4
 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETIC
 AL 16.9 KD PROTEIN.//0.47:109:28//AGROBACTERIUM TU
 MEFACIENS.//P05680
 F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIX
 X 3' REGION (ORF1).//0.57:34:38//AZORHIZOBIUM CAULI
 NODANS.//P26486
 F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTR
 Y !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN).//P391
 95
 50 F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PREC

3047

URSOR. //0.75:60:36//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS). //P78744
 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.112) (P60-SRC). //4.2e-51:72:95//GALLUS GALLUS (CHICKEN). //P00523
 F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DB P7-GCN3 INTERGENIC REGION. //0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P36121
 F-NT2RP3003809//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS). //0.028:135:35//GALLUS GALLUS (CHICKEN). //P12105
 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT). //0.0026:90:33//HORDEUM VULGARE (BARLEY). //P06472
 F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP). //5.6e-20:174:31//BOS TAURUS (BOVINE). //P02720
 F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE). //0.0017:111:38//CANIS FAMILIARIS (DOG). //P30803
 F-NT2RP3003831//ENDONUCLEASE G PRECURSOR (EC 3.1.3.0.-) (ENDO G). //1.1e-37:187:42//MUS MUSCULUS (MOUSE). //008600
 F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INT E-PIN INTERGENIC REGION. //1.0:38:39//ESCHERICHIA COLI. //P75979
 F-NT2RP3003842
 F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDCB). //0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY). //P43125
 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST84DB. //0.83:51:37//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01643
 F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2. //0.0017:151:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P17065
 F-NT2RP3003914//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT). //3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q09332
 F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33). //5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE). //Q16943
 F-NT2RP3003932
 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT. //0.96:46:32//THERMOTOGA MARITIMA. //P35874
 F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67). //0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P27476

3048

F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1). //3.6e-21:134:45//RATTUS NORVEGICUS (RAT). //P51400
 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LE F4-P33 INTERGENIC REGION. //0.00021:64:40//AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACNPV). //P41479
 F-NT2RP3004041//SPERM PROTAMINE P1. //0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS). //P35307
 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE). //0.0079:194:24//CLOSTRIDIUM PERFRINGENS. //P43153
 F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //3.4e-11:51:72//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2. //2.7e-114:243:87//MUS MUSCULUS (MOUSE). //P48379
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RH SE-NARV INTERGENIC REGION (ORFB). //8.0e-13:111:41//ESCHERICHIA COLI. //P37757
 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //1.5e-17:72:65//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! //2.6e-10:51:72//HOMO SAPIENS (HUMAN). //P39195
 F-NT2RP3004125//ZINC FINGER PROTEIN 75. //1.1e-28:18:47//HOMO SAPIENS (HUMAN). //P51815
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN. //0.012:45:33//AEROMONAS SOBRIA. //P09165
 F-NT2RP3004148//METALLOTHIONEIN-I (MT-1). //0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON). //P15786
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN CO Q7 HOMOLOG. //1.7e-82:178:89//RATTUS NORVEGICUS (RAT). //Q63619
 F-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //1.7e-11:215:24//PODOSPORA ANSERINA. //Q00808
 F-NT2RP3004206//CROOKED NECK PROTEIN. //3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT FLY). //P17886
 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR. //0.13:130:33//CAENORHABDITIS ELEGANS. //P20630
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG). //6.5e-16:207:29//HOMO SAPIENS (HUMAN). //Q13107

3049

F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 CA
NNA SUBUNIT. //1.0:69:31//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST). //P35179

F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK63
2.12 IN CHROMOSOME III. //1.1e-64:191:63//CAENORHAB
DITIS ELEGANS. //P34657

F-NT2RP3004246//RING3 PROTEIN (KIAA9001). //0.060:1
01:28//HOMO SAPIENS (HUMAN). //P25440

F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMEN
TS). //1.1e-07:184:35//BOS TAURUS (BOVINE). //P02453

F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40. //4.9e-0
8:98:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //
P32583

F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HE
AT SHOCK PROTEIN 40) (HSP40). //1.6e-63:210:61//HOM
O SAPIENS (HUMAN). //P25685

F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G4.1 IN CH
ROMOSOME II (FRAGMENT). //1.6e-29:177:38//CAENORHAB
DITIS ELEGANS. //P54073

F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LAR
GEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT). //0.03
0:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER). //P
11414

F-NT2RP3004334

F-NT2RP3004341//ALPHA-INTERNEKIN (ALPHA-INX). //0.9
1:110:26//MUS MUSCULUS (MOUSE). //P46660

F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G
6.5 IN CHROMOSOME III. //0.60:198:24//CAENORHABDITI
S ELEGANS. //P46012

F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!! //1.0e-37:60:76//HOMO SAPIENS (HUMAN). //P391
93

F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN GN
TR-CGT INTERGENIC REGION (0162). //0.0026:76:28//ES
CHERICHIA COLI. //P46854

F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROT
EIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPON
SE PROTEIN). //4.4e-109:212:96//HOMO SAPIENS (HUMA
N). //Q92674

F-NT2RP3004424//JTV-1 PROTEIN. //4.5e-18:60:70//HOM
O SAPIENS (HUMAN). //Q13155

F-NT2RP3004428//METALLOTHIONEIN-A (MTA). //0.0010:3
6:47//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA UR
CHIN). //P04734

F-NT2RP3004451//MYOSIN IC HEAVY CHAIN. //0.00072:11
3:34//ACANTHAMOEBA CASTELLANII (AMOEBA). //P10569

F-NT2RP3004454//VERPROLIN. //3.3e-07:156:29//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST). //P37370

F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215. //0.001
3:125:32//HUMAN ADENOVIRUS TYPE 2. //P03291

3050

F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C1
0.11 IN CHROMOSOME III. //1.0:33:51//CAENORHABDITIS
ELEGANS. //Q09254

F-NT2RP3004472//GERM CELL-LESS PROTEIN. //7.3e-33:1
70:40//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q0182
0

F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1
(P115) (KIAA0131). //8.4e-54:214:46//HOMO SAPIENS
(HUMAN). //P98171

F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATE
D PROTEIN VPS35. //3.9e-47:199:49//SACCHAROMYCES CE
REVISIAE (BAKER'S YEAST). //P34110

F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURS
OR (APEG PROTEIN). //0.0013:121:33//XENOPUS LAEVIS
(AFRICAN CLAWED FROG). //P17437

F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN CO
TD-KDUD INTERGENIC REGION PRECURSOR. //0.066:87:35/
BACILLUS SUBTILIS. //P50840

F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!! //2.0e-34:102:69//HOMO SAPIENS (HUMAN). //P39
194

F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40. //0.64:9
3:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P
32583

F-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1). //2.2
e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T). //P40484

F-NT2RP3004527

F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6. //0.38:148:
22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32
943

F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN 1 PRECURSOR (IGFBP-1) (IBP-1) (IGF-BINDIN
G PROTEIN 1). //0.38:89:38//RATTUS NORVEGICUS (RAT).
//P21743F-NT2RP3004544//CYTADHERENCE HIGH MOLECULA
R WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN
2). //0.0024:200:24//MYCOPLASMA PNEUMONIAE. //P7547
1

F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLGCF
17.1 (FRAGMENT). //4.6e-25:126:43//XENOPUS LAEVIS
(AFRICAN CLAWED FROG). //P18713

F-NT2RP3004569//ANKYRIN. //8.3e-07:150:28//MUS MUSC
ULUS (MOUSE). //Q02357

F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TF
IID 150 KD SUBUNIT (TAFII-150) (TAFII150). //1.6e-7
0:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q2
4325

F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROT
EIN). //1.5e-10:210:26//HOMO SAPIENS (HUMAN). //Q022
24

3051

F-NT2RP3004594//P54 PROTEIN PRECURSOR.//0.0044:23
 0:24//ENTEROCOCCUS FAECIUM (STREPTOCOCCUS FAECIU
 M).//P13692
 F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLE
 UKIN 2 RECEPTOR.//1.5e-14:113:34//MUS MUSCULUS (MO
 USE).//P15533
 F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK75
 7.3 IN CHROMOSOME III.//4.5e-08:149:30//CAENORHABD
 ITIS ELEGANS.//P34681
 F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) 10
 (EASILY SHOCKED PROTEIN).//1.0e-24:75:48//DROSOPHI
 LA MELANOGASTER (FRUIT FLY).//P54352
 F-NT2RP3004670//CUTICLE COLLAGEN 2.//0.00090:159:2
 9//CAENORHABDITIS ELEGANS.//P17656
 F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0
 e-79:243:62//BOS TAURUS (BOVINE).//P35526
 F-NT2RP4000023
 F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTR
 Y !!!!!/3.6e-06:46:67//HOMO SAPIENS (HUMAN).//P391
 94
 F-NT2RP4000049//CALDESMON (CDM).//0.41:63:34//GALL
 US GALLUS (CHICKEN).//P12957
 F-NT2RP4000051//DUALIN.//2.3e-23:195:37//GALLUS GA
 LLUS (CHICKEN).//Q90830
 F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEI
 N).//1.2e-24:182:31//DROSOPHILA MELANOGASTER (FRUI
 T FLY).//Q04652
 F-NT2RP4000102//XPAP7 PROTEIN.//1.0:54:33//BACILLU
 S LICHENIFORMIS.//Q99166
 F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:2
 30:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P2401
 4
 F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECI
 FICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNI
 T).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q10568
 F-NT2RP4000129//SE5 ANTIGEN.//0.00072:124:37//RATT
 US NORVEGICUS (RAT).//Q63003
 F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-2
 6:119:43//SACCHAROMYCESCEREVISIAE (BAKER'S YEAST).
 //P35197
 F-NT2RP4000150
 F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.
 2 IN CHROMOSOME III.//4.2e-31:180:47//CAENORHABDIT
 IS ELEGANS.//P32740
 F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:10
 7:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P143
 28
 F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SP
 X19-GCR2 INTERGENIC REGION.//2.4e-08:133:32//SACCH
 AROMYCES CEREVISIAE (BAKER'S YEAST).//P40164

3052

F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTE
 IN ICPO (VMW118 PROTEIN).//5.4e-05:143:32//HERPES
 SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).//P28284
 F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN./
 /1.8e-40:258:35//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST).//P22579
 F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PREC
 URSOR (AGSA).//1.4e-20:104:40//APLYSIA CALIFORNICA
 (CALIFORNIA SEA HARE).//P15287
 F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA T
 HERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203
 F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/1.7e-15:48:60//HOMO SAPIENS (HUMAN).//P3918
 8
 F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GA
 LLUS (CHICKEN).//Q90830
 F-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1
 (NDPP-1).//3.1e-83:207:76//MUS MUSCULUS (MOUSE)./
 /Q03173
 20 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.
 1.9).//5.5e-29:153:43//HELIANTHUS ANNUUS (COMMON S
 UNFLOWER).//023968
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT)./
 /0.98:42:40//BOS TAURUS (BOVINE).//P20072
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G
 8.09C IN CHROMOSOME I.//3.5e-71:209:66//SCHIZOSACC
 HAROMYCES POMBE (FISSION YEAST).//P87115
 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1)
 (RSP-1 PROTEIN) (RSP-1).//8.9e-22:166:37//HOMO SAP
 30 IENS (HUMAN).//Q15404
 F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST).//P37370
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.4
 2:15:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN S
 EA ANEMONE).//P01531
 F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GC
 N20-CMK1 INTERGENIC REGION.//0.75:125:29//SACCHARO
 MYCES CEREVISIAE (BAKER'S YEAST).//P43596
 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECUR
 40 SOR (CLONE PRP25) (FRAGMENT).//0.27:92:33//RATTUS
 NORVEGICUS (RAT).//P10164
 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100
 KD PROTEIN REGION.//0.99:52:32//HUMAN ADENOVIRUS
 TYPE 41.//P23691
 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEAS
 E FACTOR 1 PRECURSOR (MRF-1).//4.1e-40:163:52//HOM
 O SAPIENS (HUMAN).//075570
 F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTE
 IN (PLAP).//4.2e-59:125:80//RATTUS NORVEGICUS (RA
 50 T).//P54319

- F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246
- F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO SAPIENS (HUMAN).//Q99676
- F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
- F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.8e-25:196:40//MUS MUSCULUS (MOUSE).//P39098
- F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY!!!!//1.0e-15:72:61//HOMO SAPIENS (HUMAN).//P39195
- F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY!!!!//7.0e-23:63:82//HOMO SAPIENS (HUMAN).//P39192
- F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2).//1.3e-41:102:45//KLUYVEROMYCES LACTIS (YEAST).//P33294
- F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS (CHICKEN).//P19601
- F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009
- F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276
- F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//2.3e-05:152:23//CAENORHABDITIS ELEGANS.//Q09475
- F-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
- F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D 3.2 IN CHROMOSOME III.//1.3e-23:165:35//CAENORHABDITIS ELEGANS.//P34535
- F-NT2RP4000515//PHOSPHODIESTERASE I (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).//P1396
- F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA (BROAD BEAN).//Q41657
- F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818
- F-NT2RP4000519//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.68:55:40//BOS TAURUS (BOVINE).//P25508
- F-NT2RP4000524//IGA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0.37:187:24//STREPTOCOCCUS AGALACTIAE.//P27951
- F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755
- F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS GALLUS (CHICKEN).//P13544
- F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H 1.4 IN CHROMOSOME III.//4.3e-14:174:34//CAENORHABDITIS ELEGANS.//Q03574
- F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK75 7.1 IN CHROMOSOME III.//2.1e-19:155:36//CAENORHABDITIS ELEGANS.//P34679
- F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIRUS TYPE 2.//P03290
- F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188:44//GALLUS GALLUS (CHICKEN).//P30352
- F-NT2RP4000638//EARLY NODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:40:40//GLYCINE MAX (SOYBEAN).//Q05544
- F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-06:31:74//HOMO SAPIENS (HUMAN).//P39188
- F-NT2RP4000657//HYPOTHETICAL PROTEIN MJ1065.//2.5e-40:237:40//METHANOCOCCUS JANNASCHII.//Q58465
- F-NT2RP4000704
- F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-07:134:40//STREPTOMYCES FRADIAE.//P20186
- F-NT2RP4000724//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.1e-62:109:88//HOMO SAPIENS (HUMAN).//P10266
- F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
- F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.0e-05:114:34//HOMO SAPIENS (HUMAN).//P23246
- F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK).//P50655
- F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CP T1-SPC98 INTERGENIC REGION.//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
- F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e

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-13:79:39//HELIANTHUS ANNUUS (COMMON SUNFLOWER). //P29675
 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40. //1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32583
 F-NT2RP4000833
 F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST84D B. //0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01643
 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TF IID 90 KD SUBUNIT (TAFII-90). //0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38129
 F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B). //2.8e-64:229:53//RATTUS NORVEGICUS (RAT). //009175
 F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT). //3.6e-84:174:54//HOMO SAPIENS (HUMAN). //P16415
 F-NT2RP4000878//MYELOID UPREGULATED PROTEIN. //8.2e-88:227:74//MUS MUSCULUS (MOUSE). //035682
 F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN). //9.1e-55:268:43//HOMO SAPIENS (HUMAN). //P22314
 F-NT2RP4000907//BDNF / NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GP145-TRKB) (TRK-B). //5.4e-10:220:25//HOMO SAPIENS (HUMAN). //Q16620
 F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT). //0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //P51407
 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB. //0.00010:148:32//BACILLUS SUBTILIS. //P39217
 F-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN). //3.5e-27:220:36//HOMO SAPIENS (HUMAN). //Q06828
 F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2.9/ER2.6). //0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA). //P29128
 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAGSYNTHASE). //3.1e-104:263:66//HOMO SAPIENS (HUMAN). //Q92903
 F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION. //0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53288
 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G8.6. 50

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//2.0e-05:102:37//CAENORHABDITIS ELEGANS. //P34391
 F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BE T1-PAN1 INTERGENIC REGION. //2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40564
 F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.0041:142:33//HOMO SAPIENS (HUMAN). //P10162
 F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN. //0.77:106:33//VACCINIA VIRUS (STRAIN COPENHAGEN). //P20517
 F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E 4.4 IN CHROMOSOME III. //0.90:94:25//CAENORHABDITIS ELEGANS. //P34343
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B). //0.76:41:41//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE). //P01531
 F-NT2RP4000996//PROTEIN Q300. //0.00024:41:53//MUS MUSCULUS (MOUSE). //Q02722
 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT). //8.7e-115:261:82//RATTUS NORVEGICUS (RAT). //054888
 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT). //0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //Q42377
 F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR. //0.010:152:29//BACILLUS SUBTILIS. //P50840
 F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P08640
 F-NT2RP4001029//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1). //1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY). //P13002
 F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS). //1.5e-74:272:55//CAENORHABDITIS ELEGANS. //Q09996
 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK65 2.6 IN CHROMOSOME III. //0.0064:76:38//CAENORHABDITIS ELEGANS. //P34664
 F-NT2RP4001064//DUALIN. //2.5e-24:199:38//GALLUS GALLUS (CHICKEN). //Q90830
 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TF IID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130). //0.11:139:38//HOMO SAPIENS (HUMAN). //000268
 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC

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3.6.1.38) (GOLGI CA2+-ATPASE). //1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P13586
 F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I). //1.7e-82:178:69//SUS SCROFA (PIG). //Q29099
 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN. //0.00039:141:26//RATTUS NORVEGICUS (RAT). //P49911
 F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1). //9.9e-07:79:43//HOMO SAPIENS (HUMAN). //P78563
 F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION. //4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40032
 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT. //8.1e-115:224:99//RATTUS NORVEGICUS (RAT). //P38378
 F-NT2RP4001122//TIPD PROTEIN. //7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //015736
 F-NT2RP4001126//TRICHOHYALIN. //1.4e-19:257:28//OVIS ARIES (SHEEP). //P22793
 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-). //0.00010:204:25//METHANOCOCCUS JANNASCHII. //Q58896
 F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAP155-YMR31 INTERGENIC REGION. //4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P43616
 F-NT2RP4001148//SOF1 PROTEIN. //2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P33750
 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185). //1.3e-08:106:41//VOLVOX CARTERI. //P21997
 F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO). //3.6e-24:194:32//GALLUS GALLUS (CHICKEN). //P35331
 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2). //0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND). //Q03643
 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT). //5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER). //P52178
 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2). //0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND). //Q03643
 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1. //1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P33307
 F-NT2RP4001210//DERMOPHIN 1 PRECURSOR [CONTAINS:

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DELTORPHIN (DERMENKEPHALIN); DERMOPHIN]. //0.019:130:30//PHYLLomedusa SAUVAGEI. (SAUVAGE'S LEAF FROG). //P05422
 F-NT2RP4001213//ZINC FINGER PROTEIN 177. //3.2e-28:176:39//HOMO SAPIENS (HUMAN). //Q13360
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1). //2.4e-13:108:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q12404
 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN). //2.7e-56:242:40//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q04652
 F-NT2RP4001235//REGULATORY PROTEIN E2. //0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25. //P36787
 F-NT2RP4001256//CUTICLE COLLAGEN 1. //0.014:104:31//CAENORHABDITIS ELEGANS. //P08124
 F-NT2RP4001260//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17). //0.00077:16:68//ESCHERICHIA COLI. //P05834
 F-NT2RP4001274//HISTONE H1. M6.1. //0.98:65:35//TRYPANOSOMA CRUZI. //P40273
 F-NT2RP4001276//ELAV PROTEIN. //0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY). //P23241
 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN). //0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO). //P13983
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9. //2.3e-12:190:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P54787
 F-NT2RP4001336//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1. //0.0037:108:31//PODOSPORA ANSERINA. //Q00808
 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810. //1.2e-09:150:34//METHANOCOCCUS JANNASCHII. //Q58220
 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III. //1.4e-18:244:27//CAENORHABDITIS ELEGANS. //Q10123
 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT). //4.0e-49:212:50//GALLUS GALLUS (CHICKEN). //P53760
 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1. //5.7e-11:229:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P25386
 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1). //0.00088:84:28//HOMO SAPIENS (HUMAN). //Q15404
 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN). //1.0e-22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q08180

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F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL ANTIGEN).//0.51:92:26//ONCHOCERCA VOLVULUS.//P36991

F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//3.5e-13:146:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160

F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGENIC REGION.//1.2e-14:207:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38767

F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGE SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.073:112:33//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414

F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:233:24//HOMO SAPIENS (HUMAN).//Q02224

F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO SAPIENS (HUMAN).//Q14141

F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-85:216:56//HOMO SAPIENS (HUMAN).//P28160

F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGE SUBUNIT (EC 2.7.7.6) (VERSION 1).//0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P18616

F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:69:33//ARTEMIA SALINA (BRINE SHRIMP).//P02399

F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P21560

F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:61//HOMO SAPIENS (HUMAN).//Q02218

F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I.//2.3e-24:137:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701

F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN P0M152-REC114 INTERGENIC REGION.//6.0e-22:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40206

F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDITIS ELEGANS.//P34804

F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS), AND LACTOCOCCUS LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561

F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-1-BINDING ACTIVITY) (TRANSCR

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PTION FACTOR NTF-1).//2.8e-06:79:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NO T1/CDC39-HMR INTERGENIC REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25656

F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558

F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:158:24//MYCOBACTERIUM TUBERCULOSIS.//P96902

F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT).//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P52170

F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-22:119:42//HOMO SAPIENS (HUMAN).//Q15057

F-NT2RP4001571//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:167:28//BOS TAURUS (BOVINE).//P06836

F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620

F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTOCOCCUS PYOGENES.//P16946

F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNALIGASE) (ILERS).//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73505

F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:74:28//SUS SCROFA (PIG).//P27917

F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37//HOMO SAPIENS (HUMAN).//P02811

F-NT2RP4001634//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE (FRAGMENT).//0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462

F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN M ET18/MMS19.//4.2e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469

F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323

F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F 6.2 IN CHROMOSOME II.//3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600

F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//0.065:66:43//MYCOBACTERIUM TUBERCULOSIS.//Q10690

F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:103:72//HOMO SAPIENS (HUMAN).//P39

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F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J P
ROTEIN.//0.93:37:37//CHLORELLA VULGARIS.//P56338
F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN
BETA SUBUNIT.//4.3e-11:128:32//SCHIZOSACCHAROMYCE
S POMBE (FISSION YEAST).//Q10282
F-NT2RP4001730//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYL
TRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//4.1e-2
2:201:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q0
9332
F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H)
(HOX-1.8) (PL).//1.0:67:34//HOMO SAPIENS (HUMAN)./
/P31260
F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGE
R PROTEIN KOX1) (FRAGMENT).//1.2e-19:72:62//HOMO S
APIENS (HUMAN).//P21506
F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.
//1.8e-13:179:28//HOMOSAPIENS (HUMAN).//P11274
F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (C
TFIN51) (TRANSCRIPTIONFACTOR RU49).//7.9e-38:147:4
9//MUS MUSCULUS (MOUSE).//Q07231
F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.
40:48:39//CAENORHABDITIS ELEGANS.//P20630
F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:
173:36//HOMO SAPIENS (HUMAN).//014817
F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.
//3.3e-16:152:42//CAENORHABDITIS ELEGANS.//P34391
F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE
HP1.//P51727
F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA
1.//1.2e-07:95:31//HOMOSAPIENS (HUMAN).//Q13330
F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (ML
P) (FRAGMENT).//0.94:141:22//RATTUS NORVEGICUS (RA
T).//P98089
F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-5
2:276:45//MUS MUSCULUS(MOUSE).//P55194
F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN CA
LE-PEPT INTERGENIC REGION.//0.92:39:51//BACILLUS S
UBTILIS.//P55185
F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:
97:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HE
RPESVIRUS 4).//P03181
F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.
1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUC
LEASE 4) (FRAGMENT).//3.6e-07:124:29//MUS MUSCULUS
(MOUSE).//Q05921
F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEA
TS CONTAINING PROTEININ PMT6-PCT1 INTERGENIC REGIO
N.//3.9e-10:210:28//SACCHAROMYCES CEREVISIAE (BAKE
R'S YEAST).//P42935
- F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10)./
/2.4e-07:53:45//ORYCTOLAGUS CUNICULUS (RABBIT).//P
48038
F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM
1.//3.1e-19:170:32//SACCHAROMYCES CEREVISIAE (BAKE
R'S YEAST).//Q12024
F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-2
8:72:50//MUS MUSCULUS(MOUSE).//P24399
F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRA
NSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE MET
HYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METH
YLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL MET
HYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVU
M (WHEAT).//Q43209
F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.
7e-07:115:29//MUS MUSCULUS (MOUSE).//P11260
F-NT2RP4001953
F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.
//0.13:151:27//BACILLUS SUBTILIS.//Q07833
20 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAI
N.//0.00031:190:31//RIFTIA PACHYPTILA (TUBE WORM).
//P30754
F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEI
N).//3.5e-18:185:29//DROSOPHILA MELANOGASTER (FRUI
T FLY).//Q04652
F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE G
UF1).//4.0e-49:158:65//SACCHAROMYCES CEREVISIAE (B
AKER'S YEAST).//P46943
F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D
3.03C IN CHROMOSOME I.//0.0047:148:27//SCHIZOSACCH
AROMYCES POMBE (FISSION YEAST).//Q09844
F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR
ATP-DEPENDENT RNA HELICASE P56D2.6.//0.057:66:30//
CAENORHABDITIS ELEGANS.//Q20875
F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN
CY251.09.//0.94:45:46//MYCOBACTERIUM TUBERCULOSIS.
//Q10888
F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGUL
ATORY PROTEIN).//0.44:36:38//HUMAN IMMUNODEFICIENC
40 Y VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGE
R PROTEIN HTF10) (HPF7).//2.6e-19:46:76//HOMO SAPI
ENS (HUMAN).//Q05481
F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX
1 (RFX) (ENHANCER FACTOR C) (EF-C).//2.8e-05:196:3
1//HOMO SAPIENS (HUMAN).//P22670
F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN
(FRAGMENT).//0.0064:29:55//OWENIA FUSIFORMIS.//P21
260
50 F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-)./

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/1.1e-37:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P38938
 F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56027
 F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEMA PALLIDUM.//083371
 F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) (FRAGMENT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012
 F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:40:40//MUS MUSCULUS (MOUSE).//P02831
 F-NT2RP5003461//HYPOTHETICAL PROTEIN C22F3.14C IN CHROMOSOME I (FRAGMENT).//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
 F-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.3e-13:215:28//PODOSPORA ANSERINA.//Q00808
 F-NT2RP5003492//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.0055:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:38//MUS MUSCULUS (MOUSE).//P05142
 F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87.//0.53:21:38//DROSOPHILA MELANOGASTER (FRUIT FL Y).//P08175
 F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYCB 3' REGION PRECURSOR (ORF2) (FRAGMENT).//0.92:49:32//PARACOCCLUS DENITRIFICANS.//P29969
 F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).//P37116
 F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:125:41//RATTUS NORVEGICUS (RAT).//P02454
 F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45//HALOBACTERIUM VOLCANII (HALOPHAX VOLCANII).//Q48331
 F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMAN).//Q99501
 F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658
 F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS (RAT).//P02262
 F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87060

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F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:220:30//GALLUS GALLUS (CHICKEN).//P02457
 F-OVARC1000017//CUTICLE COLLAGEN DPY-13.//2.6e-05:97:30//CAENORHABDITIS SELEGANS.//P17657
 F-OVARC1000035
 F-OVARC1000058//RAS-RELATED PROTEIN RABC.//0.00015:110:24//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34143
 10 F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).//P80022
 F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN V-II-4).//1.0:27:44//NAJA MOSSAMBICA (MOZAMBIQUE COBRA).//P01452
 F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROTEIN 15) (PP15).//5.2e-06:115:29//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P13662
 20 F-OVARC1000085
 F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVEGICUS (RAT).//Q02874
 F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS MUSCULUS (MOUSE).//Q06666
 F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P46756
 F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53935
 30 F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600
 F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
 F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-28:57:63//HOMO SAPIENS (HUMAN).//P39194
 F-OVARC1000133
 40 F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//1.9e-09:200:29//HOMO SAPIENS (HUMAN).//Q13107
 F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q01702
 F-OVARC1000148//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.12:175:29//CANDIDA ALBICANS (Y

- EAST). //P46593
 F-OVARC1000151//HYPOTHETICAL PROTEIN KIAA0161. //5.
 6e-20:197:30//HOMO SAPIENS (HUMAN). //P50876
 F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/0.0030:77:38//HOMO SAPIENS (HUMAN). //P39188
 F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN
 WCAH. //0.95:56:35//ESCHERICHIA COLI. //P32056
 F-OVARC1000198//HISTONE H1.C2. //0.96:70:25//TRYPAN
 OSOMA CRUZI. //P40268
 F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PL 10
 B1-HXT2 INTERGENIC REGION. //2.5e-33:178:44//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //Q03677
 F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSO
 R. //1.7e-05:66:46//MUSMUSCULUS (MOUSE). //P05142
 F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTR
 Y !!!!!/1.8e-10:41:78//HOMO SAPIENS (HUMAN). //P391
 93
 F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1
 (EPAS-1) (HIF-1 ALPHA-LIKE FACTOR) (MHLF) (HIF-REL
 ATED FACTOR) (HRF). //7.4e-54:177:54//MUS MUSCULUS 20
 (MOUSE). //P97481
 F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ER
 P5-ORC6 INTERGENIC REGION. //2.9e-20:115:45//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //P38821
 F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PR
 ECURSOR (CBG) (TRANSCORTIN). //1.0:79:25//MUS MUSCU
 LUS (MOUSE). //Q06770
 F-OVARC1000304//PROTEIN MOV-10. //1.6e-79:181:83//M
 US MUSCULUS (MOUSE). //P23249
 F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2). / 30
 /6.9e-36:156:42//ASHBYA GOSSYPII (EREMOTHECIUM GOS
 SYPII). //Q00063
 F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.
 03 IN CHROMOSOME I. //5.2e-45:159:53//SCHIZOSACCHAR
 OMYCES POMBE (FISSION YEAST). //014179
 F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE IB-1. //
 0.036:67:35//HOMO SAPIENS (HUMAN). //P04281
 F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GC
 N4-WBP1 INTERGENIC REGION. //1.2e-16:200:27//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //P40004 40
 F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.
 //0.69:41:43//CYANOPHORA PARADOXA. //P48273
 F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR. //
 0.98:49:34//PSEUDOPLEURONECTA AMERICANUS (WINTER F
 LOUNDER). //P02734
 F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1)
 (FRAGMENT). //8.1e-05:115:33//XENOPUS LAEVIS (AFRIC
 AN CLAWED FROG). //Q05049
 F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD D
 YNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) 50
 (P150-GLUED). //0.00076:100:29//RATTUS NORVEGICUS
 (RAT). //P28023
 F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLT
 R-SPOI11C INTERGENIC REGION. //1.0:46:34//BACILLUS
 SUBTILIS. //P54431
 F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDO
 THELIAL COLLAGEN) (FRAGMENT). //0.0028:97:37//HOMO
 SAPIENS (HUMAN). //P25067
 F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PR
 FA-SPOI1R INTERGENIC REGION. //0.70:21:47//BACILLUS
 SUBTILIS. //P39150
 F-OVARC1000431
 F-OVARC1000437//TENSIN. //9.2e-42:195:52//GALLUS GA
 LLUS (CHICKEN). //Q04205
 F-OVARC1000440//PINCH PROTEIN (PARTICULARY INTERES
 TING NEW CYS-HIS PROTEIN). //3.4e-31:37:97//HOMO SA
 PIENS (HUMAN). //P48059
 F-OVARC1000442
 F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT). //
 0.0056:163:34//HAEMONCHUS CONTORTUS. //P16252
 F-OVARC1000461//FIXU PROTEIN. //0.36:36:44//RHIZOBI
 UM LEGUMINOSARUM (BIOVAR TRIFOLII). //P42710
 F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7. //
 2.4e-14:222:26//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST). //P11075
 F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTR
 Y !!!!!/2.3e-08:29:93//HOMO SAPIENS (HUMAN). //P391
 92
 F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATA
 SE 7 (EC 3.1.3.48) (EC3.1.3.16) (DUAL SPECIFICITY
 PROTEIN PHOSPHATASE MKP-X) (FRAGMENT). //2.8e-06:9
 6:36//RATTUS NORVEGICUS (RAT). //Q63340
 F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBU
 NIT X (PSI-K). //0.99:48:37//CYANIDIUM CALDARIUM (G
 ALDIERIA SULPHURARIA). //P31567
 F-OVARC1000486
 F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213. //1.0:
 62:32//METHANOCOCCUS JANNASCHII. //Q58610
 F-OVARC1000520//MEROZOITE SURFACE PROTEIN CMZ-8 (F
 RAGMENT). //0.0011:66:40//EIMERIA ACERVULINA. //P091
 25
 F-OVARC1000526//PROTEIN Q300. //1.2e-05:51:43//MUS
 MUSCULUS (MOUSE). //Q02722
 F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEI
 N). //0.74:43:41//HOMO SAPIENS (HUMAN). //Q16612
 F-OVARC1000543//POLYPEPTIDE N-ACETYL GALACTOSAMINYL
 TRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALA
 CTOSAMINYLTRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N-
 ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1). //2.
 3e-23:192:35//HOMO SAPIENS (HUMAN). //Q10472

- F-OVARC1000556
F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//1.6e-08:80:47//HOMO SAPIENS (HUMAN).//P3918
8
F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL
ACCESSORY PROTEIN).//0.45:32:50//HUMAN IMMUNODEFI
CIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2).//P1776
0
F-OVARC1000573
F-OVARC1000576//BETA-DEFENSIN 1 (BNDB-1).//0.47:2 10
9:41//BOS TAURUS (BOVINE).//P46159
F-OVARC1000578//COLLAGEN ALPHA 1(II) CHAIN (FRAGME
NTS).//0.023:96:36//BOS TAURUS (BOVINE).//P02459
F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEI
N L3.//0.75:57:29//HOMO SAPIENS (HUMAN).//P09001
F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38)
(GAMETE LYTIC ENZYME) (GLE).//0.91:134:28//CHLAMYD
OMONAS REINHARDTII.//P31178
F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!//2.6e-36:100:80//HOMO SAPIENS (HUMAN).//P39
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F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40
(ORF73).//0.96:34:38//ODONTELLA SINENSIS.//P49535
F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECU
RSOR (FRAGMENT).//0.0036:64:37//HELIANTHUS ANNUUS
(COMMON SUNFLOWER).//P22357
F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMEN
TS).//0.21:53:47//RATTUS NORVEGICUS (RAT).//P02466
F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR
(MCB17).//1.0:17:58//ESCHERICHIA COLI.//P05834
F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA
CHAIN (EC 2.7.7.6) (TRANSCRIPTASE OMEGA CHAIN) (RN
A POLYMERASE OMEGA SUBUNIT).//0.096:67:29//ESCHERI
CHIA COLI.//P08374
F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUS
CULUS (MOUSE).//Q02722F-OVARC1000682//PROCESSING A
LPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNO
SIDASE 1B).//7.6e-70:102:99//MUS MUSCULUS (MOUSE).
//P39098
F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).// 40
0.032:30:40//HELIX POMATIA (ROMAN SNAIL) (EDIBLE S
NAIL).//P33187
F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN
2.//0.17:60:40//RATTUSNORVEGICUS (RAT).//P02684
F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (IB
-9).//0.57:42:42//HOMOSAPIENS (HUMAN).//P02811
F-OVARC1000722//N-ACETYLLACTOSAMINE SYNTHASE (EC
2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1->4)GALACTOS
YLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A P
ROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (G 50
T).//1.1e-20:44:70//BOS TAURUS (BOVINE).//P08037
F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F
2.7 IN CHROMOSOME III.//5.2e-29:224:36//CAENORHABD
ITIS ELEGANS.//Q18262
F-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//
6.2e-12:78:48//DROSOPHILA MELANOGASTER (FRUIT FL
Y).//P25159
F-OVARC1000769
F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-4
6:121:79//HOMO SAPIENS(HUMAN), AND CANIS FAMILIARI
S (DOG).//P08886
F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATI
ON AND BRAIN-SPECIFICHOMEBOX PROTEIN 2).//0.81:3
6:52//HOMO SAPIENS (HUMAN).//P52951
F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMEN
T).//0.96:37:48//SUS SCROFA (PIG).//Q29303
F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!//2.5e-31:47:82//HOMO SAPIENS (HUMAN).//P391
89
F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.
2 IN CHROMOSOME X.//0.16:55:40//CAENORHABDITIS ELE
GANS.//Q10926
F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PA
K-ALPHA (EC 2.7.1.-) (P68-PAK) (P21- ACTIVATED KIN
ASE) (ALPHA-PAK) (PROTEIN KINASE MUK2).//0.87:140:
31//RATTUS NORVEGICUS (RAT).//P35465
F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:
109:30//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//PO
8199
F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ER
G8-UBP8 INTERGENIC REGION.//6.9e-09:180:28//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991
F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-1
7.5 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE)
(UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST).//P52490
F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8
e-39:154:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
ST).//P40484
F-OVARC1000883//METALLOTHIONEIN-I.//0.87:38:36//CA
NDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P151
13
F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//
2.8e-18:170:34//ESCHERICHIA COLI.//P37440
F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMEN
T).//0.00033:60:45//BOS TAURUS (BOVINE).//P02465
F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//H
UMAN PAPILOMAVIRUS TYPE 70.//P50774
F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF
5).//1.0:36:36//PARAMECIUM TETRAURELIA.//P15606

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F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPNPV).//010337
 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELEGANS.//Q09455
 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:115:76//HOMO SAPIENS (HUMAN).//P56524
 F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA CONSTRICTOR (BOA).//P92848
 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION.//1.0:48:33//ESCHERICHIA COLI.//P45505
 F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOMO SAPIENS (HUMAN).//P02452
 F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (MAV-1).//P12533
 F-OVARC1000948
 F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCUS JANNASCHII.//Q58343
 F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.8e-32:56:75//HOMO SAPIENS (HUMAN).//P39193
 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-IIA ANTAGONIST) (PLATELET AGGREGATION INHIBITOR) (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P28375
 F-OVARC1000971
 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECURSOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53832
 F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06138
 F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN).//0.00020:50:40//HOMO SAPIENS (HUMAN).//P20264
 F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.4e-16:43:90//HOMO SAPIENS (HUMAN).//P39195
 F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
 F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCUS JANNASCHII.//Q58336
 F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949
 F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).//Q05561

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F-OVARC1001034//METALLOTHIONEIN-IG (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640
 F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338
 F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194
 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637
 F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-STUBBLOID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319
 F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//HOMO SAPIENS (HUMAN).//P43490
 F-OVARC1001062
 F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHET E).//Q44951
 F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM.//069162
 F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0076:41:56//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO).//P46291
 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME I.//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197
 F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PET54-DIE2 INTERGENIC REGION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079
 F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P78963
 F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
 F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).//P11339
 F-OVARC1001118
 F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AEOLICUS.//066439
 F-OVARC1001154//GRANULINS PRECURSOR (ACROGRANIN).//2.3e-95:99:77//MUS MUSCULUS (MOUSE).//P28798
 F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//0.17:87:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177
 F-OVARC1001162
 F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA

CHIA COLI.//P41070
 F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.82:35:40//MUSMUSCULUS (MOUSE).//P97323
 F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIENS (HUMAN).//P02814
 F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00023:28:75//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001173
 F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510
 F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN VM A7-RPS25A INTERGENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53215
 F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NS P1-KAR2 INTERGENIC REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47057
 F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METHANOCOCCUS JANNASCHII.//Q58633
 F-OVARC1001240
 F-OVARC1001243
 F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAPIENS (HUMAN).//P25440
 F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MUS MUSCULUS (MOUSE).//Q06666
 F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4).//0.71:43:41//PSEUDOMONAS AERUGINOSA.//P24563
 F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVS W-UVSY INTERGENIC REGION.//1.0:44:29//BACTERIOPHAGE T4.//P32281
 F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSOME III PRECURSOR.//0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504
 F-OVARC1001282
 F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
 F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01 IN CHROMOSOME I.//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013695
 F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//1.3e-14:150:28//ZEA MAIZE (MAIZE).//P49133

F-OVARC1001330
 F-OVARC1001339//RIBONUCLEOPROTEIN RB97D.//0.0013:55:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02926
 F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
 F-OVARC1001342
 F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:23//STAPHYLOCOCCUS CARNOSUS.//P36253
 10 F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05890
 F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (H LA-B-ASSOCIATED TRANSCRIPT 2).//0.86:109:31//HOMO SAPIENS (HUMAN).//P48634
 F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:124:36//BOS TAURUS (BOVINE).//P02465
 F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGENIC REGION PRECURSOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMONAS SP. (STRAIN B13).//Q47100
 20 F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-24:96:61//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.1.34) (SUL-ATPASE EPSILON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIUS.//P23039
 F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00024:189:29//HOMO SAPIENS (HUMAN).//P10162
 30 F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.062:18:77//HOMO SAPIENS (HUMAN).//P39195
 F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSOME III.//0.010:185:23//CAENORHABDITIS ELEGANS.//Q03570
 F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAMELPOX VIRUS (STRAIN CP-1).//Q05482
 F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//HOMO SAPIENS (HUMAN).//Q03692
 F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//P36283
 40 F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HELOBDELLA TRISERIALIS (LEECH).//P17138
 F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.74:19:47//MUS MUSCULUS (MOUSE).//P28184
 F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53290
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F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:134:32//MUS MUSCULUS (MOUSE).//Q02788
 F-OVARC1001489//HYPOTHETICAL PROTEIN HI1270.//0.98:30:43//HAEMOPHILUS INFLUENZAE.//P44149
 F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HOMO SAPIENS (HUMAN).//P56545
 F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN).//P98161
 F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14).//1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077
 F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B).//0.69:57:33//HOMO SAPIENS (HUMAN).//P35325
 F-OVARC1001547
 F-OVARC1001555//NGG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53081
 F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//8.8e-38:94:81//GALLUS GALLUS (CHICKEN).//P30352
 F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV1-R8A2B.//P15898
 F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898
 F-OVARC1001611
 F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.30:43:34//CAENORHABDITIS EL EGANS.//Q11116
 F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0e-19:45:82//HOMO SAPIENS (HUMAN).//P39192
 F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMAN).//O60248
 F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINENUCLEOTIDE-BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE PROTEIN MAG-1).//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514
 F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1B).//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267
 F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.5e-20:46:67//BOS TAURUS (BOVINE).//P07106
 F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIM I (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES

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1).//0.59:23:56//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921
 F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-75:176:87//XENOPUS LAEVIS (AFRICAN CRAWLED FROG).//Q01173
 F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SPV1-R8A2 B.//P15902
 F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945
 F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CIS-TRANSISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLEOLAR PROLINEISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38911
 F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//0.99:113:27//ESCHERICHIA COLI.//P23839
 F-OVARC1001768
 F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MP T5-SAE2 INTERGENIC REGION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46945
 F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPB A-GP46 INTERGENIC REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878
 F-OVARC1001802//PLECTOXIN VIII (PLT-VIII) (PLTVIII).//0.41:19:36//PLECTREURYS TRISTIS (SPIDER).//P36984
 F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14796
 F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:31//RATTUS NORVEGICUS (RAT).//P02454
 F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:28:42//HALICHOERUS GRYPUS (GRAY SEAL).//P38592
 F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562
 F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260
 F-OVARC1001828
 F-OVARC1001846
 F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATESSA (PLAICE).//P07216
 F-OVARC1001873
 F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EED 8.6 IN CHROMOSOME II.//2.3e-05:73:31//CAENORHABDITIS

- IS ELEGANS.//Q09296
 F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812
 F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.3e-16:86:59//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F22B 7.5 IN CHROMOSOME III.//0.0053:48:47//CAENORHABDITIS ELEGANS.//P34408
 F-OVARC1001901
 F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P34789
 F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//0.00082:114:27//HOMO SAPIENS (HUMAN).//P98174
 F-OVARC1001928//FERREDOXIN III (FDIII).//1.0:64:2920 //ANABAENA VARIABILIS.//P46050
 F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945
 F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK65 2.6 IN CHROMOSOME III.//1.7e-23:147:43//CAENORHABDITIS ELEGANS.//P34664
 F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360
 F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//0.011:57:47//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001987//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.39:14:64//MUS MUSCULUS (MOUSE).//P02319
 F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//2.4e-13:55:72//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1002044
 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO SAPIENS (HUMAN).//P46939
 F-OVARC1002066
 F-OVARC1002082
 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.99:149:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
 F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874
 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.002 50 3:95:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG).//6.4e-51:198:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328
 F-OVARC1002143
 F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CP T1-SPC98 INTERGENIC REGION.//0.00010:64:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LE F4-P33 INTERGENIC REGION.//8.2e-07:119:35//AUTOGRA PHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).//P41479
 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204
 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964
 F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A 2.05C IN CHROMOSOME I.//8.8e-05:148:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725
 F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722
 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547
 F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//0.00036:63:39//HOMO SAPIENS (HUMAN).//P19474
 F-PLACE1000031
 F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY!!!!//4.4e-12:97:41//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP. (STRAIN C-125).//P38373
 F-PLACE1000050//COLLAGEN ALPHA 1(III) CHAIN.//0.00062:190:33//BOS TAURUS (BOVINE).//P04258
 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS (CHICKEN).//P32046
 F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO SAPIENS (HUMAN).//Q92934
 F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS MUSCULUS (MOUSE).//P06

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F-PLACE1000094

F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290

F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.8e-12:104:34//HOMO SAPIENS (HUMAN).//P30084

F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924

F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10C PRECURSOR.//0.11:48:33//MYCOBACTERIUM TUBERCULOSIS.//Q10637

F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640

F-PLACE1000214

F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GALLUS GALLUS (CHICKEN).//P02457

F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINEHERPESVIRUS TYPE 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2).//Q00039

F-PLACE1000292

F-PLACE1000308//EARLY NODULIN 75 (N-75) (NCM-75) (FRAGMENT).//0.049:28:42//MEDICAGO SATIVA (ALFALFA).//P11728

F-PLACE1000332

F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALLIDUM.//O83435

F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLMURAMIDASE C).//1.0:63:25//ORYCTOLAGUS CUNICULUS (RABBIT).//P16973

F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027

F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q13496

F-PLACE1000401//ELASTIN PRECURSOR (TROPOLASTIN).//0.00023:145:30//MUS MUSCULUS (MOUSE).//P54320

F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:90:63//HOMO SAPIENS (HUMAN).//Q15233

F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//4.7e-07:134:29//MUS MUSCULUS (MOUSE).//P53368

F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C11D3.01C IN CHROMOSOME I.//0.48:72:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080

F-PLACE1000424

F-PLACE1000435

F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.0e-31:129:63//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q02722

F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMOSAPIENS (HUMAN).//P08547

F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P80723

F-PLACE1000540

F-PLACE1000547//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940

F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS JANNASCHII.//Q57982

F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37//HOMO SAPIENS (HUMAN).//P15803

F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-45:192:47//HOMO SAPIENS (HUMAN).//P51522

30 F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINENUCLEOTIDE-BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//P32455

F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//HUMANADENOVIRUS TYPE 12.//P36707

F-PLACE1000610

40 F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MC K1-RPS19B INTERGENIC REGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48558

F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891

F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE).//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09687

50 F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.0029:75:33//NICOTIANA

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TIANA TABACUM (COMMON TOBACCO). //P13983
 F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR
 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATE
 D PROTEIN 1). //1.1e-38:180:42//HOMO SAPIENS (HUMA
 N). //Q13263
 F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN C
 Y441.05 PRECURSOR. //0.93:49:34//MYCOBACTERIUM TUBE
 RCULOSIS. //P71934
 F-PLACE1000716
 F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SP 10
 AT 3' REGION (ORF-11). //0.90:53:37//SHIGELLA FLEXNE
 RI. //P55794
 F-PLACE1000749//HYPOTHETICAL PROTEIN MG148. //0.001
 4:142:27//MYCOPLASMA GENITALIUM. //P47394
 F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN C
 HROMOSOME III. //1.1e-15:98:48//CAENORHABDITIS ELEG
 ANS. //P34529
 F-PLACE1000769//VIGILIN. //0.51:60:33//GALLUS GALLU
 S (CHICKEN). //P81021
 F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C1 20
 0.04. //1.0:22:45//MYCOBACTERIUM TUBERCULOSIS. //006
 360
 F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK63
 2.12 IN CHROMOSOME III. //2.6e-38:159:51//CAENORHAB
 DITIS ELEGANS. //P34657
 F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROT
 EIN (VASP). //0.0097:128:30//HOMO SAPIENS (HUMAN). /
 /P50552
 F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/9.4e-07:47:61//HOMO SAPIENS (HUMAN). //P3918 30
 8
 F-PLACE1000841
 F-PLACE1000849//ELAV PROTEIN. //3.5e-05:140:35//DRO
 SOPHILA VIRILIS (FRUITFLY). //P23241
 F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008. //0.9
 5:100:23//METHANOCOCCUSJANNASCHII. //Q60319
 F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOM
 AL PROTEIN YHR148W. //2.3e-46:172:54//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST). //P32899
 F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) 40
 (ERYTHROCYTE ANKYRIN). //0.00022:105:35//HOMO SAPIE
 NS (HUMAN). //P16157
 F-PLACE1000931//KILLER TOXIN HM-1. //0.95:24:33//WI
 LLIOPSIS MRKII (YEAST) (HANSENULA MRKII). //P1041
 0
 F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAN
 D). //0.97:52:40//HOMO SAPIENS (HUMAN). //P49771
 F-PLACE1000972//MYOSIN ID HEAVY CHAIN. //1.9e-06:7
 9:43//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //P341
 09

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F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D
 4.5 IN CHROMOSOME III. //2.5e-23:105:41//CAENORHABD
 ITIS ELEGANS. //P46941
 F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER
 PROTEIN KOX4) (ZINC FINGER PROTEIN HF.16). //0.91:
 83:30//HOMO SAPIENS (HUMAN). //P17097
 F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G
 7.02 IN CHROMOSOME I. //0.10:128:24//SCHIZOSACCHARO
 MYCES POMBE (FISSION YEAST). //Q09796
 F-PLACE1001000
 F-PLACE1001007//ZYXIN. //2.2e-05:135:30//GALLUS GAL
 LUS (CHICKEN). //Q04584
 F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR
 COMPONENT PRECURSOR (BUNGAROTOXIN, B1 CHAIN). //1.
 0:30:40//BUNGARUS MULTICINCTUS (MANY-BANDEDKRAIT).
 //P00987
 F-PLACE1001015
 F-PLACE1001024
 F-PLACE1001036
 F-PLACE1001054//HOLOTRICIN 3 PRECURSOR. //0.0044:5
 6:39//HOLOTRICHIA DIOMPHALIA. //Q25055
 F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+,
 L-GLUTAMATE FORMING]
 (EC 1.5.1.10). //0.0013:38:52//SACCHAROMYCES CEREVI
 SIAE (BAKER'S YEAST). //P38999
 F-PLACE1001076
 F-PLACE1001088//EARLY NODULIN 75 (N-75) (NGM-75)
 (FRAGMENT). //0.95:32:50//MEDICAGO SATIVA (ALFALF
 A). //P11728
 F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NS
 P1-KAR2 INTERGENIC REGION. //0.0026:81:35//SACCHARO
 MYCES CEREVISIAE (BAKER'S YEAST). //P47057
 F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN CO2F
 12.7 IN CHROMOSOME X. //0.00063:125:32//CAENORHABDI
 TIS ELEGANS. //Q11102
 F-PLACE1001118//ZINC FINGER PROTEIN MLZ-4 (ZINC FI
 NGER PROTEIN 46). //2.6e-77:209:63//MUS MUSCULUS (M
 OUSE). //Q03309
 F-PLACE1001136//ALPHA-N-ACETYL GALACTOSAMINIDASE PR
 ECURSOR (EC 3.2.1.49) (ALPHA- GALACTOSIDASE B). //0.
 99:107:30//HOMO SAPIENS (HUMAN). //P17050
 F-PLACE1001168
 F-PLACE1001171//RETROVIRUS-RELATED POLYPROTEIN
 (FRAGMENT). //0.00012:37:59//HOMO SAPIENS (HUMAN).
 //P12895
 F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN UR
 E2-SSU72 INTERGENIC REGION. //3.6e-12:88:36//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //P53867
 F-PLACE1001238
 50 F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMEN

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T). //0.13:30:53//COLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE). //P27087
 F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN). //4.1e-24:125:46//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q04652
 F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSGA 3' REGION (ORF L5) (FRAGMENT). //1.0:24:45//MYCOPLASMA CAPRICOLUM. //P43040
 F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-II-3). //0.98:31:41//NAJA MOSSAMBICA (MOZAMBIQUE COBRA). //P01470
 F-PLACE1001280//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]. //0.0051:156:32//MUS MUSCULUS (MOUSE). //P28481
 F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154. //3.7e-56:109:93//MUS MUSCULUS (MOUSE). //P50636
 F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35). //3.2e-30:75:57//MUS MUSCULUS (MOUSE). //P15620
 F-PLACE1001311//ALU SUBFAMILY SB WARNING ENTRY 11111//2.7e-31:66:66//HOMO SAPIENS (HUMAN). //P39189
 F-PLACE1001323
 F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANS ACTIVATOR PROTEIN) (ART/TRS). //0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 ISOLATE) (SIV-AGM). //P27971
 F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12). //0.070:18:33//NAJA HAJE ANNULIFERA (BANDED EGYPTIAN COBRA). //P01422
 F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION ACTIVATION INHIBITOR). //4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDIAN GREEN TREE VIPER) (GREEN HABU SNAKE). //P17495
 F-PLACE1001383//M PROTEIN, SEROTYPE 49 PRECURSOR. //0.080:136:24//STREPTOCOCCUS PYOGENES. //P16947
 F-PLACE1001384
 F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. //1.9e-22:142:39//HOMO SAPIENS (HUMAN). //Q12929
 F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASI A-MOTA INTERGENIC REGION. //0.98:67:34//BACTERIOPHAGE GE T4. //P22917
 F-PLACE1001399//ALU SUBFAMILY SQ WARNING ENTRY 11111//3.1e-32:47:74//HOMO SAPIENS (HUMAN). //P39194
 F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC) (GLYCOCONNECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD). //0.00021:125:36//HOMO SAPIENS (HUMAN). //P04921

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F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITOR S 2 TO 5. //0.99:37:35//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES). //P07852
 F-PLACE1001440//PROLINE-RICH PEPTIDE P-B. //0.35:16:50//HOMO SAPIENS (HUMAN). //P02814
 F-PLACE1001456//RELAXIN. //0.48:38:36//BALAENOPTERA ACUTOROSTRATA (MINKEWHALE) (LESSER RORQUAL). //P11184
 F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602. //0.10:86:32//METHANOCOCCUS JANNASCHII. //Q58019
 F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNA C-RPLI INTERGENIC REGION. //1.0:47:34//BACILLUS SUBTILIS. //P37480
 F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR. //0.00029:118:34//BOS TAURUS (BOVINE). //P23206
 F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G 5.8 IN CHROMOSOME III. //2.2e-07:107:30//CAENORHABDITIS ELEGANS. //P34561
 F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2 (SI ALPHA-2). //0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM). //P21924
 F-PLACE1001534//PUTATIVE GENE PROTEIN 54. //0.43:44:40//BACTERIOPHAGE SPO1. //048408
 F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENIC REGION. //0.99:70:32//ESCHERICHIA COLI. //P37795
 F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32. //1.0:66:28//MARCHANTIA POLYMORPHA (LIVERWORT). //P12196
 F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN). //0.024:120:27//HOMO SAPIENS (HUMAN). //Q15431
 F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1). //1.1e-30:90:78//MUS MUSCULUS (MOUSE). //Q60809
 F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT). //0.054:77:33//RATTUS NORVEGICUS (RAT). //P10164
 F-PLACE1001608
 F-PLACE1001610//PROBABLE E4 PROTEIN. //0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28. //P51896
 F-PLACE1001611//METALLOTHIONEIN-1G (MT-1G). //0.35:30:40//HOMO SAPIENS (HUMAN). //P13640
 F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2). //3.6e-28:144:43//HOMO SAPIENS (HUMAN). //P51523
 F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN. //1.0:36:41//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA). //019926
 F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN). //0.24:47:38//HUMAN IMMUNODEFICIENCY

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Y VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804
 F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/1.0:27:66//HOMOSAPIENS (HUMAN).//P39188
 F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PI
 K1-POL2 INTERGENIC REGION.//0.40:81:33//SACCHAROMY
 CES CEREVISIAE (BAKER'S YEAST).//P53842
 F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOEST
 ERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE I
 I).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08
 635
 F-PLACE1001705
 F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H
 9.01 IN CHROMOSOME I.//6.1e-07:157:29//SCHIZOSACCH
 AROMYCES POMBE (FISSION YEAST).//013798
 F-PLACE1001720
 F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMEN
 T).//6.5e-05:196:32//MUS MUSCULUS (MOUSE).//P05143
 F-PLACE1001739//NEUROFILAMENT TRIPLET M PROTEIN (1
 60 KD NEUROFILAMENT PROTEIN) (NF-M).//0.00050:213:
 23//RATTUS NORVEGICUS (RAT).//P12839
 F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/2.4e-17:90:56//HOMO SAPIENS (HUMAN).//P3918
 8
 F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.
 96:38:36//HOMO SAPIENS (HUMAN).//Q14138
 F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.
 98:23:43//LUPINUS ANGUSTIFOLIUS (NARROW-LEAVED BLU
 E LUPINE).//P09930
 F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC1
 19.17.//2.9e-28:167:38//SCHIZOSACCHAROMYCES POMBE
 (FISSION YEAST).//042908
 F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTR
 Y !!!!!/9.2e-43:126:77//HOMO SAPIENS (HUMAN).//P39
 189
 F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:4
 2:38//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)./
 /P56057
 F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE
 PROTEIN.//4.8e-35:223:40//DROSOPHILA MELANOGASTER
 (FRUIT FLY).//P48994
 F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DS
 K2-CAT8 INTERGENIC REGION.//9.5e-41:194:46//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262
 F-PLACE1001799
 F-PLACE1001810
 F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING],
 BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SY
 NTHETASE, BETA CHAIN) (SCS-BETA).//2.8e-40:115:61/
 /NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587
 F-PLACE1001821

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F-PLACE1001844//IG KAPPA CHAIN V-I REGION (HAU).//
 0.59:89:35//HOMO SAPIENS (HUMAN).//P01600
 F-PLACE1001845
 F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SA
 CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53583
 F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADEND
 RON LIGA (ARGENTINE MISTLETOE).//P01540
 F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.5
 7:44:45//ASTROTIA STOKESI (STOKES'S SEA SNAKE) (DI
 10 STEIRA STOKESI).//P01381
 F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEI
 N GP4) (GPF).//0.89:75:29//BACTERIOPHAGE NF.//P098
 77
 F-PLACE1001928
 F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.
 0049:51:45//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PR
 V).//P33479
 F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.
 9e-08:125:36//MORAXELLA CATARRHALIS.//Q49091
 20 F-PLACE1002004
 F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:8
 4//MUS MUSCULUS (MOUSE).//Q61211
 F-PLACE1002052
 F-PLACE1002066
 F-PLACE1002072//ANTER-SPECIFIC PROLINE-RICH PROTEI
 N APC PRECURSOR.//0.16:77:31//ARABIDOPSIS THALIANA
 (MOUSE-EAR CRESS).//P40602
 F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C
 1.1 IN CHROMOSOME III.//4.0e-11:174:28//CAENORHABD
 30 ITIS ELEGANS.//Q09564
 F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD
 PROTEIN (SRP72).//2.8e-57:112:99//HOMO SAPIENS (HU
 MAN).//076094
 F-PLACE1002115//P8 MTCP-1 PROTEIN (MATURE T-CELL P
 ROLIFERATION-1 TYPE A) (MTCP-1 TYPE A) (P8MTCP1).//
 1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908
 F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CY
 CLOHEXIMIDE-INDUCED) (CHX1) (IMMEDIATE EARLY RESPO
 NSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS (MOU
 40 SE).//P17950
 F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MO
 BL 3' REGION (ORF 4).//0.0086:39:46//THIOBACILLUS F
 ERROOXIDANS.//P20088
 F-PLACE1002150
 F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTR
 Y !!!!!/2.4e-34:56:82//HOMO SAPIENS (HUMAN).//P391
 89
 F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRURO
 IDES SCULPTURATUS (BARK SCORPION).//P01492
 50 F-PLACE1002170

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F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591
 F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOBI-SGA1 INTERGENIC REGION.//0.77:21:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490
 F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738
 F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIX W 5' REGION.//0.41:49:36//RHIZOBIUM LEGUMINOSARUM.//P14310
 F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITISELEGANS.//P24890
 F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508
 F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32219
 F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM VIVAX.//P08677
 F-PLACE1002399
 F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYN-EIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023
 F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS (MOUSE).//P41233
 F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC REGION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545
 F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
 F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O13765
 F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555
 F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.15:65:41//HOMO SAPIENS (HUMAN).//P39193
 F-PLACE1002493//SEMOGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS MACAQUE).//Q95196
 F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN CO2B 8.6 IN CHROMOSOME X.//2.9e-11:67:35//CAENORHABDITI

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S ELEGANS.//Q11096
 F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPHUS.//P13512
 F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (071).//1.0:15:60//ESCHERICHIA COLI.//P46878
 F-PLACE1002529
 F-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (MOUSE).//P70396
 F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-18:51:86//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P45890
 F-PLACE1002578
 F-PLACE1002583
 F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BOVINE).//Q92176
 F-PLACE1002598
 F-PLACE1002604
 F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781
 F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:89//MUS MUSCULUS (MOUSE).//Q60604
 F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILLUS FERROOXIDANS.//P20086
 F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCES EXIGUUS (YEAST).//P38479
 F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//RATTUS NORVEGICUS (RAT).//Q62839
 F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P47749
 F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS (MOUSE).//P35378
 F-PLACE1002772
 F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//O14007
 F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROPHUS.//P13512
 F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAENORHABDITIS ELEGANS.//P20630
 F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITO

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R (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C). //1.1e-09:137:34//MUS MUSCULUS (MOUSE). //Q60772
 F-PLACE1002815//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT). //0.46:35:42//HORDEUM VULGARE (BARLEY). //P17991
 F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116). //1.0e-86:201:74//HOMO SAPIENS (HUMAN). //P56524
 F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1). //1.6e-30:54:96//HOMO SAPIENS (HUMAN). //P51522
 F-PLACE1002839//METALLOTHIONEIN-I (MT-I). //1.0:43:37//MUS MUSCULUS (MOUSE). //P02802
 F-PLACE1002851//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI). //0.77:35:37//VICIA ANGUSTIFOLIA (COMMON VETCH). //P01065
 F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5' REGION (ORF1). //1.0:18:55//LYMANTRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIRUS (LDMPV). //P36866
 F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-27:91:70//HOMO SAPIENS (HUMAN). //P39188
 F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III. //2.0e-31:148:46//CAENORHABDITIS ELEGANS. //P34548
 F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-11:40:85//HOMO SAPIENS (HUMAN). //P39195
 F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT). //0.90:38:36//CANIS FAMILIARIS (DOG). //P13206
 F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT). //0.97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION). //P01496
 F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4). //3.3e-20:120:41//METHANOCOCCUS JANNASCH II. //Q58560
 F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F158). //0.0045:93:23//ESCHERICHIA COLI. //P52121
 F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATED CLONE 22 HOMOLOG). //0.17:91:29//GALLUS GALLUS (CHICKEN). //Q91012
 F-PLACE1003025//SUPPRESSOR PROTEIN IN SRP40. //0.0079:214:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32583
 F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III. //1.3e-49:167:63//CAENORHABDITIS ELEGANS. //P34609
 F-PLACE1003044//SPORE COAT PROTEIN D. //0.97:24:45//BACILLUS SUBTILIS. //P07791
 F-PLACE1003045
 F-PLACE1003092
 F-PLACE1003100//HEP27 PROTEIN (PROTEIN D). //3.9e-51:188:57//HOMO SAPIENS (HUMAN). //Q13268
 F-PLACE1003108
 F-PLACE1003136
 F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT). //0.00 50

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024:170:24//BOS TAURUS (BOVINE). //P18892
 F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT). //1.0:32:37//LOCUSTA MIGRATORIA (MIGRATORY LOCUST). //Q01777
 F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42). //6.3e-05:54:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //P42743
 F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PC S60-ABD1 INTERGENIC REGION. //0.24:74:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38319
 F-PLACE1003190//SOF1 PROTEIN. //1.0e-52:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P33750
 F-PLACE1003200
 F-PLACE1003205//SPERM PROTAMINE P1. //0.074:20:45//CAENOLESTES FULIGINOSUS. //P42131
 F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001. //0.013:20:55//HOMO SAPIENS (HUMAN). //Q15391
 F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125. //0.98:48:37//HOMO SAPIENS (HUMAN). //Q14138
 F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SHAKER PEPTIDE). //0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE). //P01522
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN. //4.1e-18:70:47//CAENORHABDITIS ELEGANS. //P21541
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE. //0.063:160:24//HOMO SAPIENS (HUMAN). //P11277
 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1). //9.4e-69:84:94//HOMO SAPIENS (HUMAN). //P51522
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN). //0.029:125:24//RATTUS NORVEGICUS (RAT). //Q63083
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84B. //0.97:44:40//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01643
 F-PLACE1003343//GENE 11 PROTEIN. //1.0:37:37//SPIROPLASMA VIRUS SPV1-R8A2B. //P15902
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2). //6.4e-05:69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P87378
 F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.6e-23:66:75//HOMO SAPIENS (HUMAN). //P39192
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1. //0.62:19:57//HOMO SAPIENS (HUMAN). //P35326
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR. //4.3e-06:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32323

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- F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE).//Q02722
- F-PLACE1003375//OLFACTORY RECEPTOR 11 (M49) (FRAGMENT).//0.99:46:34//MUS MUSCULUS (MOUSE).//Q60890
- F-PLACE1003383
- F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTUS NORVEGICUS (RAT).//P35287
- F-PLACE1003401
- F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W.//8.1e-17:138:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556
- F-PLACE1003454
- F-PLACE1003478
- F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:123:32//HOMO SAPIENS (HUMAN).//Q13201
- F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68:76//HOMO SAPIENS (HUMAN).//P08547
- F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//9.2e-17:77:50//HOMO SAPIENS (HUMAN).//P391820
- F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWLPOX VIRUS (ISOLATE HP-438[MUNICH]).//P14366
- F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:32:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
- F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q01436
- F-PLACE1003553
- F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWLPOX VIRUS (ISOLATE HP-438[MUNICH]).//P14366
- F-PLACE1003575
- F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAVIRUS TYPE 35.//P27226
- F-PLACE1003584
- F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PHI-80.//P05998
- F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:42:30//OVIS ARIES (SHEEP).//078751
- F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//6.3e-87:238:67//CAENORHABDITIS ELEGANS.//P46975
- F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FA A3-MAS3 INTERGENIC REGION.//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40554
- F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02516
- F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:43//CANIS FAMILIARIS (DOG).//P04542
- F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:229:58//HOMO SAPIENS (HUMAN).//P08547
- F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//PROTEUS MIRABILIS.//P42275
- F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE).//Q02722
- F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).//P22793
- F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08170
- F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CC T3-CCT8 INTERGENIC REGION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47074
- F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-IV).//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724
- F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70).//6.0e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270
- F-PLACE1003738//OOCTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//2.5e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
- F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSOMA BRUCEI BRUCEI.//P00164
- F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//024058
- F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:123:37//HOMO SAPIENS (HUMAN).//P08547
- F-PLACE1003771
- F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//ALLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634
- F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SP X19-GCR2 INTERGENIC REGION.//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
- F-PLACE1003795//EC PROTEIN I/II (ZINC-METALLOTHIONEIN CLASS II).//0.67:53:30//TRITICUM AESTIVUM (WHEAT).//P30569
- F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523
- F-PLACE1003850
- F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28:42//LITHOBIUS FORFICATUS.//Q02030
- F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR.//0.0046:116:31//ACTINOBACILLUS ACTINOMYCE

3091

TEMCOMITANS (HAEMOPHILUS ACTINOMYCETEMCOMITANS). // 052727
 F-PLACE1003870
 F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT). //1.6e-92:166:75//HOMO SAPIENS (HUMAN). //P51003
 F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180. //0.54:96:34//PSEUDORABIESVIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV). //P11675
 F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT). //8.8e-54:260:46//BOS TAURUS (BOVINE). //P10895
 F-PLACE1003892//PROBABLE E5 PROTEIN. //1.0:13:61//HUMAN PAPILLOMAVIRUS TYPE 18. //P06792
 F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME I (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS). //0.58:49:36//DAUCUS CAROTA (CARROT). //P80065
 F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LI GASE) (CTP SYNTHETASE). //3.8e-52:92:85//HOMO SAPIENS (HUMAN). //P17812
 F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE-TRNA LI GASE) (ARGRS). //2.6e-26:202:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q05506
 F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-TRNALI GASE) (HISRS). //0.94:65:29 //STREPTOCOCCUS EQUISIMILIS. //P30053
 F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION. //0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53074
 F-PLACE1003936
 F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN). //4.7e-68:164:78//RATTUS NORVEGICUS (RAT). //P80385
 F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!! //1.9e-14:60:73//HOMO SAPIENS (HUMAN). //P39192
 F-PLACE1004104//EXOCYST COMPLEX COMPONENT SEC5. //0.020:202:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P89102
 F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!! //2.1e-15:69:60//HOMO SAPIENS (HUMAN). //P39188
 F-PLACE1004118//REGULATORY PROTEIN E2. //0.73:58:36 //CANINE ORAL PAPILLOMAVIRUS (COPV). //Q89420
 F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN

3092

BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4). //7.7e-62:108:100//MUS MUSCULUS (MOUSE). //P29387
 F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN. //0.0011:73:42//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV). //P33485
 F-PLACE1004156//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT). //0.00061:39:48//OWENIA FUSIFORMIS. //P21260
 F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMENT). //0.033:108:27//STREPTOCOCCUS P YOGENES. //P49054
 F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CD C12-ERP5 INTERGENIC REGION. //4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38817
 F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT). //5.9e-11:208:27//MUS MUSCULUS (MOUSE). //Q62556
 F-PLACE1004203//PROTEIN A39. //8.5e-18:139:33//VACCINIA VIRUS (STRAIN COPENHAGEN). //P21062
 F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN. //1.0:28:42//PISUM SATIVUM (GARDEN PEA). //P13555
 F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D). //0.73:134:25//CAENORHABDITIS ELEGANS. //P02567
 F-PLACE1004257//HYPOTHETICAL PROTEIN HI0490. //0.13:75:29//HAEMOPHILUS INFLUENZAE. //P44006
 F-PLACE1004258//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGEN) (FRAGMENT). //0.027:128:35//HOMO SAPIENS (HUMAN). //P25067
 F-PLACE1004270//LARGE TEGUMENT PROTEIN. //1.8e-10:100:44//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). //P03186
 F-PLACE1004274//HYPOTHETICAL PROTEIN E-95. //0.44:61:42//HUMAN ADENOVIRUS TYPE 2. //P03286
 F-PLACE1004277//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS). //0.0013:55:38//BOS TAURUS (BOVINE). //P25508
 F-PLACE1004284//7 KD PROTEIN (ORF 4). //1.0:63:23//CHRYSANTHEMUM VIRUS B(CVB). //P37990
 F-PLACE1004289//SPERM PROTAMINE P3. //0.00057:22:77 //MUS MUSCULUS (MOUSE). //Q62100
 F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AF SK (EC 2.7.1.-). //0.0065:148:29//STREPTOMYCES COELICOLOR. //P54741
 F-PLACE1004316//AUTOPHAGY PROTEIN APC5. //8.8e-06:117:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q12380
 F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR. //0.0027:83:36//HOMO SAPIENS (HUMAN). //P53420
 F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR. //2.9e-05:200:33//CALLUS CALLUS (CHICKEN). //P02457

- F-PLACE1004376//AXONE-ASSOCIATED PROTEIN MST101 (2).//2.4e-05:179:29//DROSOPHILA HYDEI (FRUIT FLY).//Q08696
- F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-28:46:76//HOMO SAPIENS (HUMAN).//P39194
- F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN AC S1-GCV3 INTERGENIC REGION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
- F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYLNEURAMINYLLACTOSE-BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING SUBUNIT) (NLBH) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT).//0.93:74:33//HELI COBACTER ACINONYX.//Q47947
- F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.81:70:42//HOMO SAPIENS (HUMAN).//P39195
- F-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.9e-31:203:39//RATTUS NORVEGICUS (RAT).//Q63448
- F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD], MITOCHONDRIAL SUBUNIT BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) (FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28479
- F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00013:40:62//HOMO SAPIENS (HUMAN).//P39188
- F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25823
- F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-10:33:87//HOMO SAPIENS (HUMAN).//P39193
- F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-56:92:58//HOMO SAPIENS (HUMAN).//P51522
- F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSOME I.//0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09844
- F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19903
- F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LAGE-1).//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358
- F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TF IID 150 KD SUBUNIT (TAFII-150) (TAFII150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325
- F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH PROTEINS (FRAGMENT).//0.95:62:29//PULMONARIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14587
- F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//MYTILUS EDULIS (BLUE MUSSEL).//P80248
- F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYZOLAGUS CUNICULUS (RABBIT).//P19518
- F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS.//P17656
- F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568
- F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438
- F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR II B HOMOLOG (TFIIB).//0.00036:100:30//PYROCOCOCCUS FURIOSUS.//Q51731
- F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA PNEUMONIAE.//Q48481
- F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32//MUS MUSCULUS (MOUSE).//Q03391
- F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN F A4-HOR7 INTERGENIC REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781
- F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME I.//7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704
- F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815
- F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).//Q60809
- F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:48:62//HOMO SAPIENS (HUMAN).//P39192
- F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//P55946
- F-PLACE1004693
- F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (AGL).//1.0:27:37//PAN PANISCUS (PYGMY CHIMPANZEE) (BONOB0).//Q35587
- F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CL A4-MID1 INTERGENIC REGION.//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565
- F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN N AP-22.//0.014:163:30//RATTUS NORVEGICUS (RAT).//Q05175

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F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/1.9e-09:37:70//HOMO SAPIENS (HUMAN).//P391
94

F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN AL
GR3 3' REGION.//0.99:72:33//PSEUDOMONAS AERUGINOSA.
//P21484

F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALAC
TOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-)
(BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (S
T3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-
C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (H
UMAN).//Q11206

F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2)
(ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO SAPIE
NS (HUMAN).//P16157

F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALP
HA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//RATTU
S NORVEGICUS (RAT).//P30337

F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PR
OTEIN GP52; COAT PROTEIN GP36].//0.00062:106:25//M
OUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259
F-PLACE1004804

F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:2
2:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P1677
7

F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B049
5.8 IN CHROMOSOME II.//2.8e-06:136:25//CAENORHABDI
TIS ELEGANS.//Q09217

F-PLACE1004815

F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN M
UP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST).//P53236

F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLA
L 3' REGION (ORF3).//0.54:25:56//BACILLUS LICHENIFO
RMIS.//P22754

F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT)./
/0.0066:12:66//BOS TAURUS (BOVINE).//P20072

F-PLACE1004838

F-PLACE1004840

F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-1
6:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)./
/Q08891

F-PLACE1004885

F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PR
ECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//AP
IS MELLIFERA (HONEYBEE).//P01499

F-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR
ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//7.3e-15:
94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)./
/042643

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F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BCS
A-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUB
TILIS.//P54165

F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RP
S21B-MRS3 INTERGENIC REGION.//0.98:50:34//SACCHARO
MYCES CEREVISIAE (BAKER'S YEAST).//P47012

F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.8
2:44:36//METHANOCOCCUSJANNASCHII.//Q57982

F-PLACE1004934

10 F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEA
TS CONTAINING PROTEINC57A10.05C IN CHROMOSOME I.//
9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION
YEAST).//P87053

F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B041
6.5 IN CHROMOSOME X.//4.0e-14:184:25//CAENORHABDIT
IS ELEGANS.//Q11073

F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-II) (BRO
MELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS C
OMOSUS (PINEAPPLE).//P27478

20 F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTR
Y !!!!!/5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P391
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F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR
(FRAGMENT).//0.00049:124:27//STREPTOCOCCUS PYOGENE
S.//P19401

F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.3
4) (AGL).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON
EARTHWORM).//Q34942

F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG. /
/0.0011:179:27//EUPLOTES CRASSUS.//Q06183

F-PLACE1005027

F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT)./
/0.082:44:36//BOS TAURUS (BOVINE).//P20072

F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST84D
D.//0.38:36:44//DROSOPHILA MELANOGASTER (FRUIT FL
Y).//Q01645

F-PLACE1005055

F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEI
N).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUI
T FLY).//Q04652

F-PLACE1005077

F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:3
6:33//BUTHUS OCCITANUSTUNETANUS (COMMON EUROPEAN S
CORPION).//P55902

F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P391
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F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGM
ENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P497

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F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821

F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359

F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608

F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708

F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075

F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1005176

F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831

F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//NEUROSPORA CRASSA.//P38678

F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511

F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218

F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS.//Q01577

F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003

F-PLACE1005266

F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287

F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352

F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760

F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020

F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEU X-FECE INTERGENIC REGION (067).//0.15:36:41//ESCHE 50

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RICHIA COLI.//P39355

F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808

F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMOSAPIENS (HUMAN).//P11274

F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067

10 F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINESYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//0.010:96:28//SACCAROMYCES CEREVISIAE (BAKER'S YEAST).//P48567

F-PLACE1005374

F-PLACE1005409

F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).//P07979

20 F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER GULL).//P02451

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS).//Q37598

F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137.//9.6e-13:115:38//MUS MUSCULUS (MOUSE).//P11260

F-PLACE1005480//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.97:33:30//HORDEUM VULGARE (BARLEY).//P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT).//0.30:52:38//APIS MELLIFERA (HONEYBEE).//P31504

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN.//3.9e-05:87:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P19334

F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180.//4.6e-05:132:32//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

40 F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-09:31:74//HOMO SAPIENS (HUMAN).//P39195

F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//9.7e-50:148:58//CAENORHABDITIS ELEGANS.//Q09251

F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III.//3.0e-21:127:37//CAENORHABDITIS ELEGANS.//P34524

F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO

- RAT). //P16359
 F-PLACE1005557//60S RIBOSOMAL PROTEIN L27. //4.8e-09:60:48//CRYPTOCOCCUSNEOFORMANS (FILOBASIDIELLA NEOFORMANS). //P46288
 F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //0.89:44:29//BOS TAURUS (BOVINE). //P03929
 F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87 F. //0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY). //P08175
 F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180. //0.00048:162:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV). //P11675
 F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN). //0.00034:83:30//TETRAHYMENA PYRIFORMIS. //P40625
 F-PLACE1005611//DNAJ PROTEIN. //8.6e-20:108:48//CLOSTRIDIUM ACETOBUTYLICUM. //P30725
 F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.-) (ERK5) (ERK4) (BMK1 KINASE). //0.80:116:31//HOMO SAPIENS (HUMAN). //Q13164
 F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT-B-CELL GROWTH FACTOR) (HMW-B CGF). //0.0024:74:39//HOMO SAPIENS (HUMAN). //P40222
 F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT P85) (FRAGMENT). //0.72:18:61//RATTUS NORVEGICUS (RAT). //Q62894
 F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10. //4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO). //P46942
 F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE). //3.7e-64:133:75//MESOCRICETUS AURATUS (GOLDEN HAMSTER). //Q60561
 F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28. //0.57:36:41//PORPHYRA PURPUREA. //P51224
 F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3' REGION (ORFC) (FRAGMENT). //0.50:61:29//BACILLUS SUBTILIS. //P40405
 F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APC (PROTEIN CEX) (FRAGMENT). //0.46:27:51//BRASSICA NAPUS (RAPE). //P40603
 F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT). //0.95:21:52//ORYCTOLAGUS CUNICULUS (RABBIT). //P02456
 F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11. //3.4e-46:111:53//MUS MUSCULUS (MOUSE). //Q60710
 F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GS H1-CHS6 INTERGENIC REGION. //2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P42951
 F-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE I1). //1.5e-26:69:57//RATTUS NORVEGICUS (RAT). //P08635
 F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN). //0.028:96:32//HOMO SAPIENS (HUMAN). //P26371
 F-PLACE1005802//PROTEIN PROSPERO. //0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY). //P29617
 F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116. //1.0:95:25//MUS MUSCULUS (MOUSE). //P17564
 F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSEDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSEDASE 1B). //2.8e-73:198:73//MUS MUSCULUS (MOUSE). //P39098
 F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NS P1-KAR2 INTERGENIC REGION. //0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P47057
 F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! //1.8e-23:56:76//HOMO SAPIENS (HUMAN). //P39195
 F-PLACE1005834//LATE CONTROL GENE B PROTEIN (GPB). //0.97:33:39//BACTERIOPHAGE 186. //P08711
 F-PLACE1005845
 F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //5.5e-28:96:73//HOMO SAPIENS (HUMAN). //P39194
 F-PLACE1005851
 F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT). //2.2e-99:155:95//BOS TAURUS (BOVINE). //Q10568
 F-PLACE1005884
 F-PLACE1005890//BEM46 PROTEIN (FRAGMENT). //1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //P54069
 F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ). //0.77:58:34//HOMO SAPIENS (HUMAN). //000483
 F-PLACE1005921//AIG1 PROTEIN. //1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //P54120
 F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16). //0.90:118:28//PARAMECIUM TETRAURELIA. //P15617
 F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN. //0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11). //Q01010
 F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN). //0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO). //P13983
 F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LAR

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GEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT). //0.4
 0:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER). //P1
 1414
 F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGUL
 ATORY PROTEIN). //0.50:15:66//HUMAN IMMUNODEFICIENC
 Y VIRUS TYPE 1 (CLONE 12) (HIV-1). //P04326
 F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDR
 OXYPROLINE-RICH GLYCOPROTEIN). //0.0025:135:32//NIC
 OTIANA TABACUM (COMMON TOBACCO). //P13983
 F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN 10
 (HIP1P). //0.64:57:33//RHODOFERAX FERMENTANS. //P80
 882
 F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ER
 P5-ORC6 INTERGENIC REGION. //1.0e-32:110:50//SACCHA
 ROMYCES CEREVISIAE (BAKER'S YEAST). //P38821
 F-PLACE1005966//TACHYPLESIN II PRECURSOR. //0.97:3
 1:35//TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE C
 RAB). //P14214
 F-PLACE1005968//GATA FACTOR SREP. //0.17:52:40//PEN
 ICILLIUM CHRYSOGENUM. //Q92259
 F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED
 PROTEIN. //0.36:55:36//EMERICELLA NIDULANS (ASPERGI
 LLUS NIDULANS). //P36011
 F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTR
 Y !!!!//1.5e-36:102:75//HOMO SAPIENS (HUMAN). //P39
 192
 F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX
 3-NAD1 INTERGENIC REGION (ORF 61). //1.0:22:40//MAR
 CHANTIA POLYMORPHA (LIVERWORT). //P38473
 F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC
 2.4.2.30) (PARP) (ADPRT) (NAD(+)) ADP- RIBOSYLTRANS
 FERASE) (POLY[ADP-RIBOSE] SYNTHETASE). //2.8e-21:16
 3:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //Q11
 207
 F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTR
 Y !!!!//1.1e-10:43:67//HOMO SAPIENS (HUMAN). //P391
 92
 F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTC I)
 [CONTAINS: LIPOVITELLIN1 (LV1); PHOSVITIN (PV); LI
 POVITELLIN 2 (LV2)]. //0.00019:123:37//FUNDULUS HET
 EROCLITUS (KILLIFISH) (MUMMICHOG). //Q90508
 F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19
 (ARPP-19). //3.2e-40:110:76//HOMO SAPIENS (HUMAN). /
 /P56211
 F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBI
 TOR A-II. //0.99:30:40//ARACHIS HYPOGAEA (PEANUT). /
 /P01066
 F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHER
 IN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5). //8.8e-
 94:218:76//HOMO SAPIENS (HUMAN). //000410

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F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PR
 ECURSOR. //0.00092:228:26//SACCHAROMYCES CEREVISIAE
 (BAKER'S YEAST). //P32323
 F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SA
 P155-YMR31 INTERGENIC REGION. //5.9e-55:128:50//SACC
 HAROMYCES CEREVISIAE (BAKER'S YEAST). //P43616
 F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTR
 Y !!!!//1.4e-25:107:63//HOMO SAPIENS (HUMAN). //P39
 194
 F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL
 LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE
 -ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (C
 D62E). //1.3e-21:168:32//SUS SCROFA (PIG). //P98110
 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIR1 PR
 ECURSOR (SERINE-RICH PROTEIN 1). //0.46:98:29//SACC
 HAROMYCES CEREVISIAE (BAKER'S YEAST). //P10863
 F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHA
 IN 4L (EC 1.6.5.3). //0.70:28:42//ARTEMIA SALINA (B
 RINE SHRIMP). //P19049
 20 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC
 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPH
 A-D-GLUCAN GLUCOHYDROLASE). //8.9e-05:167:32//SACCH
 AROMYCES CEREVISIAE (BAKER'S YEAST). //P08640
 F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY
 PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD CO
 ATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR H
 A2/AP2 ADAPTIN ALPHA C SUBUNIT). //1.1e-67:157:88//
 MUS MUSCULUS (MOUSE). //P17427
 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E. //5.6e-75:2
 24:62//HOMO SAPIENS (HUMAN). //P24864
 30 F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENT
 ERON PROTEIN). //0.99:177:29//DROSOPHILA MELANOGAST
 ER (FRUIT FLY). //P55965
 F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICAS
 E C12C2.06. //2.0e-33:183:46//SCHIZOSACCHAROMYCES P
 OMBE (FISSION YEAST). //Q09747
 F-PLACE1006205
 F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENO
 PROTEIN (MCS). //0.00015:22:50//MUS MUSCULUS (MOUS
 E). //P15265
 F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PRO
 TEIN). //1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TY
 PE 1 (NDK ISOLATE) (HIV-1). //P18805
 F-PLACE1006236
 F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (F
 RAGMENT). //0.48:23:52//ARABIDOPSIS THALIANA (MOUSE
 -EAR CRESS). //P51407
 F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-S
 IA-TR). //0.012:84:30//MUS MUSCULUS (MOUSE). //Q6142

- F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (N OPP140).//0.017:203:22//RATTUS NORVEGICUS (RAT).//P41777
- F-PLACE1006262//L-FUCULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52//HAEMOPHILUS INFLUENZAE.//P44777
- F-PLACE1006288
- F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231
- F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918
- F-PLACE1006335//PROLINE-RICH PEPTIDE P-B.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814
- F-PLACE1006357
- F-PLACE1006360
- F-PLACE1006368//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380
- F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P49777
- F-PLACE1006382//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION).//P01482
- F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RP S5-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
- F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547
- F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676
- F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910
- F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876
- F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550
- F-PLACE1006470
- F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595
- F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004
- F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN C56F8.13 IN CHROMOSOME I.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261
- F-PLACE1006506
- F-PLACE1006521
- F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZK75 7.3 IN CHROMOSOME III.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681
- F-PLACE1006534
- F-PLACE1006540
- F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
- F-PLACE1006598//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.17:43:51//HOMO SAPIENS (HUMAN).//P39190
- F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
- F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPLICATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861
- F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//2.9e-10:73:46//CAENORHABDITIS ELEGANS.//P34529
- F-PLACE1006629//HYPOTHETICAL PROTEIN BB0410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//051371
- F-PLACE1006640
- F-PLACE1006673
- F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
- F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) [CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN].//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295
- F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENES).//Q59263
- F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CGM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198
- F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941
- F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NJA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517
- F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875
- F-PLACE1006792
- F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PR

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OTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOG
 ASTER (FRUIT FLY).//P17972
 F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.9
 9:62:33//VACCINIA VIRUS(STRAIN COPENHAGEN).//P2056
 9
 F-PLACE1006805
 F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:
 146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16
 818
 F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOL 10
 OG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROL
 ASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (U
 BIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUI
 TINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CE
 REVISIAE (BAKER'S YEAST).//P50102
 F-PLACE1006860
 F-PLACE1006867
 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOB
 L 3' REGION (ORF 3).//0.85:27:37//THIOBACILLUS FERR 20
 OOXIDANS.//P20087
 F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DI
 HYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSC
 ULUS (MOUSE).//P48281
 F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.9
 9:55:23//VACCINIA VIRUS(STRAIN COPENHAGEN).//P2056
 7
 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEI
 N.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P2
 2015
 F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B1
 1.5 IN CHROMOSOME II.//6.9e-15:101:45//CAENORHABDI
 TIS ELEGANS.//Q09442
 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLY
 PEPTIDE.//0.089:28:39//HELI COBACTER PYLORI (CAMPYL
 OBACTER PYLORI).//Q48251
 F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.
 6 IN CHROMOSOME III.//0.93:35:48//CAENORHABDITIS E
 LEGANS.//Q10000
 F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TF 40
 IID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-1
 30) (TAFII130).//0.00079:122:36//HOMO SAPIENS (HUM
 AN).//000268
 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SH
 OCK 70-RELATED PROTEINAPG-1).//8.8e-70:140:98//MUS
 MUSCULUS (MOUSE).//P48722
 F-PLACE1006961
 F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-
 C1).//1.0:25:40//PAPIOHAMADRYAS (HAMADRYAS BABOO
 N).//P34929

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F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SS
 B2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCH
 AROMYCES CEREVISIAE (BAKER'S YEAST).//P40160F-PLAC
 E1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN
 P37 5' REGION.//0.15:46:32//MYCOPLASMA HYORHINIS./
 /P32083
 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DEL
 AYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:
 120:29//HOMO SAPIENS (HUMAN).//Q14542
 F-PLACE1007021//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/0.00046:42:59//HOMO SAPIENS (HUMAN).//P3918
 8
 F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.
 1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260
 F-PLACE1007053//SMALL PROLINE RICH PROTEIN II (SPR
 -II) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMA
 N).//P22531
 F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR
 (EC 1.4.3.13) (LYSYLOXIDASE).//0.0040:113:39//GAL
 LUS GALLUS (CHICKEN).//Q05063
 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE6
 5-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPH A C
 ALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).//P
 41663
 F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A1
 0.10 IN CHROMOSOME I.//2.9e-33:219:37//SCHIZOSACCH
 AROMYCES POMBE (FISSION YEAST).//013730
 F-PLACE1007111
 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.4
 7:75:28//ESCHERICHIA COLI.//P03853
 F-PLACE1007132//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/1.8e-11:56:57//HOMO SAPIENS (HUMAN).//P3918
 8
 F-PLACE1007140//GAR2 PROTEIN.//0.72:185:24//SCHIZO
 SACCHAROMYCES POMBE (FISSION YEAST).//P41891
 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.
 40C.//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS.//Q10
 826
 F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN GS
 HB-ANSB INTERGENIC REGION (0378).//1.9e-15:123:32/
 /ESCHERICHIA COLI.//P52062
 F-PLACE1007238//MYOSIN HEAVY CHAIN IB (MYOSIN HEAV
 Y CHAIN IL).//5.5e-10:98:44//ACANTHAMOEBA CASTELLA
 NII (AMOEBA).//P19706
 F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-
 II (TRANSCRIPTION ELONGATION FACTOR A).//3.9e-19:9
 6:57//HOMO SAPIENS (HUMAN).//P23193
 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION ST
 IMULATOR RALGDS FORM B(RALGEF).//1.0:132:30//RATTU
 S NORVEGICUS (RAT).//Q03386

3107

F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HT8-CAN1 INTERGENIC REGION.//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981

F-PLACE1007257//DIAPHANOUS PROTEIN.//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608

F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT).//0.054:60:30//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187

F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1).//1.0:42:28//SUS SCROFA (PIG). 10 //062697

F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3).//P11200

F-PLACE1007286

F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749

F-PLACE1007317

F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002

F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318

F-PLACE1007367//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189

F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//4.7e-07:71:39//CAENORHABDITIS ELEGANS.//P27715

F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561

F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).//0.99:63:36//CITROBACTER FR EUNDII.//069280

F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P10090

F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487

F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN K0X27) (FRAGMENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038

F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CC 50

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P1-MET1 INTERGENIC REGION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149

F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//CHLAMYDOMONAS REINHARDTII.//Q06480

F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (AGL).//0.93:45:33//SUS SCROFA (PIG).//Q35914

F-PLACE1007478//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (MOUSE).//P11369

F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION.//0.87:43:37//ESCHERICHIA COLI.//P03849

F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:31//HOMO SAPIENS (HUMAN).//P98174

F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TA60-GAP1 INTERGENIC REGION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139

F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//2.1e-45:209:48//BOSTAURUS (BOVINE).//P08728

F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20550

F-PLACE1007525

F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144

F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479

F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537

F-PLACE1007557

F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT).//P06600

F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936

F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808

F-PLACE1007621//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMO

NAS AERUGINOSA. //P23621

F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT). //0.70:110:34//BOSTAURUS (BOVINE). //P02465

F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //0.99:20:45//STRUTHIO CAMELUS (OSTRICH). //021401

F-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P08640

F-PLACE1007677//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.0:47:46//HOMO SAPIENS (HUMAN). //P39192

F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG). //2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO). //Q26457

F-PLACE1007690//SPERM PROTAMINE P1. //0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA). //P35311

F-PLACE1007697//SPERM PROTAMINE P1. //0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPLOSSUM), AND MONDELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM). //P35305

F-PLACE1007705//BIH PROTEIN. //0.015:97:29//ESCHERICHIA COLI. //P13001

F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1). //5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32898

F-PLACE1007725

F-PLACE1007729//PROTEASE (EC 3.4.23.-). //1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6). //P10271

F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT). //0.0031:77:40//HOMO SAPIENS (HUMAN). //P81489

F-PLACE1007737//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.78:39:56//HOMO SAPIENS (HUMAN). //P39195

F-PLACE1007743

F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT). //0.0066:168:25//HOMO SAPIENS (HUMAN). //Q14690

F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT). //0.62:17:41//LITHOBIUS FORFICATUS. //Q01872

F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION. //1.0:40:30//BACILLUS SUBTILIS. //P54446

F-PLACE1007810//ANTHOPLEURIN A (TOXIN AP-A). //0.79:28:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE). //P01530

F-PLACE1007829//SPORE COAT PROTEIN G. //1.0:65:38// 50 0

BACILLUS SUBTILIS. //P39801

F-PLACE1007843

F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //1.5e-32:37:94//HOMO SAPIENS (HUMAN). //P08547

F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOB (GTP-BINDING PROTEIN TTF). //8.7e-05:138:30//HOMO SAPIENS (HUMAN). //Q15669

F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN. //0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P50275

F-PLACE1007866

F-PLACE1007877

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTOGLYCOPROTEIN I) (PGP-1) (HUTCH-I) (EXTRACELLULAR MATRIX RECEPTOR-III) (ECMR-III) (GP90 LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM-1 ANTIGEN). //0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER). //Q60522

F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.5e-28:61:65//HOMO SAPIENS (HUMAN). //P39192

F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC. //0.84:48:37//PSEUDOMONAS AERUGINOSA. //P04139

F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GIP1 INTERGENIC REGION. //0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38226

F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II. //0.00027:255:23//CAENORHABDITIS ELEGANS. //Q09625

F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17). //1.7e-09:127:30//MUS MUSCULUS (MOUSE). //P70453

F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION. //2.4e-05:104:37//AUTORAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV). //P41479

F-PLACE1007990//SPERM PROTAMINE P1. //0.78:36:47//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS). //P35307

F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93). //1.2e-16:128:39//RATTUS NORVEGICUS (RAT). //Q63622

F-PLACE1008002

F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105). //3.9e-106:208:93//RATTUS NORVEGICUS (RAT). //P5259

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F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//3.9e-09:49:53//BOS TAURUS (BOVINE).//P25508
 F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//0.00025:100:27//EGGPLANT MOSAIC VIRUS.//P20126
 F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO).//0.90:74:25//MYCOBACTERIUM TUBERCULOSIS.//053230
 F-PLACE1008111//HYPOTHETICAL PROTEIN MJCS12.//0.30:38:42//METHANOCOCCUSJANNASCHII.//Q60311
 F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN).//0.0085:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40091
 F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//1.8e-06:154:36//CALLUS CALLUS (CHICKEN).//P02467
 F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.4e-13:227:36//CAENORHABDITIS ELEGANS.//Q09531
 F-PLACE1008177//TRICHOHYALIN.//2.7e-10:230:26//OVIS ARIES (SHEEP).//P22793
 F-PLACE1008181
 F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A.//3.0e-05:82:37//MICROPTERUS SALMOIDES (LARGEMOUTH BASS).//P38621
 F-PLACE1008209//METALLOTHIONEIN-I (MT-I).//0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P02797
 F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN) (PARP).//0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI.//P08469
 F-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.2e-23:148:38//PODOSPORA ANSERINA.//Q00808
 F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.1e-97:222:81//BOS TAURUS (BOVINE).//P53620
 F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//5.8e-20:161:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12689
 F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.1e-23:124:42//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.06C IN CHROMOSOME I.//0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014302
 F-PLACE1008329//PUTATIVE Z PROTEIN.//0.73:52:28//0 50

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VIS ARIES (SHEEP).//P08105
 F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-37:75:81//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-08:70:50//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1008356//FRUIT PROTEIN PRIWI501.//0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO).//P43393
 F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:205:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-PLACE1008369
 F-PLACE1008392
 F-PLACE1008398//GENE 33 POLYPEPTIDE.//1.5e-102:225:84//RATTUS NORVEGICUS(RAT).//P05432
 F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//2.9e-08:186:34//MUS MUSCULUS (MOUSE).//P05143
 F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//9.4e-105:207:98//BOS TAURUS (BOVINE).//P41541
 F-PLACE1008405
 F-PLACE1008424//PROTEIN UL56.//1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 /STRAIN HFEM).//P36297
 F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSINII).//4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q99323
 F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.00054:172:25//RATTUS NORVEGICUS (RAT).//Q05175
 F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME III.//1.9e-23:226:34//CAENORHABDITIS ELEGANS.//P34681
 F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN).//0.97:23:52//BUDGERIGAR FLEDGLING DISEASE VIRUS (BFDV).//P13893
 F-PLACE1008457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-12:89:47//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN KOX29) (FRAGMENT).//0.00017:23:43//HOMO SAPIENS (HUMAN).//P17040
 F-PLACE1008488//HYPOTHETICAL PROTEIN UL61.//9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
 F-PLACE1008524//HOMEODOMAIN PROTEIN HLX1 (HOMEODOMAIN PROTEIN HB24).//0.95:74:36//HOMO SAPIENS (HUMAN).//Q14774
 F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY

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Y 1111//3.1e-05:86:45//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SM P1-MBA1 INTERGENIC REGION.//3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38298
 F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME I.//3.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09830
 F-PLACE1008568//NEURONATIN.//0.046:34:52//HOMO SAPIENS (HUMAN).//Q16517
 F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT).//0.94:30:43//LITHOBIUS FORFICATUS.//Q02030
 F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//3.9e-123:224:96//RATTUS NORVEGICUS (RAT).//P37199
 F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//5.0e-05:31:67//HOMO SAPIENS (HUMAN).//P20931
 F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.87:17:52//ORNITHODOROS MOUTON (SOFT TICK).//P36235
 F-PLACE1008626//METALLOTHIONEIN-I (MT-I).//0.77:33:36//SCYLLA SERRATA (MUD CRAB).//P02805
 F-PLACE1008627//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB).//0.14:44:31//HOMO SAPIENS (HUMAN).//P25713
 F-PLACE1008629
 F-PLACE1008630//PROTAMINE Z3 (SCYLLIORHININE Z3).//0.78:33:36//SCYLLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK).//P30258
 F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//1.7e-30:220:41//HOMO SAPIENS (HUMAN).//Q14624
 F-PLACE1008650//PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1.//2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42384
 F-PLACE1008693//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//1.0:36:38//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321
 F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (CI-23KD) (TYKY SUBUNIT).//4.8e-14:47:80//HOMO SAPIENS (HUMAN).//000217
 F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION.//0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38834

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F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VM A7-RPS25A INTERGENIC REGION.//0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
 F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3).//0.60:44:34//ESCHERICHIA COLI.//P33669
 F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.0e-69:191:80//MUS MUSCULUS (MOUSE).//035345
 10 F-PLACE1008798//BACTERIOCIN LACTOBIN A.//1.0:34:41//LACTOBACILLUS AMYLOVORUS.//P80696
 F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.91:77:36//HOMOSAPIENS (HUMAN).//P08547
 F-PLACE1008808//REC1 PROTEIN.//0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS).//P14746
 F-PLACE1008813
 F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DUR1,2 INTERGENIC REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38309
 20 F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
 F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.65:61:36//SOLANUM TUBEROSUM (POTATO).//P15478
 F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:180:54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-PLACE1008902
 30 F-PLACE1008920
 F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAP-RND INTERGENIC REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242
 F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5' REGION (ORF3) (FRAGMENT).//0.14:77:45//GLUCONOBACTER SUBOXIDANS.//005543
 F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPIENS (HUMAN).//Q15928
 F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790
 F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS TAURUS (BOVINE).//P20072
 F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.39:57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301
 F-PLACE1009039
 F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENIC REGION (F83).//0.48:32:43//ESCHERICHIA COLI.//P46879
 50

- F-PLACE1009048
F-PLACE1009050
F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E1
2.1 IN CHROMOSOME III.//4.9e-23:244:31//CAENORHABD
ITIS ELEGANS.//P34552
F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:2
7:51//MYCOPLASMA GENITALIUM.//P47439
F-PLACE1009091
F-PLACE1009094//NEL-LIKE PROTEIN (FRAGMENT).//3.6e
-15:180:30//HOMO SAPIENS (HUMAN).//Q92832
F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (M
KR4 PROTEIN) (FRAGMENT).//1.4e-94:228:71//MUS MUSC
ULUS (MOUSE).//P10077
F-PLACE1009110//HIRUDIN HV1 (BUFRUDIN).//1.0:49:34
//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!//1.4e-05:30:83//HOMO SAPIENS (HUMAN).//P391
95
F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT)./
/0.032:40:52//BOS TAURUS (BOVINE).//P20072
F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.
3e-37:214:38//HOMO SAPIENS (HUMAN).//Q15034
F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!//1.6e-32:56:76//HOMO SAPIENS (HUMAN).//P391
95
F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!//1.2e-17:101:57//HOMO SAPIENS (HUMAN).//P39
194
F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFX (J11)./
/0.0058:73:42//HUMAN CYTOMEGALOVIRUS (STRAIN AD16
9).//P09711
F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE
(EC 3.1.3.5).//0.0086:96:30//HOMO SAPIENS (HUMAN).
//P49902
F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAP
A-RND INTERGENIC REGION.//1.0:19:52//ESCHERICHIA C
OLI.//P76246
F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!//3.1e-17:47:82//HOMO SAPIENS (HUMAN).//P391
94
F-PLACE1009183
F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13C
6.04 IN CHROMOSOME I.//0.019:62:24//SCHIZOSACCHARO
MYCES POMBE (FISSION YEAST).//Q09783
F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.
2) (LONG-CHAIN FATTY-ACYL-COA HYDROLASE) (FRAGMEN
T).//0.027:53:28//RATTUS NORVEGICUS (RAT).//P80250
F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!//5.4e-28:84:71//HOMO SAPIENS (HUMAN).//P391
94
- F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!//2.8e-12:50:74//HOMO SAPIENS (HUMAN).//P391
89
F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE C
OMPLEX 7.8 KD PROTEIN (EC 1.10.2.2) (MITOCHONDRIAL
HINGE PROTEIN) (CR7).//1.0:17:52//SOLANUM TUBEROSU
M (POTATO).//P48504
F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATE
D PROTEIN VPS35.//6.6e-41:177:53//SACCHAROMYCES CE
REVISIAE (BAKER'S YEAST).//P34110
F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX
PROTEIN (UHS KERATIN).//0.00034:108:33//HOMO SAPIE
NS (HUMAN).//P26371
F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PS
D-95).//5.3e-16:84:50//HOMO SAPIENS (HUMAN).//P783
52
F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOL
OG.//6.9e-82:263:67//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:7
1:36//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE),
AND RATTUS NORVEGICUS (RAT).//P02433
F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY
AND ENHANCER OF SPLITS).//0.90:42:40//MUS MUSCULUS
(MOUSE).//P70120
F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE IB-1.//
0.013:33:48//HOMO SAPIENS (HUMAN).//P04281
F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D1
0.1 IN CHROMOSOME III.//0.0022:135:21//CAENORHABDI
TIS ELEGANS.//P34492
F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!//4.8e-22:73:65//HOMO SAPIENS (HUMAN).//P391
95
F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGE
R PROTEIN HPF2).//8.1e-83:223:65//HOMO SAPIENS (HU
MAN).//P51523
F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SU
BUNIT PW212 PRECURSOR.//0.047:145:29//TRITICUM AES
TIVUM (WHEAT).//P08489
F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:
47//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).
//P18329
F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUB
UNIT K (EC 1.6.5.3) (FRAGMENT).//0.81:61:29//ANTHO
CEROS FORMOSAE.//Q31791
F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62
(SAP 62) (SF3A66).//9.1e-05:93:32//MUS MUSCULUS (M
OUSE).//Q62203
F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPH
A (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI
4K-ALPHA).//6.4e-15:41:97//HOMO SAPIENS (HUMAN).//

- P42356
F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G1
2.11C IN CHROMOSOME I.//0.0011:119:31//SCHIZOSACCH
AROMYCES POMBE (FISSION YEAST).//Q09874
F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTE
IN (PLAP).//4.2e-34:101:75//RATTUS NORVEGICUS (RA
T).//P54319
F-PLACE1009476//DNA-BINDING P52/P100 COMPLEX, 100
KD SUBUNIT (FRAGMENTS).//0.086:21:52//HOMO SAPIENS
(HUMAN).//P30808
F-PLACE1009477
F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B041
6.1 IN CHROMOSOME X.//1.4e-18:138:39//CAENORHABDIT
IS ELEGANS.//Q11069
F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER
(ARNO PROTEIN) (ARF EXCHANGE FACTOR).//9.4e-80:15
5:85//HOMO SAPIENS (HUMAN).//Q99418
F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAN/TC
4.//1.0:76:26//GIARDIALAMBLIA (GIARDIA INTESTINALI
S).//P38543
F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//0.00016:31:77//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34)
(SUBUNIT I).//0.88:116:29//STREPTOCOCCUS PNEUMONI
AE.//Q59952
F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.0002
3:37:51//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS
CAPSULATA).//P30788
F-PLACE1009595
F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEA
TS CONTAINING PROTEINC14B1.4 IN CHROMOSOME III.//
2.1e-36:116:49//CAENORHABDITIS ELEGANS.//Q17963
F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//1.8e-43:73:69//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE1009613
F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG
2.//0.91:29:44//HOMO SAPIENS (HUMAN).//Q13891
F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//
1.3e-22:132:47//DROSOPHILA MELANOGASTER (FRUIT FL
Y).//P25159
F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CF
XA 3' REGION.//0.30:28:57//BACTEROIDES VULGATUS.//P
30905
F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE
HELPER PROTEIN).//0.23:79:31//PSEUDOMONAS AERUGIN
OSA.//Q04591
F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2
(BRAIN PROTEIN H19) (MH19) (FRAGMENT).//3.9e-126:2 50
27:96//MUS MUSCULUS (MOUSE).//P28660
F-PLACE1009665//IG KAPPA CHAIN V-I REGION (HAU).//
0.52:89:35//HOMO SAPIENS (HUMAN).//P01600
F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERA
SE PRECURSOR (EC 2.4.1.19) (CYCLODEXTRIN-GLYCOSYL
TRANSFERASE) (CGTASE).//0.16:114:29//PAENIBACILLUS
MACERANS (BACILLUS MACERANS).//P31835
F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPE
ATS CONTAINING PROTEINC12G12.13C IN CHROMOSOME I.//
9.6e-19:156:36//SCHIZOSACCHAROMYCES POMBE(FISSION
YEAST).//Q09876
F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SAC
CHAROMYCES CEREVISIAE(BAKER'S YEAST).//P35200
F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARAB
IDOPSIS THALIANA (MOUSE-EAR CRESS).//P54120
F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H
6.12C IN CHROMOSOME I.//8.3e-42:171:51//SCHIZOSACC
HAROMYCES POMBE (FISSION YEAST).//Q09765F-PLACE100
9794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.9
20 9:36:33//HORDEUM VULGARE (BARLEY).//P17991
F-PLACE1009798//HYPOTHETICAL PROTEIN C22F3.14C IN
CHROMOSOME I (FRAGMENT).//2.6e-34:191:38//SCHIZOSA
CCHAROMYCES POMBE (FISSION YEAST).//Q09779
F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PR
OTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST).//P38968
F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.
1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688
F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL
30 22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//A
STASIA LONGA (EUGLENOPHYCEAN ALGA).//P34779F-PLACE
1009886
F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAIN
S: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:3
3:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896
F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C
3F10.16C IN CHROMOSOMEI.//3.1e-42:205:46//SCHIZOSA
CCHAROMYCES POMBE (FISSION YEAST).//Q10190
F-PLACE1009921
F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34)
(PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRUCEI BRU
CEI.//P24499
F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIA
L (EC 3.6.1.34).//0.99:111:27//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST).//P30902
F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.06
3:75:32//METHANOCOCCUSJANNASCHII.//Q57706
F-PLACE1009947//NEUROGRANIN (NG) (P17) (B-50 IMMUN
OREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//
/0.33:51:45//BOS TAURUS (BOVINE).//P35722

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F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575
 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497
 F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTM1.//0.052:185:22//CLONA INTESTINALIS.//Q07068
 F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FACTOR DMS-II) (TFIIS).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232
 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C27F 2.7 IN CHROMOSOME III.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262
 F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOGRAPH A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV).//P41479
 F-PLACE1010053//HYPOTHETICAL PROTEIN HI0593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022
 F-PLACE1010069
 F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
 F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790
 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171
 F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (KIAA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818
 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671
 F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649
 F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-PLACE1010106//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369
 F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN NUT1-A02 INTERGENIC REGION.//4.0e-28:78:76//SACCH

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AROMYCES CEREVISIAE (BAKER'S YEAST).//P53115
 F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574
 F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87 F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:43//GALLUS GALLUS (CHICKEN).//P30352
 F-PLACE1010202//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36).//0.094:109:29//RATTUS NORVEGICUS (RAT).//P47973
 F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR.//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068
 F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25722
 F-PLACE1010270
 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN C4F8.01 IN CHROMOSOME I.//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014177
 F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY 30 !!!!!/3.9e-26:94:64//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1010310//SYNAPSINS IA AND IB.//5.7e-09:89:37//RATTUS NORVEGICUS (RAT).//P09951
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:48//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567
 F-PLACE1010329//TOXIN S5C10.//1.0:39:33//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P01419
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY 9 !!!!!/0.0049:49:55//HOMO SAPIENS (HUMAN).//P39189
 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PL C).//0.0034:89:30//TRYPANOSOMA CRUZI.//015886
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17

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SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B17)
(CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q29259
F-PLACE1010383
F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (N
OPP140).//0.10:174:22//RATTUS NORVEGICUS (RAT).//P
41777
F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B028
5.5 IN CHROMOSOME III.//1.5e-21:170:35//CAENORHABD
ITIS ELEGANS.//P46555
F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MO
B1-SGA1 INTERGENIC REGION.//1.0:31:41//SACCHAROMYC
ES CEREVISIAE (BAKER'S YEAST).//P40490
F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G1
2.11C IN CHROMOSOME I.//0.77:97:30//SCHIZOSACCHARO
MYCES POMBE (FISSION YEAST).//Q09874
F-PLACE1010522//SMALL PROLINE RICH PROTEIN II (SPR
-II) (CLONE 930).//0.74:45:37//HOMO SAPIENS (HUMA
N).//P22531
F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SY
NTHETASE (P5CS) [CONTAINS: GLUTAMATE 5-KINASE (EC
2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK); GAMM
A-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41)
(GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMY
L-GAMMA-SEMIALDEHYDE DEHYDROGENASE)].//0.70:58:39/
/VIGNA ACONITIFOLIA (MOTHBEAN).//P32296
F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BU
D9-RME1 INTERGENIC REGION.//0.17:68:39//SACCHAROMY
CES CEREVISIAE (BAKER'S YEAST).//P53227
F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN
L33.//0.50:48:29//PORPHYRA PURPUREA.//P51255
F-PLACE1010579//HYPOTHETICAL PROTEIN HI1571.//0.2
9:37:43//HAEMOPHILUS INFLUENZAE.//P44260
F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICAS
E C12C2.06.//3.3e-38:178:48//SCHIZOSACCHAROMYCES P
OMBE (FISSION YEAST).//Q09747
F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PER10
(PEROXIN-14).//4.6e-17:192:31//PICHIA ANGUSTA (YE
AST) (HANSENUA POLYMORPHA).//P78723
F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNP
A 3' REGION.//0.44:32:37//PSEUDOMONAS PUTIDA.//P257
53
F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PR
ECURSOR.//5.0e-06:102:42//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P32323
F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO
(ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.
00036:134:32//HOMO SAPIENS (HUMAN).//P10162
F-PLACE1010628
F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN).//P391

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94
F-PLACE1010630
F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:6
2:30//EUMECES SKILTONIANUS (WESTERN SKINK).//P2811
8
F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//
1.0:95:30//DROSOPHILA PSEUDOOBSCURA (FRUIT FLY).//
Q24617
F-PLACE1010662//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYL
TRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.2e-0
5:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//QO
9332
F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:
117:62//HOMO SAPIENS (HUMAN).//014628
F-PLACE1010714
F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-
C.//1.1e-64:176:76//XENOPUS LAEVIS (AFRICAN CLAWED
FROG).//P50532
F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGUL
ATORY PROTEIN) (FRAGMENT).//0.97:31:41//HUMAN IMMU
NODEFICIENCY VIRUS TYPE 1 (BH5 ISOLATE) (HIV-1).//
P04612
F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMEN
T).//3.8e-05:253:30//MUS MUSCULUS (MOUSE).//P05143
F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B049
5.8 IN CHROMOSOME II.//1.5e-14:175:25//CAENORHABDI
TIS ELEGANS.//Q09217
F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN
HCNGP.//1.3e-120:216:89//MUS MUSCULUS (MOUSE).//QO
2614
F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.9
7:133:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P5
4623
F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TR
AX-FINO INTERGENIC REGION (ORFC).//0.0060:111:31//
ESCHERICHIA COLI.//Q99390
F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.
82:44:29//BACILLUS SP. (STRAIN TB-90).//Q07415
F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:
38//ECTOTHIORHODOSPIRAHALOCHLORIS.//P38587
F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//
2.8e-09:90:34//HOMO SAPIENS (HUMAN).//P41208
F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.
0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).
//P55848
F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:7
3:34//GORILLA GORILLAGORILLA (LOWLAND GORILLA).//P
20758
F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGE
R PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HOMO SAP

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IENS (HUMAN).//Q05481
 F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277
 F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN IN BLT R-SPO11C INTERGENIC REGION.//0.95:51:27//BACILLUS SUBTILIS.//P54436
 F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PT K1/STK1 (EC 2.7.1.-).//0.98:71:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36002
 F-PLACE1010900//HYPOTHETICAL PROTEIN HI0840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897
 F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN N, I1B3.//0.060:59:35//OVIS ARIES (SHEEP).//P02444
 F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMERPROTEIN).//0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191
 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19285
 F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.011:51:45//HOMO SAPIENS (HUMAN).//Q92558
 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15(PROTEIN EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567
 F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:38//BOS TAURUS (BOVINE).//P41987
 F-PLACE1010947
 F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:144:26//HOMO SAPIENS (HUMAN).//P09493
 F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT FLY).//P45890
 F-PLACE1010965
 F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT FLY).//Q03293
 F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNA SE HI) (RIBONUCLEASE H) (RNASE H).//1.0:32:37//SALMONELLA TYPHIMURIUM.//P23329
 F-PLACE1011041//HOMEBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEGANS.//Q93899
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGICUS (RAT).//P10687

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F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).//P08283
 F-PLACE1011057
 F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TW T1-FL05 INTERGENIC REGION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892
 F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//5.4e-25:63:88//RATTUS NORVEGICUS (RAT).//Q07803
 F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157:45//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09916
 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.5S ALPHA-1-GLYCOPROTEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743
 F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE 31.//P17385
 F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:27//GLYCINE MAX (SOYBEAN).//Q02917
 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586
 F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.4e-13:98:50//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1011203
 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (AGL).//1.0:48:27//EQUUS ASINUS (DONKEY).//P92479
 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//1.9e-15:162:31//STREPTOMYCES ANTIBIOTICUS.//Q03326
 F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MUNICH]).//P14369
 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107
 F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485
 F-PLACE1011273
 F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD P

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ROTEIN (FRAGMENTS). //0.011:36:50//RATTUS NORVEGICUS (RAT). //P20468

F-PLACE1011296//HOMEBOX PROTEIN DLX-6. //0.76:55:32//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO). //Q98877

F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.34) (LIPID-BINDING PROTEIN). //0.46:43:44//PETUNIA SP. (PETUNIA). //Q07060

F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME 1. //0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10411

F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR. //7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //Q05211

F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-07:40:62//HOMO SAPIENS (HUMAN). //P39188

F-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2). //2.2e-54:227:44//MUS MUSCULUS (MOUSE). //Q61703

F-PLACE1011375//PROBABLE E5 PROTEIN. //0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 5.1. //P26553

F-PLACE1011399//HISTONE H2B-IV. //0.19:129:27//VOLVOX CARTERI. //P16868

F-PLACE1011419

F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT). //3.4e-05:133:24//GALLUS GALLUS (CHICKEN). //P55879

F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //3.9e-25:76:63//HOMO SAPIENS (HUMAN). //P08547

F-PLACE1011465//ECTODERMA

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L DYSPLASIA PROTEIN (EDA PROTEIN). //0.97:36:41//HOMO SAPIENS (HUMAN). //Q92838

F-PLACE1011472//METALLOTHIONEIN-1 (CUMT-1). //0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER). //P29499

F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1). //0.028:129:34//CLOSTRIDIUM THERMOCELLUM. //Q06852

F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT). //2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER). //P52178

F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (O86). //0.66:32:40//ESCHERICHIA COLI. //P52102

F-PLACE1011520

F-PLACE1011563//LORICRIN. //0.00023:112:39//HOMO SAPIENS (HUMAN). //P23490

30 F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.2e-31:78:76//HOMO SAPIENS (HUMAN). //P39195

F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //1.5e-32:45:86//HOMO SAPIENS (HUMAN). //Q05481

F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT). //0.26:81:37//HOMO SAPIENS (HUMAN). //Q00975

40 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE180. //0.00045:170:30//PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV). //P11675

F-PLACE1011641

F-PLACE1011643//CUTICLE COLLAGEN 40. //1.0:128:32//CAENORHABDITIS ELEGANS. //P34804

F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:44:63//HOMO SAPIENS (HUMAN). //P39188

F-PLACE1011649//HYPOTHETICAL PROTEIN F-215. //0.48:106:34//HUMAN ADENOVIRUS TYPE 2. //P03291

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F-PLACE1011650
 F-PLACE1011664//CROOKED NECK PROTEIN. //1.2e-79:20
 1:68//DROSOPHILA MELANOGASTER (FRUIT FLY). //P17886
 F-PLACE1011675//FERREDOXIN. //1.0:44:29//METHANOCOC
 CUS THERMOLITHOTROPHICUS. //P21305
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS
 26A-COX4 INTERGENIC REGION. //1.0:40:22//SACCHAROMY
 CES CEREVISIAE (BAKER'S YEAST). //P53098
 F-PLACE1011719//NEUROTOXIN TX2-6. //0.90:31:35//PHO
 NEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER). //P29 10
 425
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BO
 NE 63 KD CALCIUM-BINDING PROTEIN). //0.0065:125:25/
 /RATTUS NORVEGICUS (RAT). //Q63083
 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMEN
 T). //0.97:48:39//EUBLEPHARIS MACULARIUS. //P40654
 F-PLACE1011749
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D
 BOX-BINDING PROTEIN). //0.028:91:39//MUS MUSCULUS
 (MOUSE). //Q60925
 F-PLACE1011778
 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION F
 ACTOR 1 PRECURSOR (GDF-1). //0.97:48:43//MUS MUSCUL
 US (MOUSE). //P20863
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR. //0.
 0027:154:33//BOS TAURUS (BOVINE). //P23206
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCH
 L A PROTEIN) (BCP). //1.0:60:26//PROSTHECOCHLORIS A
 ESTUARI. //P11741
 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP5 30
 4-ALT INTERGENIC REGION. //0.99:34:35//BACTERIOPHAG
 E T4. //P39495
 F-PLACE1011891//SMOOTHELIN. //0.018:122:31//HOMO SA
 PIENS (HUMAN). //P53814
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURS
 OR (APEC PROTEIN). //6.3e-09:203:35//XENOPUS LAEVIS
 (AFRICAN CLAWED FROG). //P17437
 F-PLACE1011922//CRYPTIDIN-RELATED PROTEIN 4C-2 PREC
 URSOR (CRS4C). //0.067:37:48//MUS MUSCULUS (MOUSE).
 //P50715
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SN
 K (EC 2.7.1.-) (SERUMINDUCIBLE KINASE). //1.5e-83:1
 75:89//MUS MUSCULUS (MOUSE). //P53351
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PREC
 URSOR. //0.50:46:41//SCHIZOPHYLLUM COMMUNE (BRACKET
 FUNGUS). //Q02593
 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOL
 OG. //1.6e-05:47:51//NYCTICEBUS COUCANG (SLOW LORI
 S). //P08548
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSO 50

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R (MEROZOITE SURFACE ANTIGEN). //0.98:83:31//PLASMO
 DIUM FRAGILE. //P22622
 F-PLACE1011995
 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254. //0.
 032:62:33//HOMO SAPIENS (HUMAN). //Q92543
 F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTR
 Y !!!!!//5.4e-18:63:73//HOMO SAPIENS (HUMAN). //P391
 93
 F-PLACE2000006//ANNEXIN VII (SYNEXIN) (FRAGMENT). /
 /0.14:20:50//BOS TAURUS (BOVINE). //P20072
 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMEN
 T). //0.0045:176:30//MUS MUSCULUS (MOUSE). //P05143
 F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTR
 Y !!!!!//3.6e-25:57:78//HOMO SAPIENS (HUMAN). //P391
 94
 F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN C
 HROMOSOME III. //0.00013:237:27//CAENORHABDITIS ELE
 GANS. //Q09475
 F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTR
 Y !!!!!//1.4e-33:60:80//HOMO SAPIENS (HUMAN). //P391
 93
 F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR
 -BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL
 /PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FB
 P). //1.0:83:31//HOMO SAPIENS (HUMAN). //P14207
 F-PLACE2000021//EPHRIN TYPE-A RECEPTOR 4 PRECURSOR
 (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR
 CEK8). //0.99:103:26//GALLUS GALLUS (CHICKEN). //Q07
 496
 F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84D
 A. //0.69:29:44//DROSOPHILA MELANOGASTER (FRUIT FL
 Y). //Q01642
 F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-
 -). //1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS. //Q0
 3326
 F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPR
 OTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1). //
 6.7e-18:191:35//HOMO SAPIENS (HUMAN). //Q02246
 F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYH
 C) (MAP 1C). //4.7e-80:163:96//RATTUS NORVEGICUS (R
 AT). //P38650
 F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENT
 RY !!!!!//6.4e-06:63:49//HOMO SAPIENS (HUMAN). //P39
 191
 F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTR
 Y !!!!!//3.2e-22:74:64//HOMO SAPIENS (HUMAN). //P391
 92
 F-PLACE2000061
 F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTE
 IN B (GENERAL STRESS PROTEIN B). //1.9e-06:108:37//

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BACILLUS SUBTILIS.//P26907
 F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:
 175:49//HOMO SAPIENS (HUMAN).//P49910
 F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.2
 7.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDATRA ZIB
 ETHICUS (MUSKRAT).//P00681
 F-PLACE2000100
 F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).
 //0.18:32:37//ZEA MAYS(MAIZE).//P33626
 F-PLACE2000111//CMRF35 ANTIGEN PRECURSOR.//0.056:1 10
 07:27//HOMO SAPIENS (HUMAN).//Q08708
 F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.
 1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:52//CLOST
 RIDIUM PERFRINGENS.//Q46185
 F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTR
 Y !!!!!/3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39
 194
 F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//
 0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HU
 MAN HERPESVIRUS 4).//P03224
 F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE
 RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLAT
 E CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTO
 R) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:6
 5:32//MUS MUSCULUS(MOUSE).//P41588
 F-PLACE2000140
 F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DIC
 TYOSTELIUM DISCOIDEUM(SLIME MOLD).//015736
 F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BM1 P
 RECURSOR (CARNOBACTERIOCIN B1).//1.0:30:26//CARNOB 30
 ACTERIUM PISCICOLA.//P38579
 F-PLACE2000172
 F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.7
 6:44:43//ARCHAEOGLOBUSFULGIDUS.//029724
 F-PLACE2000187//EM-LIKE PROTEIN GE46.//0.84:42:35/
 /ARABIDOPSIS THALIANA(MOUSE-EAR CRESS).//Q02973
 F-PLACE2000216
 F-PLACE2000223//NEUROTOXIN III (LQX III).//0.99:3
 8:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGY
 PTIAN SCORPION).//P01487
 F-PLACE2000235
 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEI
 N).//5.1e-37:121:42//DROSOPHILA MELANOGASTER (FRUI
 T FLY).//Q04652
 F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENT
 RY !!!!!/2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39
 191
 F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-
 46:232:45//TRIPNEUSTESGRATILLA (HAWAIIAN SEA URCHI
 N).//P23098

3130

F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORY
 CTOLAGUS CUNICULUS (RABBIT).//P37709
 F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY
 !!!!!/5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P3918
 8
 F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:
 33//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).
 //P18329
 F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTR
 Y !!!!!/7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P391
 95
 F-PLACE2000341//SODIUM/GLUCOSE COTRAPORTER 1 (NA
 (+)/GLUCOSE COTRAPORTER 1) (HIGH AFFINITY SODIUM
 -GLUCOSE COTRAPORTER).//0.014:141:24//ORYCTOLAGU
 S CUNICULUS (RABBIT).//P11170
 F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LE
 F4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAP
 HA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNP
 V).//P41479
 20 F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:
 49:53//HOMO SAPIENS (HUMAN).//Q13360
 F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTR
 Y !!!!!/7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P391
 94
 F-PLACE2000366
 F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOL
 UYSIAN ATROPHY PROTEIN).//1.5e-05:216:29//HOMO SAP
 IENS (HUMAN).//P54259
 F-PLACE2000373//MAX BINDING PROTEIN MNT (ROX PROTE
 IN) (MYC ANTAGONIST MNT).//0.27:63:33//HOMO SAPIEN
 S (HUMAN).//Q99583
 F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.7
 2:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)
 (EHV-1).//P28978
 F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (IB
 -9).//0.95:40:42//HOMOSAPIENS (HUMAN).//P02811
 F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.
 -).//0.88:88:31//AEROMONAS HYDROPHILA.//Q07465
 F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRE
 40 CURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7)./
 /7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P14209
 F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (E
 C 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//1.7e-9
 4:243:64//CAENORHABDITIS ELEGANS.//Q09996
 F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATA
 SE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T)
 (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULUS (MO
 USE).//Q06076
 F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY
 50 !!!!!/2.6e-20:61:62//HOMO SAPIENS (HUMAN).//P3918

8
F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MS
B2-UGA1 INTERGENIC REGION.//0.98:75:32//SACCHAROMY
CES CEREVISIAE (BAKER'S YEAST).//P53211
F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CE
RCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30
407
F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//7.5e-07:65:50//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE2000435
F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK68
8.8 IN CHROMOSOME III.//4.7e-66:178:47//CAENORHABD
ITIS ELEGANS.//P34678
F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!//2.1e-23:88:62//HOMO SAPIENS (HUMAN).//P391
95
F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGME
NT).//0.093:18:44//CENTRUROIDES LIMPIDUS LIMPIDUS
(MEXICAN SCORPION).//P45630
F-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR
PRECURSOR (FAT PROTEIN).//3.1e-23:165:40//DROSOPHI
LA MELANOGASTER (FRUIT FLY).//P33450
F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//3.6e-23:73:63//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!//4.4e-37:90:78//HOMO SAPIENS (HUMAN).//P391
94
F-PLACE3000004//EYES ABSENT HOMOLOG 3.//1.1e-09:2
7:100//MUS MUSCULUS (MOUSE).//P97480
F-PLACE3000009//PUTATIVE CUTICLE COLLAGEN C09G5.6.
//0.0061:148:34//CAENORHABDITIS ELEGANS.//Q09457
F-PLACE3000020//ADENYLATE CYCLASE, OLFACTIVE TYPE
(EC 4.6.1.1) (TYPE III) (ATP PYROPHOSPHATE-LYASE)
(ADENYLYL CYCLASE).//8.8e-93:193:92//RATTUS NORVEGI
CUS (RAT).//P21932
F-PLACE3000029//50S RIBOSOMAL PROTEIN L31E.//0.15:
50:38//METHANOCOCCUS JANNASCHII.//P54009
F-PLACE3000059//TCP1-CHAPERONIN COFACTOR A.//0.96:
50:34//BOS TAURUS (BOVINE).//P48427
F-PLACE3000070//HYPOTHETICAL 17.1 KD PROTEIN IN PU
R5 3' REGION.//0.29:22:59//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P38898
F-PLACE3000103//LYSIS PROTEIN (E PROTEIN) (GPE).//
0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280
F-PLACE3000119//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!//5.4e-41:87:78//HOMO SAPIENS (HUMAN).//P391
89
F-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN 50

SEC15.//1.0e-07:269:22//SACCHAROMYCES CEREVISIAE
(BAKER'S YEAST).//P22224
F-PLACE3000124//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//1.2e-29:97:73//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE3000136//PARS INTERCEREBRALIS MAJOR PEPTIDE
D1 (PMP-D1).//0.77:26:42//LOCUSTA MIGRATORIA (MIG
RATORY LOCUST).//P80059
F-PLACE3000142//HYPOTHETICAL 7.1 KD PROTEIN IN NAD
2 3' REGION (ORF 63).//0.82:34:41//MARCHANTIA POLYM
ORPHA (LIVERWORT).//P38468
F-PLACE3000145//TENSIN.//3.5e-91:238:74//CALLUS GA
LLUS (CHICKEN).//Q04205
F-PLACE3000147//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!//4.4e-30:61:65//HOMO SAPIENS (HUMAN).//P391
94
F-PLACE3000148//POL POLYPROTEIN [CONTAINS: PROTEAS
E (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.4
9); ENDONUCLEASE].//1.4e-18:226:34//GIBBON APE LEU
20 KEMIA VIRUS.//P21414
F-PLACE3000155//EXTENSIN PRECURSOR (PROLINE-RICH G
LYCOPROTEIN).//0.00014:107:33//ZEA MAYS (MAIZE).//
P14918
F-PLACE3000156//POL POLYPROTEIN [CONTAINS: PROTEAS
E (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.4
9); ENDONUCLEASE].//2.7e-19:169:30//BABOON ENDOGEN
OUS VIRUS (STRAIN M7).//P10272
F-PLACE3000157//PROBABLE SERINE/THREONINE-PROTEIN
KINASE CY50.16 (EC 2.7.1.-).//0.0061:92:30//MYCOBA
30 CTERIUM TUBERCULOSIS.//Q11053
F-PLACE3000158//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!//5.7e-49:56:80//HOMO SAPIENS (HUMAN).//P391
89
F-PLACE3000160//DNA TRANSFORMATION PROTEIN TFOX (C
OMPETENCE ACTIVATOR) (PROTEIN SXY).//0.39:94:34//H
AEMOPHILUS INFLUENZAE.//P43779
F-PLACE3000169//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!//5.6e-28:99:59//HOMO SAPIENS (HUMAN).//P391
93
F-PLACE3000194//PROLINE-RICH PROTEIN LAS17.//0.91:
80:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
Q12446
F-PLACE3000197//NEUROFILAMENT TRIPLET M PROTEIN (1
60 KD NEUROFILAMENT PROTEIN) (NF-M).//0.24:119:32/
/GALLUS GALLUS (CHICKEN).//P16053
F-PLACE3000199//EXTENSIN PRECURSOR (CELL WALL HYDR
OXYPROLINE-RICH GLYCOPROTEIN).//0.76:87:37//NICOTI
ANA TABACUM (COMMON TOBACCO).//P13983
F-PLACE3000207//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//4.5e-09:32:78//HOMO SAPIENS (HUMAN).//P3918

- 8
F-PLACE3000208
F-PLACE3000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY
Y !!!!!/7.2e-34:96:70//HOMO SAPIENS (HUMAN).//P391
94
F-PLACE3000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC
ACID-CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BG
P).//0.46:13:53//CANIS FAMILIARIS (DOG).//P81455
F-PLACE3000221//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/2.8e-24:178:45//HOMO SAPIENS (HUMAN).//P391
88
F-PLACE3000226//30S RIBOSOMAL PROTEIN S18.//0.98:3
8:34//NEISSERIA GONORRHOEA.//007815
F-PLACE3000230//METALLOTHIONEIN (MT).//0.97:25:48/
/OREOCHROMIS MOSSAMBICUS (MOZAMBIQUE TILAPIA) (TIL
APIA MOSSAMBICA).//P52726
F-PLACE3000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAC
E-8 ANTIGEN).//8.0e-21:121:39//HOMO SAPIENS (HUMA
N).//P43361
F-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT
REGULATOR).//2.3e-125:264:87//MUS MUSCULUS (MOUS
E).//P53995
F-PLACE3000254//RTOA PROTEIN (RATIO-A).//0.99:142:
23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
F-PLACE3000271//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/2.2e-12:63:53//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE3000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECU
RSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38//HOMO SAPI
ENS (HUMAN).//P27658
F-PLACE3000304//DNA-BINDING P52/P100 COMPLEX, 100
KD SUBUNIT (FRAGMENTS).//0.0028:31:54//HOMO SAPIEN
S (HUMAN).//P30808
F-PLACE3000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOL
UYSIAN ATROPHY PROTEIN).//0.98:82:34//RATTUS NORVE
GICUS (RAT).//P54258
F-PLACE3000320
F-PLACE3000322//GLYCINE-RICH CELL WALL STRUCTURAL
PROTEIN 1 PRECURSOR.//2.2e-22:61:52//ORYZA SATIVA
(RICE).//P25074
F-PLACE3000331//SMALL PROLINE-RICH PROTEIN II (SPR
-II) (CLONE 174N).//0.32:15:53//HOMO SAPIENS (HUMA
N).//P22532
F-PLACE3000339//CHORION PROTEIN S19.//0.34:89:37//
DROSOPHILA VIRILIS (FRUIT FLY).//P24516
F-PLACE3000341//NADH-UBIQUINONE OXIDOREDUCTASE CHA
IN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38//COTURNIX
COTURNIX JAPONICA (JAPANESE QUAIL).//P24968
F-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SU
LU (EC 2.7.1.-).//3.9e-50:168:60//CAENORHABDITIS E 50
LEGANS.//P46549
F-PLACE3000352//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/7.8e-29:76:71//HOMO SAPIENS (HUMAN).//P391
94
F-PLACE3000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYL
TRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYL GALA
CTOSAMINYLTRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N-
ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//3.
0e-09:100:41//HOMO SAPIENS (HUMAN).//Q10472
F-PLACE3000362//HYPOTHETICAL PROTEIN TP0064.//1.0:
75:26//TREPONEMA PALLIDUM.//083103
F-PLACE3000363//METALLOTHIONEIN (MT).//0.067:42:33
//ASTACUS FLUVIATILIS (BROAD-FINGERED CRAYFISH) (AS
TACUS ASTACUS).//P55951
F-PLACE3000365//LYSIS PROTEIN (E PROTEIN) (GPE).//
1.0:65:27//BACTERIOPHAGE PHI-K.//Q38040
F-PLACE3000373//RETROVIRUS-RELATED ENV POLYPROTEIN
N.//1.5e-18:90:47//HOMOSAPIENS (HUMAN).//P10267
F-PLACE3000388
F-PLACE3000399//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!!/6.3e-45:60:75//HOMO SAPIENS (HUMAN).//P391
93
F-PLACE3000400
F-PLACE3000401//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/3.6e-09:46:73//HOMO SAPIENS (HUMAN).//P3918
8
F-PLACE3000402//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/0.036:43:44//HOMO SAPIENS (HUMAN).//P39188
F-PLACE3000405//POSTERIOR PITUITARY PEPTIDE.//0.7
0:25:40//BOS TAURUS (BOVINE).//P01154
F-PLACE3000406//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!/4.3e-09:49:67//HOMO SAPIENS (HUMAN).//P391
95
F-PLACE3000413//MALE SPECIFIC SPERM PROTEIN MST87
F.//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FL
Y).//P08175
F-PLACE3000416//CYLICIN I (MULTIPLE-BAND POLYPEPTI
DE I).//0.67:236:21//BOS TAURUS (BOVINE).//P35662
F-PLACE3000425//PROLINE-RICH PEPTIDE P-B.//0.45:1
9:42//HOMO SAPIENS (HUMAN).//P02814
F-PLACE3000455//AMELOGENIN, CLASS I PRECURSOR.//0.
0073:81:43//BOS TAURUS (BOVINE).//P02817
F-PLACE3000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.
//1.0:53:32//TACHYPLEUS TRIDENTATUS (JAPANESE HORS
ESHOE CRAB).//P81281
F-PLACE3000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:5
5:32//DENDROASPIS ANGSTICEPS (EASTERN GREEN MAMB
A).//P80970
F-PLACE4000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE
ISOFORM (SMHHC) (FRAGMENT).//7.0e-19:180:27//HOMO

SAPIENS (HUMAN). //P35749
 F-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP). //3.2e-15:193:30//HOMO SAPIENS (HUMAN). //P46100
 F-PLACE4000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR. //0.0024:97:29//DROSOPHILA MELANOGASTER (FRUIT FLY). //P22815
 F-PLACE4000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-32:79:75//HOMO SAPIENS (HUMAN). //P39194
 F-PLACE4000052//ATP-BINDING CASSETTE TRANSPORTER 1. //2.2e-99:178:97//MUS MUSCULUS (MOUSE). //P41233
 F-PLACE4000063//IMMEDIATE-EARLY PROTEIN. //0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11). //Q01042
 F-PLACE4000089
 F-PLACE4000093
 F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-14:68:60//HOMO SAPIENS (HUMAN). //P39188
 F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE; METHYLTRANSFERASE]. //1.0:46:41//BROAD BEAN MOTTLE VIRUS. //Q00020
 F-PLACE4000128//HYPOTHETICAL PROTEIN E-115. //0.00020:101:30//HUMAN ADENOVIRUS TYPE 2. //P03290
 F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN). //0.15:57:31//HOMO SAPIENS (HUMAN). //P22528
 F-PLACE4000131
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR. //1.0:45:24//BACILLUS SUBTILIS. //P45453
 F-PLACE4000156//ZINC FINGER PROTEIN 136. //2.1e-88:194:59//HOMO SAPIENS (HUMAN). //P52737
 F-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654). //0.083:148:26//HOMO SAPIENS (HUMAN). //P52746
 F-PLACE4000211//CALPHOTIN. //0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q02910
 F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:20:85//HOMO SAPIENS (HUMAN). //P39188
 F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE SYNTHASE (EC 2.1.1.45) (DHFR-TS). //1.0:96:28//TRYPANOSOMA BRUCEI BRUCEI. //Q27783
 F-PLACE4000233
 F-PLACE4000247//METALLOTHIONEIN (MT). //1.0e-05:34:41//PLEURONECTES PLATESSA (PLAICE). //P07216
 F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN). //0.99:33:42//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV). //P31834
 F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST84D

B. //0.42:24:45//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01643
 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-). //3.5e-09:189:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32639
 F-PLACE4000261//PEREGRIN (BR140 PROTEIN). //5.0e-11:103:37//HOMO SAPIENS (HUMAN). //P55201
 F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01. //0.037:181:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P25386
 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21). //1.0:46:39//MUS MUSCULUS (MOUSE). //P70375
 F-PLACE4000300//50S RIBOSOMAL PROTEIN L32. //0.81:28:46//THERMUS AQUATICUS (SUBSP. THERMOPHILUS). //P80339
 F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN). //1.6e-29:44:93//HOMO SAPIENS (HUMAN). //P42345
 F-PLACE4000323
 F-PLACE4000326//PARATHYMOXIN. //0.0018:54:48//HOMO SAPIENS (HUMAN). //P20962
 F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT). //0.97:28:42//SUS SCROFA (PIG). //Q00968
 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-I) (SHNA) (NEUROTOXIN SHI). //1.0:33:36//STOICHACTIS HELIANTHUS (CARRIBEAN SEA ANEMONE) (STICHODACTYLA HELIANTHUS). //P19651
 F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN). //0.071:42:42//SORGHUM VULGARE (SORGHUM). //P24152
 F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-16:54:77//HOMO SAPIENS (HUMAN). //P39193
 F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR. //0.25:21:52//HORDEUM VULGARE (BARLEY), AND SECALE CEREALE (RYE). //P25877
 F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOME FERRO-LYASE) (HEME SYNTHETASE) (FRAGMENT). //0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS. //Q05338
 F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-29:96:67//HOMO SAPIENS (HUMAN). //P39194
 F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-18:41:73//HOMO SAPIENS (HUMAN). //P39188
 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-). //5.4e-21:237:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32639
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SD

LI 5' REGION PRECURSOR.//0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40442
 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION FACTOR HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//P23922
 F-PLACE4000465//METALLOTHIONEIN-1L (MT-1L) (MT1X).//0.20:18:38//HOMO SAPIENS (HUMAN).//P80297
 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY!!!!//1.5e-19:73:52//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE4000489
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.17:130:30//MUS MUSCULUS (MOUSE).//Q03173
 F-PLACE4000521//RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] (FRAGMENT).//3.0e-05:50:36//MUS MUSCULUS (MOUSE).//P10400
 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.//1.8e-45:231:47//RATTUS NORVEGICUS (RAT).//Q07008
 F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHORHODOSPIRAHALOPHILA.//P00122
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55824
 F-PLACE4000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM 3).//9.7e-11:166:28//HOMO SAPIENS (HUMAN).//P16109
 F-PLACE4000590//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.6e-17:134:35//GIBBON APE LEUKEMIA VIRUS.//P21414
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//1.0:54:29//RATTUS NORVEGICUS (RAT).//P30969
 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COATPROTEIN P12; CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLONEY MURINE SARCOMA VIRUS (STRAIN TS110).//P32594
 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NRDB-INAA INTERGENIC REGION.//0.65:37:40//ESCHERICHIA COLI.//P37910
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN KOX9) (FRAGMENT).//1.0:33:33//HOMO SAPIENS (HUMAN).//P17020

F-PLACE4000654
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RP B5-CDC28 INTERGENIC REGION.//1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33313
 F-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//060100
 F-SKNMC1000013//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).//0.0013:128:35//GALLUS GALLUS (CHICKEN).//Q98937
 F-SKNMC1000046//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS ELEGANS.//P08124
 F-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.2e-41:87:98//HOMO SAPIENS (HUMAN).//P17655
 F-SKNMC1000091//NTAK PROTEIN (NEURAL- AND THYMUS-DERIVED ACTIVATOR FORERBB KINASES).//0.0032:154:35//HOMO SAPIENS (HUMAN).//014511
 F-THYR01000017//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMO OXIDASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.//Q20939
 F-THYR01000026//!!!! ALU SUBFAMILY SC WARNING ENTRY!!!!//3.0e-13:54:66//HOMO SAPIENS (HUMAN).//P39192
 F-THYR01000034//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS B VIRUS (SUBTYPE AYW).//P03163
 F-THYR01000035//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CDW52) (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763
 F-THYR01000040//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//BOS TAURUS (BOVINE).//P79244
 F-THYR01000070//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:133:36//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).//010341
 F-THYR01000072//C-PROTEIN, SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:205:29//HOMO SAPIENS (HUMAN).//Q00872
 F-THYR01000085
 F-THYR01000092//SPERM MITOCHONDRIAL CAPSULE SELENO PROTEIN (MCS).//0.063:59:33//HOMO SAPIENS (HUMAN).//P49901
 F-THYR01000107
 F-THYR01000111//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:110:67//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-THYR01000121//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66).//2.6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203

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F-THYRO1000124//TENECIN 3 PRECURSOR.//0.047:76:35/
/TENEBRIO MOLITOR (YELLOW MEALWORM).//Q27270
F-THYRO1000129//FIBROSIN (FRAGMENT).//0.35:43:34//
MUS MUSCULUS (MOUSE).//Q60791
F-THYRO1000132//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!//8.7e-14:104:42//HOMO SAPIENS (HUMAN).//P391
88
F-THYRO1000156
F-THYRO1000163//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!//3.7e-20:71:71//HOMO SAPIENS (HUMAN).//P391 10
89
F-THYRO1000173//CLATHRIN COAT ASSEMBLY PROTEIN AP4
7 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI A
DAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CL
ATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1
MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOU
SE).//P35585
F-THYRO1000186//!!!! ALU SUBFAMILY SC WARNING ENTR
Y !!!!!//2.9e-24:72:77//HOMO SAPIENS (HUMAN).//P391
92
F-THYRO1000187
F-THYRO1000190//PROTEIN TRANSPORT PROTEIN SEC61 BE
TA 2 SUBUNIT.//0.060:50:42//SACCHAROMYCES CEREVISI
AE (BAKER'S YEAST).//P52871
F-THYRO1000197
F-THYRO1000199//HYPOTHETICAL 49.8 KD PROTEIN D200
7.5 IN CHROMOSOME III.//2.0e-06:88:35//CAENORHABDI
TIS ELEGANS.//P34379
F-THYRO1000206
F-THYRO1000221
F-THYRO1000241//HYPOTHETICAL 11.8 KD PROTEIN IN HE
65-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPH A C
ALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMPV).//P
41661
F-THYRO1000242//ZINC FINGER PROTEIN 84 (ZINC FINGE
R PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HU
MAN).//P51523
F-THYRO1000253//DNA-BINDING P52/P100 COMPLEX, 100
KD SUBUNIT (FRAGMENTS).//0.11:21:52//HOMO SAPIENS
(HUMAN).//P30808
F-THYRO1000270//WDNM1 PROTEIN PRECURSOR.//0.40:52:
32//MUS MUSCULUS (MOUSE).//Q62477
F-THYRO1000279//BETA CRYSTALLIN A4.//0.97:64:26//B
OS TAURUS (BOVINE).//P11842
F-THYRO1000288//POTENTIAL CAAX PRENYL PROTEASE 1
(EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEA
SE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMY
CES POMBE (FISSION YEAST).//Q10071
F-THYRO1000320//ZINC FINGER PROTEIN 14 (ZFP-14) (K
ROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCUL 50

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US (MOUSE).//P10755
F-THYRO1000327//HYPOTHETICAL 64.7 KD PROTEIN F26E
4.11 IN CHROMOSOME I.//0.00010:75:26//CAENORHABDIT
IS ELEGANS.//P90859
F-THYRO1000343//CHROMOGRANIN A PRECURSOR (CGA) [CO
NTAINS: PANCREASTATIN; BETA-CRANIN; WE-14].//0.88:1
07:26//MUS MUSCULUS (MOUSE).//P26339
F-THYRO1000358//SELENIUM-BINDING LIVER PROTEIN.//
4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563
F-THYRO1000368//LOCOMOTION-RELATED PROTEIN HIKARU
GENKI PRECURSOR.//1.0:136:26//DROSOPHILA MELANOGAS
TER (FRUIT FLY).//Q09101
F-THYRO1000381//GAG POLYPROTEIN [CONTAINS: CORE PR
OTEIN P15; INNER COATPROTEIN P12; CORE SHELL PROTE
IN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN S
ARCOMA VIRUS.//P03330
F-THYRO1000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.3
4) (A6L).//0.90:46:30//HALICHOERUS GRYPUS (GRAY SE
AL).//P38592
20 F-THYRO1000394//SMALL PROLINE RICH PROTEIN II (SPR
-II) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HU
MAN).//P22531
F-THYRO1000395//RING CANAL PROTEIN (KELCH PROTEI
N).//1.2e-33:186:38//DROSOPHILA MELANOGASTER (FRUI
T FLY).//Q04652
F-THYRO1000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAG
MENT).//0.57:67:31//STAPHYLOCOCCUS AUREUS.//P48860
F-THYRO1000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.3
4) (A6L).//1.0:42:38//STRONGYLOCENTROTUS PURPURATU
30 S (PURPLE SEA URCHIN).//P15997
F-THYRO1000452//BACTERIOCIN CARNOBACTERIOCIN A PRE
CURSOR (PISCICOLIN 61).//0.31:34:44//CARNOBACTERIU
M PISCICOLA.//P38578
F-THYRO1000471//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!//2.1e-31:94:72//HOMO SAPIENS (HUMAN).//P391
94
F-THYRO1000484//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!//5.9e-08:30:86//HOMO SAPIENS (HUMAN).//P391
95
40 F-THYRO1000488//EARLY NODULIN 55-2 PRECURSOR (N-55
-2) (NODULIN-315).//0.93:98:27//GLYCINE MAX (SOYBE
AN).//Q02917
F-THYRO1000501//DOWN REGULATORY PROTEIN OF INTERLE
UKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MO
USE).//P15533
F-THYRO1000502//HUNCHBACK PROTEIN (FRAGMENT).//0.8
4:41:43//APIS MELLIFERA (HONEYBEE).//P31504
F-THYRO1000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:
231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN H
50 ERPESVIRUS 4).//P03181

3141

F-THYR01000558//ANTITHROMBIN-III PRECURSOR (ATIII)
(FRAGMENT).//0.47:58:37//GALLUS GALLUS (CHICKEN).
//Q03352
F-THYR01000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMEN
TS).//0.00048:64:42//RATTUS NORVEGICUS (RAT).//P02
454
F-THYR01000570//HYPOTHETICAL 11.6 KD PROTEIN IN AC
S1-GCV3 INTERGENIC REGION.//0.94:61:32//SACCHAROMY
CES CEREVISIAE (BAKER'S YEAST).//P39725
F-THYR01000585//SPLICING FACTOR, ARGININE/SERINE-R
ICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:10
4:36//HOMO SAPIENS (HUMAN).//Q13247
F-THYR01000596//INFECTED CELL PROTEIN ICP34.5 (NEU
ROVIRULENCE FACTOR ICP34.5).//0.99:37:40//HERPES S
IMPLEX VIRUS (TYPE 1 / STRAIN MGH-10).//P37319
F-THYR01000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.
88:61:34//EIMERIA ACERVULINA.//P21959
F-THYR01000605//SUPPRESSOR PROTEIN SRP40.//0.0016:
116:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
P32583
F-THYR01000625//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/3.4e-33:88:78//HOMO SAPIENS (HUMAN).//P391
94
F-THYR01000637//METALLOTHIONEIN A (MT A).//1.0:23:
43//SPARUS AURATA (GILTHEAD SEA BREAM).//P52727
F-THYR01000641//PHOTOSYSTEM II 10 KD PHOSPHOPROTEI
N.//0.99:26:46//CYANIDIUM CALDARIUM (GALDIERIA SUL
PHURARIA).//O19925
F-THYR01000658//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!/1.5e-49:116:69//HOMO SAPIENS (HUMAN).//P39
189
F-THYR01000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//
3.7e-15:119:43//ESCHERICHIA COLI.//Q47155
F-THYR01000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-4
4:232:41//CHLAMYDOMONAS REINHARDTII.//P46870
F-THYR01000676//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!!/2.1e-15:144:39//HOMO SAPIENS (HUMAN).//P39
193
F-THYR01000684//HYPOTHETICAL 73.5 KD PROTEIN IN SC
S3-RPS2 INTERGENIC REGION.//0.00033:84:30//SACCHAR
OMYCES CEREVISIAE (BAKER'S YEAST).//P53129
F-THYR01000699//!!!! ALU SUBFAMILY SC WARNING ENTR
Y !!!!!/0.97:20:85//HOMO SAPIENS (HUMAN).//P39192
F-THYR01000712//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/4.2e-10:69:59//HOMO SAPIENS (HUMAN).//P3918
8
F-THYR01000715//SALIVARY PROLINE-RICH PROTEIN PREC
URSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PE
PTIDE 1B-6; PEPTIDE P-H].//4.6e-10:204:32//HOMO SA
PIENS (HUMAN).//P04280

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F-THYR01000734
F-THYR01000748//HYPOTHETICAL PROTEIN KIAA0411 (FRA
GMENT).//1.8e-46:130:70//HOMO SAPIENS (HUMAN).//04
3295
F-THYR01000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPH
A-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACII
I) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS (RAT)./
/Q64686
F-THYR01000777//CUTICLE COLLAGEN 2C (FRAGMENT).//
0.0031:119:34//HAEMONCHUS CONTORTUS.//P16252
F-THYR01000783//MYOSIN IC HEAVY CHAIN.//0.0014:12
1:37//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-THYR01000787//HUNCHBACK PROTEIN (FRAGMENT).//0.5
4:25:52//PHOLCUS PHALANGIODES.//Q02031
F-THYR01000793//PRE-MRNA SPLICING FACTOR PRP9.//0.
91:30:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P19736
F-THYR01000796
F-THYR01000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100
KD PROTEIN REGION.//0.081:31:38//HUMAN ADENOVIRUS
TYPE 41.//P23691
F-THYR01000815//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!/6.0e-30:81:70//HOMO SAPIENS (HUMAN).//P391
95
F-THYR01000829//NEUROTOXIN III (BOM III).//0.022:3
2:34//BUTHUS OCCITANUS MARDOCHEI (MOROCCAN SCORPIO
N).//P13488
F-THYR01000843//HYPOTHETICAL 7.7 KD PROTEIN IN GEN
ES 5-4 INTERGENIC REGION (ORF 109).//0.98:25:44//B
ACTERIOPHAGE P22.//P26750
F-THYR01000852//SULFATED SURFACE GLYCOPROTEIN 185
(SSG 185).//7.3e-09:83:42//VOLVOX CARTERI.//P21997
F-THYR01000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//
1.0:54:35//PSEUDOPLEURONECTA AMERICANUS (WINTER FL
OUNDER).//P02734
F-THYR01000865//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/5.2e-17:66:57//HOMO SAPIENS (HUMAN).//P3918
8
F-THYR01000895//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!/1.0e-12:58:62//HOMO SAPIENS (HUMAN).//P391
89
F-THYR01000916//!!!! ALU SUBFAMILY SB WARNING ENTR
Y !!!!!/2.0e-32:101:69//HOMO SAPIENS (HUMAN).//P39
189
F-THYR01000926//NITROGEN FIXATION REGULATORY PROTE
IN.//5.5e-05:108:27//KLEBSIELLA OXYTOCA.//P56267
F-THYR01000934//PYRROLINE-5-CARBOXYLATE REDUCTASE
(EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//3.9e-50:147:
40//HOMO SAPIENS (HUMAN).//P32322
50 F-THYR01000951//DIHYDROXYACETONE KINASE (EC 2.7.1.

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29) (GLYCERONE KINASE).//1.8e-31:136:56//CITROBACTER FREUNDII.//P45510
 F-THYRO1000952//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
 F-THYRO1000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PRECURSOR.//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32580
 F-THYRO1000975
 F-THYRO1000983//HYPOTHETICAL 48.1 KD PROTEIN B040 3.2 IN CHROMOSOME X.//1.3e-20:96:51//CAENORHABDITIS ELEGANS.//Q11076
 F-THYRO1000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROTEIN.//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160
 F-THYRO1000988
 F-THYRO1001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSC L-RPLQ INTERGENIC REGION.//0.97:60:31//ESCHERICHIA COLI.//P36675
 F-THYRO1001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.5e-18:56:66//HOMO SAPIENS (HUMAN).//P39195
 F-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:126:35//HOMO SAPIENS (HUMAN).//P31948
 F-THYRO1001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-35:97:79//HOMO SAPIENS (HUMAN).//P39194
 F-THYRO1001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN).//P39194
 F-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS (HUMAN).//P98168
 F-THYRO1001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).//0.00068:160:31//HOMO SAPIENS (HUMAN).//Q15427
 F-THYRO1001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME I.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
 F-THYRO1001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN).//P39188
 F-THYRO1001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161
 F-THYRO1001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN).//P39194
 F-THYRO1001173//CYTOCHROME C OXIDASE POLYPEPTIDE V

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11S (EC 1.9.3.1).//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610
 F-THYRO1001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN).//P39192
 F-THYRO1001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:165:39//MUS MUSCULUS (MOUSE).//P08043
 F-THYRO1001204//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//0.67:42:42//HOMOSAPIENS (HUMAN).//P02811
 F-THYRO1001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMAN).//P39194
 F-THYRO1001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN).//P39193
 F-THYRO1001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62:126:30//STREPTOMYCES FRADIAE.//P20186
 F-THYRO1001287//HYPOTHETICAL 91.2 KD PROTEIN IN RP S4B-SCH9 INTERGENIC REGION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
 F-THYRO1001290//GIANT HEMOGLOBIN A1V CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413
 F-THYRO1001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5.//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
 F-THYRO1001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258
 F-THYRO1001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN).//P39188
 F-THYRO1001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21123
 F-THYRO1001347//TOXIN F-VIII PRECURSOR (TOXIN TA2) (TOXIN DAF8).//0.94:61:36//DENDROASPIS ANGUSTICEPS (EASTERN GREEN MAMBA).//P01404
 F-THYRO1001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0025:23:73//HOMO SAPIENS (HUMAN).//P39188
 F-THYRO1001365//MERSACIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).//P43683
 F-THYRO1001374//PROTEIN VDL.//1.6e-13:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//005729
 F-THYRO1001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.047:43:48//HOMO SAPIENS (HUMAN).//P39192
 F-THYRO1001403
 F-THYRO1001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:42//HOMO SAPIENS (HUMAN).//P22531

- F-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK
-I (EC 1.1.1.-) //3.1e-81:97:83//MUS MUSCULUS (MOU
SE) //070503
- F-THYRO1001411//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!!/1.9e-26:89:74//HOMO SAPIENS (HUMAN) //P391
93
- F-THYRO1001426//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!!/1.4e-09:55:61//HOMO SAPIENS (HUMAN) //P391
93
- F-THYRO1001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-
4) //0.68:44:34//BOS TAURUS (BOVINE) //P46162
- F-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE
B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-
B) //3.8e-64:216:62//HOMO SAPIENS (HUMAN) //P35580
- F-THYRO1001480//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/9.3e-29:88:75//HOMO SAPIENS (HUMAN) //P391
94
- F-THYRO1001487//HOMEBOX PROTEIN HOX-B4 (HOX-2.6).
//0.99:59:37//MUS MUSCULUS (MOUSE) //P10284
- F-THYRO1001534//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/1.4e-14:40:82//HOMO SAPIENS (HUMAN) //P391
94
- F-THYRO1001537//HYPOTHETICAL 33.8 KD PROTEIN IN TW
T1-FL05 INTERGENIC REGION. //2.4e-07:142:32//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST) //P38892
- F-THYRO1001541//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!/0.98:26:61//HOMO SAPIENS (HUMAN) //P39195
- F-THYRO1001559//PROTEIN Q300. //2.6e-05:20:75//MUS
MUSCULUS (MOUSE) //Q02722
- F-THYRO1001570
- F-THYRO1001573//SPERM MITOCHONDRIAL CAPSULE SELENO
PROTEIN (MCS) //0.033:71:36//MUS MUSCULUS (MOUSE).
//P15265
- F-THYRO1001584//SUPPRESSOR PROTEIN SRP40. //2.1e-0
5:188:27//SACCHAROMYCESCEREVISIAE (BAKER'S YEAST).
//P32583
- F-THYRO1001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1)
(RSP-1 PROTEIN) (RSP-1) //6.1e-21:35:91//HOMO SAPI
ENS (HUMAN) //Q15404
- F-THYRO1001602//TRK SYSTEM POTASSIUM UPTAKE PROTEI
N TRKH. //1.0:57:42//HAEMOPHILUS INFLUENZAE. //P4484
3
- F-THYRO1001605//VENOM BASIC PROTEASE INHIBITORS IX
AND VIIIB. //1.0:34:38//BUNGARUS FASCIATUS (BANDED
KRAIT) //P25660
- F-THYRO1001617//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/7.0e-18:55:81//HOMO SAPIENS (HUMAN) //P391
94
- F-THYRO1001637//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!/0.00020:25:80//HOMO SAPIENS (HUMAN) //P391
- 95
- F-THYRO1001656//PROLINE-RICH PROTEIN MP-2 PRECURSO
R. //0.0091:54:42//MUSMUSCULUS (MOUSE) //P05142
- F-THYRO1001661//HYPOTHETICAL 21.1 KD PROTEIN IN SS
R-SERA INTERGENIC REGION (0182) //0.033:77:35//ESC
HERICHIA COLI. //P09160
- F-THYRO1001671//((2'-5')) OLIGOADENYLATE SYNTHETASE 1
(EC 2.7.7.-) ((2-5')) OLIGO(A) SYNTHETASE 1) (2-5A
SYNTHETASE 1) (P46/P41) (E18/E16) //4.3e-34:207:34
//HOMO SAPIENS (HUMAN) //P00973
- F-THYRO1001673//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/3.9e-08:49:65//HOMO SAPIENS (HUMAN) //P391
94
- F-THYRO1001703//HYPOTHETICAL 69.8 KD PROTEIN IN BD
F1-SFP1 INTERGENIC REGION. //6.4e-16:134:35//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST) //Q06053F-THYRO
1001706
- F-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEI
N) //2.7e-27:191:36//DROSOPHILA MELANOGASTER (FRUI
T FLY) //Q04652
- F-THYRO1001738//MATING PROCESS PROTEIN MID2 (SERIN
E-RICH PROTEIN SMS1) (PROTEIN KINASE A INTERFERENC
E PROTEIN) //0.0032:105:32//SACCHAROMYCES CEREVISI
AE (BAKER'S YEAST) //P36027
- F-THYRO1001745
- F-THYRO1001746//GENE 10 PROTEIN. //1.0:55:30//SPIRO
PLASMA VIRUS SPV1-R8A2B. //P15901
- F-THYRO1001772//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/1.2e-05:41:63//HOMO SAPIENS (HUMAN) //P3918
- 30 8
- F-THYRO1001793//HYPOTHETICAL 21.6 KD PROTEIN F37A
4.2 IN CHROMOSOME III. //1.5e-26:161:42//CAENORHABD
ITIS ELEGANS. //P41880
- F-THYRO1001809//LATENCY-RELATED PROTEIN 2. //0.49:7
4:27//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F) //P
17589
- F-THYRO1001828//PROTEINASE INHIBITOR. //0.11:34:50/
/SOLANUM MELONGENA (EGGPLANT) (AUBERGINE) //P01078
- F-THYRO1001854//ACYL-COA-BINDING PROTEIN HOMOLOG
(ACBP) (DIAZEPAM BINDING INHIBITOR HOMOLOG) (DBI).
//0.63:50:38//RANA RIDIBUNDA (LAUGHING FROG) (MARSH
FROG) //P45883
- F-THYRO1001895//!!!! ALU SUBFAMILY J WARNING ENTRY
!!!!/6.1e-09:72:47//HOMO SAPIENS (HUMAN) //P3918
8
- F-THYRO1001907//TRYPOMASTIGOTE DECAY-ACCELERATING
FACTOR (T-DAF) (FRAGMENT) //0.79:36:44//TRYPANOSOM
A CRUZI. //Q26327
- F-VESEN1000122//HOMEBOX PROTEIN HB9. //0.57:64:32/
/HOMO SAPIENS (HUMAN) //P50219
- 50

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F-Y79AA1000013//METALLOTHIONEIN B (MT-B). //0.034: 35:48//SALMO SALAR (ATLANTIC SALMON). //P52720
 F-Y79AA1000033//CHOLECYSTOKININ. //0.97:49:30//PSEUDEMYS SCRIPTA (SLIDERTURTLE). //P80345
 F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1. //1.4e-23:80:60//HOMO SAPIENS (HUMAN). //P35226
 F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556. //0.0075:127:36//STREPTOMYCES FRADIAE. //P20186
 F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.022:135:29//HOMO SAPIENS (HUMAN). //P10162
 F-Y79AA1000131//REGULATORY PROTEIN E2. //1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24. //P50770
 F-Y79AA1000181//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //1.4e-06:187:29//MUS MUSCULUS (MOUSE). //P05143
 F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT). //6.2e-09:47:53//OWENIA FUSIFORMIS. //P21260
 F-Y79AA1000214//HISTONE H2A VARIANT. //1.7e-50:107:100//GALLUS GALLUS (CHICKEN). //P02272
 F-Y79AA1000230//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HORMONE-RELEASING HORMONE I) (GONADOTROPIN-RELEASING HORMONE I) (GNRH I) (LULIBERIN I). //0.27:64:34//HOMO SAPIENS (HUMAN). //P01148
 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN M021B04.12. //2.5e-72:277:53//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //004658
 F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR. //2.8e-08:174:35//MUS MUSCULUS (MOUSE). //P05142
 F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT). //0.00020:176:33//RATTUS NORVEGICUS (RAT). //P13941
 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A3.1 IN CHROMOSOME III. //0.092:127:21//CAENORHABDITIS ELEGANS. //Q09260
 F-Y79AA1000328//SEL-10 PROTEIN. //5.3e-05:129:28//CAENORHABDITIS ELEGANS. //Q93794
 F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN). //1.0:73:30//OVIS ARIES (SHEEP). //P26372
 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP). //1.8e-95:205:83//BOS TAURUS (BOVINE). //P53620
 F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR. //0.036:37:54//PSEUDOPLEURONECTA AMERICANUS (WINTER FLOUNDER). //P02734
 F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME III. //0.0031:106:28//CAENORHABDITIS ELEGANS. //Q10120

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F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161. //1.4e-16:208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P25343
 F-Y79AA1000405//LIGHT-HARVESTING PROTEIN B-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN C) (LH II-C ALPHA). //0.98:50:30//RHODOPSEUDOMONAS PALUSTRIS. //P35103
 F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!! //7.9e-20:62:79//HOMO SAPIENS (HUMAN). //P39194
 F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UM E3-HDA1 INTERGENIC REGION. //1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53970
 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F44B9.5 IN CHROMOSOME III. //2.8e-34:211:40//CAENORHABDITIS ELEGANS. //P34426
 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN C1F3.09 IN CHROMOSOME I. //3.9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10414
 F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!! //0.37:41:48//HOMO SAPIENS (HUMAN). //P39195
 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //1.8e-21:190:37//HOMO SAPIENS (HUMAN). //Q08170
 F-Y79AA1000540//SPERM PROTAMINE P1. //0.00045:66:45//DASYRUS VIVERRINUS (SOUTHEASTERN QUOLL), AND DASYRUS HALLUCATUS. //P42135
 F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR H A2/AP2 ADAPTIN ALPHA C SUBUNIT). //1.6e-79:186:87//MUS MUSCULUS (MOUSE). //P17427
 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-.-) (FRAGMENT). //0.010:35:60//STREPTOMYCES PEUCETIUS. //P32009
 F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION. //4.5e-27:197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P28320
 F-Y79AA1000627//ZINC FINGER PROTEIN 134. //1.6e-34:191:35//HOMO SAPIENS (HUMAN). //P52741
 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION. //8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P31380
 F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A). //0.00037:108:27//CANDIDA BOIDINII (YEAST). //Q00316
 F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III. //1.0e-23:210:34//CAENORHABDITIS ELEGANS. //Q09316
 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIB

3149

ONUCLEOPROTEIN X (HNRNP X) (CBP). //1.4e-53:156:68/
/MUS MUSCULUS (MOUSE). //Q61990

F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RR
N10-MCM2 INTERGENIC REGION. //1.2e-11:231:26//SACCH
AROMYCES CEREVISIAE (BAKER'S YEAST). //P38205

F-Y79AA1000782//CUTICLE COLLAGEN 2. //0.012:56:35//
CAENORHABDITIS ELEGANS. //P17656

F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECUR
SOR. //1.3e-08:82:39//PLASMODIUM LOPHURAE. //P04929

F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100
KD SUBUNIT (FRAGMENTS). //0.043:13:53//HOMO SAPIENS
(HUMAN). //P30808

F-Y79AA1000800//PRIA PROTEIN PRECURSOR. //0.031:94:
34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS
EDODES). //Q01200

F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RP
S3-PSD1 INTERGENIC REGION. //0.26:186:23//SACCHAROM
YCES CEREVISIAE (BAKER'S YEAST). //P53882

F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADE
NYLATE DEAMINASE). //0.99:78:35//SCHIZOSACCHAROMYCE
S POMBE (FISSION YEAST). //P50998

F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MO
L1-NAT2 INTERGENIC REGION. //3.4e-44:111:49//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST). //P48234

F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN. //0.004
6:187:33//EPSTEIN-BARRVIRUS (STRAIN B95-8) (HUMAN
HERPESVIRUS 4). //P03181

F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN. //1.0e-75:23
9:66//CRICETULUS GRISEUS (CHINESE HAMSTER). //P0520
9

F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN II (SPR
-II) (CLONE 174N). //0.0078:57:31//HOMO SAPIENS (HU
MAN). //P22532

F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH
MUSCLE. //8.5e-11:241:26//GALLUS GALLUS (CHICKEN).
//P10587

F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34)
(PROTEIN 6). //0.69:122:31//TRYPANOSOMA BRUCEI BRU
CEI. //P24499

F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-
2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).
//3.3e-102:211:93//RATTUS NORVEGICUS (RAT). //P7054
1

F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECU
RSOR. //1.0:67:38//GALLUS GALLUS (CHICKEN). //P02457

F-Y79AA1000976//INVOLUCRIN. //0.99:66:31//CEBUS ALB
IFRONS (WHITE-FRONTEDCAPUCHIN). //P24709

F-Y79AA1000985//PERICENTRIN. //1.1e-24:116:59//MUS
MUSCULUS (MOUSE). //P48725

F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN A 50

3150

AC3-RFC5 INTERGENIC REGION. //0.37:79:27//SACCHAROM
YCES CEREVISIAE (BAKER'S YEAST). //P38250

F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CON
TAINS: SPERM PROTAMINESP1]. //0.93:43:39//SEPIA OFF
ICINALIS (COMMON CUTTLEFISH). //P80001

F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-
CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD). //
1.5e-51:211:52//BOS TAURUS (BOVINE). //P48818

F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTR
Y !!!!!/3.8e-25:85:69//HOMO SAPIENS (HUMAN). //P391
94

F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PREC
URSOR [CONTAINS: CHONDROCALCIN]. //0.0015:207:33//M
US MUSCULUS (MOUSE). //P28481

F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PRO
TEIN 11.9 (ACP 11.9). //0.99:36:41//ARANEUS DIADEMA
TUS (SPIDER). //P80515

F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN KO2D1
0.1 IN CHROMOSOME III. //1.0e-06:197:23//CAENORHABD
ITIS ELEGANS. //P34492

F-Y79AA1001105//HOMEODOMAIN PROTEIN OTX2. //2.9e-62:16
3:79//MUS MUSCULUS (MOUSE). //P80206

F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTR
Y !!!!!/0.024:42:59//HOMO SAPIENS (HUMAN). //P39195

F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP
2-VLF1 INTERGENIC REGION. //0.96:20:50//AUTOGRAPHIA
CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACMNPV). //
P41471

F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN. //3.9e-
05:135:34//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMA
N HERPESVIRUS 4). //P03181

F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.
//0.00017:93:38//CAENORHABDITIS ELEGANS. //Q09456

F-Y79AA1001211

F-Y79AA1001216//TENSIN. //0.012:134:32//GALLUS GALL
US (CHICKEN). //Q04205

F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCI
N 2). //0.088:75:34//HOMO SAPIENS (HUMAN). //Q02817

F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1
(EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTER
OID DEHYDROGENASE 1). //1.1e-40:139:51//RATTUS NORV
EGICUS (RAT). //P51657

F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN OR
C2-TIP1 INTERGENIC REGION. //2.0e-22:108:53//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST). //P38238

F-Y79AA1001281

F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGEN
T). //0.0022:49:44//MUSMUSCULUS (MOUSE). //P05143

F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROP
LAST PRECURSOR. //0.98:117:25//ARABIDOPSIS THALIANA

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(MOUSE-EAR CRESS). //P92959
 F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN 1) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP). //0.082:44:40//SUS SCROFA (PIG). //P35323
 F-Y79AA1001384//APOLIPROTEIN C-III PRECURSOR (APO-CIII). //0.99:47:40//MUS MUSCULUS (MOUSE). //P33622
 F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J). //9.8e-58:157:62//HOMOSAPIENS (HUMAN). //P31271
 F-Y79AA1001394//TRICHOHYALIN. //4.7e-08:121:36//HOMO SAPIENS (HUMAN). //Q07283
 F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ER F. //0.0087:81:33//MUS MUSCULUS (MOUSE). //P70459
 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B040 3.2 IN CHROMOSOME X. //4.5e-21:125:44//CAENORHABDITIS ELEGANS. //Q11076
 F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PF K1-TDS4 INTERGENIC REGION. //2.3e-17:249:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53313
 F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE I 49 K D POLYPEPTIDE (EC 2.7.7.6) (A49). //0.0099:155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q01080
 F-Y79AA1001541
 F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN). //P39192
 F-Y79AA1001555//MAJOR SURFACE ANTIGEN. //0.046:62:29//HEPATITIS B VIRUS. //P31873
 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME). //8.6e-11:144:31//ESCHERICHIA COLI. //P27550
 F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENO PROTEIN (MCS). //0.012:64:40//MUS MUSCULUS (MOUSE). //P15265
 F-Y79AA1001594//CORNIFIN BETA. //0.61:88:31//MUS MUSCULUS (MOUSE). //009116
 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TF IID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130). //0.024:170:30//HOMO SAPIENS (HUMAN). //000268
 F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1). //4.5e-09:136:27//HOMO SAPIENS (HUMAN). //P28698
 F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY27 7.20C. //0.093:94:26//MYCOBACTERIUM TUBERCULOSIS. //P71779
 F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1). //0.79:90:26//MUS MUSCULUS (MOUSE). //P40764

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F-Y79AA1001679//LAMBDA-CRYSTALLIN. //1.6e-95:224:81//ORYCTOLAGUS CUNICULUS (RABBIT). //P14755
 F-Y79AA1001692//GERM CELL-LESS PROTEIN. //3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01820
 F-Y79AA1001696//INSULIN. //1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL). //P42633
 F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN. //0.0013:192:33//EPSTEIN-BARRVIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). //P03181
 10 F-Y79AA1001711//PARATHYMOSIN (ZINC-BINDING 11.5 KD PROTEIN). //0.032:38:34//RATTUS NORVEGICUS (RAT). //P04550
 F-Y79AA1001781
 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP). //0.0063:128:30//HOMO SAPIENS (HUMAN). //P50552
 F-Y79AA1001827//SPERM PROTAMINE P1. //0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OP OSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM). //P35305
 20 F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN). //P39188
 F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT). //1.8e-10:63:44//PSYCHODA CINEREA. //Q02035
 F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10). //0.00036:108:37//MUS MUSCULUS (MOUSE). //Q61967
 F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN). //3.2e-07:100:35//HOMO SAPIENS (HUMAN). //P43489
 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD). //0.020:25:64//HOMO SAPIENS (HUMAN). //P20931
 F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.016:83:36//HOMO SAPIENS (HUMAN). //P10162
 F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C. //8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //042643
 F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42). //9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //P42743
 F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS). //0.036:53:45//HOMO SAPIENS (HUMAN). //P30808
 50 F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN FO2A

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9.4 IN CHROMOSOME III. //0.12:171:22//CAENORHABDITI
S ELEGANS. //P34384
F-Y79AA1002093//MAX PROTEIN. //3.1e-07:111:29//BRAC
HYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO). //P52161
F-Y79AA1002103//SHORT NEUROTOXIN C. //0.040:21:47//
AIPYSURUS LAEVIS (OLIVE SEA SNAKE). //P19958
F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827. //0.8
4:68:30//METHANOCOCCUSJANNASCHII. //Q58237
F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN PO
M152-REC114 INTERGENIC REGION. //3.4e-29:197:39//SAC 10
CHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40206
F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1). //
1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FL
Y). //Q24133
F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6). //
0.0011:162:32//MUS MUSCULUS (MOUSE). //P70327
F-Y79AA1002208//ANKYRIN. //2.9e-08:231:29//MUS MUSC
ULUS (MOUSE). //Q02357
F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHOND
RIAL PRECURSOR (EC 6.1.1.1) (TYROSINE--TRNA LIGAS 20
E) (TYRRS). //3.7e-23:170:32//SACCHAROMYCES CEREVIS
IAE (BAKER'S YEAST). //P48527
F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PRO
TEIN IA) (SPR-IA) (SPRK). //0.0061:69:31//HOMO SAPI
ENS (HUMAN). //P35321
F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTR
Y !!!!!/9.2e-10:43:62//HOMO SAPIENS (HUMAN). //P391
93
F-Y79AA1002220
F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F 30
8.17C IN CHROMOSOME I. //1.9e-21:147:40//SCHIZOSACC
HAROMYCES POMBE (FISSION YEAST). //Q10264
F-Y79AA1002234
F-Y79AA1002246//MYOSIN IC HEAVY CHAIN. //0.00066:13
1:34//ACANTHAMOEBA CASTELLANII (AMOEB). //P10569
F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK37
0.3 IN CHROMOSOME III. //4.3e-45:164:48//CAENORHABD
ITIS ELEGANS. //Q02328
F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO
(ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0. 40
0063:99:31//HOMO SAPIENS (HUMAN). //P10161
F-Y79AA1002307
F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G
6.5 IN CHROMOSOME III. //0.75:198:24//CAENORHABDITI
S ELEGANS. //P46012
F-Y79AA1002351//CUTICLE COLLAGEN 34. //0.74:128:35/
/CAENORHABDITIS ELEGANS. //P34687
F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2. //0.05
0:71:29//SACCHAROMYCESCEREVISIAE (BAKER'S YEAST). //
/P40036

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F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROT
EIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN
-BINDING PROTEIN P-57). //1.0:89:30//CARASSIUS AURA
TUS (GOLDFISH). //P17691
F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YG
P1-YCK2 INTERGENIC REGION. //3.7e-16:232:28//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST). //P53899
F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AM
MONIA LIGASE) (CTP SYNTHETASE). //6.7e-72:162:84//H
OMO SAPIENS (HUMAN). //P17812
F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR
-II) (CLONE 930). //0.81:34:41//HOMO SAPIENS (HUMA
N). //P22531
F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68. /
/0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S
YEAST). //P32558
F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35). //
2.3e-60:217:44//MUS MUSCULUS (MOUSE). //P15620
F-Y79AA1002482//ZINC FINGER PROTEIN 141. //2.0e-31:
90:55//HOMO SAPIENS (HUMAN). //Q15928
F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEA
TS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I. //
0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEA
ST). //P87053

【1123】 同源性検索結果データ 2.

5'末端クローン配列に対するESTとSTSを除いたGenBank
同源性検索結果データ

各データはクローン配列名、トップヒットデータのDefi
nition、P値:比較配列の長さ (base):同源性(%), トップ
ヒットデータのAccession No.の順に//で区切って記載
した。なお、同源性のスコアのP値が1より大であった
場合はデータは示さない。

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein
1 mRNA, complete cds. //3.4e-106:695:86//L16953
F-HEMBA1000012//Caenorhabditis elegans cosmid C16C
10, complete sequence. //1.5e-24:374:66//Z46787
F-HEMBA1000020//Homo sapiens beta 2 gene. //3.5e-11
2:529:90//X02344
F-HEMBA1000030//Rattus norvegicus G protein-couple
d receptor kinase-associated ADP ribosylation fact
or GTPase-activating protein (GIT1) mRNA, complete
cds. //5.6e-124:743:88//AF085693
F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone
pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pi
eces. //1.1e-25:529:65//AC004581
F-HEMBA1000046//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 12513, WORKING DRAFT SE
QUENCE. //3.2e-11:330:63//AL033528
F-HEMBA1000050//Homo sapiens DNA sequence from PAC
172K10 on chromosome6q24. Contains STS, GSS and c

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hromosome 6 fragment, complete sequence.//0.32:40
7:59//AL022477
F-HEMBA1000076//Homo sapiens full length insert cD
NA clone ZB97G06.//6.2e-135:594:98//AF086182
F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sa
piens genomic clone 2291M18, genomic survey sequen
ce.//2.8e-16:132:79//AQ004134
F-HEMBA1000129//Homo sapiens chromosome 17, clone
HCIT48C15, complete sequence.//8.6e-98:230:93//AC0
03104
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 pro
tein, partial cds.//2.1e-167:791:98//AB018340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 pro
tein, partial cds.//2.2e-44:242:96//AB018331
F-HEMBA1000156//Rattus norvegicus scaffold attachm
ent factor B mRNA, complete cds.//1.1e-10:409:60//
AF056324
F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial
cds.//1.6e-35:365:73//U80741
F-HEMBA1000168//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 321D2, WORKING DRAFT SE
QUENCE.//0.99:290:61//AL031033
F-HEMBA1000180//rat u2 small nuclear rna gene and
flanks.//3.7e-18:112:98//K00034
F-HEMBA1000185
F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:1
91:67//L19476
F-HEMBA1000201//Human Ini1 mRNA, complete cds.//2.
0e-73:440:92//U04847
F-HEMBA1000213//Plasmodium falciparum MAL3P7, comp
lete sequence.//0.90:332:59//AL034559
F-HEMBA1000216//Mus musculus hypoxia inducible fac
tor three alpha mRNA, complete cds.//4.8e-117:585:8
3//AF060194
F-HEMBA1000227//H.sapiens CpG island DNA genomic M
sel fragment, clone 179h6, reverse read cpg179h6.r
tla.//1.9e-14:95:98//Z64921
F-HEMBA1000231//H.sapiens CpG island DNA genomic M
sel fragment, clone 90a5, reverse read cpg90a5.rtl
a.//5.1e-34:186:97//Z56144
F-HEMBA1000243//Human DNA sequence from PAC 440021
on chromosome X contains ESTs and STS.//4.1e-67:2
91:82//Z84481
F-HEMBA1000244//M.musculus Ank-1 mRNA for erythroi
d ankyrin.//0.029:316:59//X69065
F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 f
rom 7q11.23-q21.1, complete sequence.//0.35:467:60
//AC004454
F-HEMBA1000264
F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORK

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ING DRAFT SEQUENCE, 2unordered pieces.//8.9e-20:21
8:78//AC004825
F-HEMBA1000282//Homo sapiens chromosome Y, clone 2
64.H.20, complete sequence.//4.2e-08:134:77//AC004
617
F-HEMBA1000288//345L5.TPB CIT978SKA1 Homo sapiens
genomic clone A-345L05, genomic survey sequence.//
1.1e-06:152:73//B17459
F-HEMBA1000290//Human ornithine decarboxylase gen
e, complete cds.//3.2e-11:507:62//M33764
F-HEMBA1000302//CIT-HSP-2169N13.TF CIT-HSP Homo sa
piens genomic clone 2169N13, genomic survey sequen
ce.//5.4e-06:86:88//B90730
F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH)
mRNA, complete cds.//7.9e-111:701:86//AF030131
F-HEMBA1000304//HS_3006_A1_A09_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3006 Col=17 Row=A, genomic surveysequenc
e.//5.2e-40:240:92//AQ118226
F-HEMBA1000307//Mus musculus mRNA for CDV-1R prote
in.//7.9e-127:815:84//Y10495
F-HEMBA1000327//HS_3124_B2_H08_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3124 Col=16 Row=P, genomic surveysequenc
e.//1.4e-11:87:96//AQ187492
F-HEMBA1000333
F-HEMBA1000338//Homo sapiens chromosome X, PAC 671
D9, complete sequence.//4.0e-66:271:84//AF031078
F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 f
rom 7q11.23-q21, complete sequence.//0.64:334:60//
AC004848
F-HEMBA1000355//Pseudorabies virus serine/threonin
e kinase (ULPK) gene, partial cds and alkaline nucl
ease (AN) gene, complete cds.//0.017:313:63//U2505
6
F-HEMBA1000356//Oryctolagus cuniculus troponin T c
ardiac isoform mRNA, 3' end of cds.//0.87:198:61//
L40178
F-HEMBA1000357//HS_3194_A1_D05_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3194 Col=9 Row=G, genomic survey sequenc
e.//6.5e-90:436:98//AQ173748
F-HEMBA1000366//HS_3027_B2_G06_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3027 Col=12 Row=N, genomic surveysequenc
e.//0.0074:192:64//AQ128843
F-HEMBA1000369//Human DNA sequence from clone 1039
K5 on chromosome 22q12.3-13.2 Contains gene simila
r to PICK1 perinuclear binding protein, genesimila
r to monocarboxylate transporter (MCT3), ESTs, ST

3157

S, CSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587
 F-HEMBA1000376//Homo sapiens chromosome 19, BAC CI T-B-393115 (BC301323), complete sequence.//1.6e-22:659:63//AC006116
 F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPC111-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122
 F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from 7p15, complete sequence.//3.5e-111:284:95//AC004520
 F-HEMBA1000392//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984
 F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460
 F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409
 F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584
 F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112
 F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554
 F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393
 F-HEMBA1000442
 F-HEMBA1000456//RPC111-30J5.TV RPC111 Homo sapiens genomic clone RPC111-30J5, genomic survey sequence.//6.3e-06:62:96//B85188
 F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808
 F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//2.8e-154:746:98//AC004839
 F-HEMBA1000464//Homo sapiens, clone hRPK.15_A.1, complete sequence.//4.8e-25:397:72//AC006213
 F-HEMBA1000469//CIT-HSP-2167P21.TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160
 F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PACC Clone p_m11 In BCRL2-CGT Region, complete sequence.//4.2e-53:312:93//AC004033
 F-HEMBA1000490//Campylobacter jejuni groES, groEL 50

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genes.//0.59:451:62//Y13334
 F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transforming p21 gene.//8.6e-06:338:58//X00740
 F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence.//9.4e-41:591:69//AC005884
 F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666
 F-HEMBA1000505
 F-HEMBA1000508//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTCS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661
 F-HEMBA1000518//Caenorhabditis elegans cosmid C17H12.//0.96:425:58//AF045642
 F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616
 F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006
 F-HEMBA1000523
 F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.//3.9e-35:290:80//U08215
 F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177_H_5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973
 F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project).//0.057:265:63//AL033545
 F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//1.2e-110:572:88//D89340
 F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z49237
 F-HEMBA1000555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//3.2e-175:838:98//AL034555
 F-HEMBA1000557//CIT-HSP-2369F15.TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence.//2.8e-32:315:78//AQ074611
 F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//3.4e-69:665:72//U92564
 F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.59:261:61//AC005504

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F-HEMBA1000568//HS_3243_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=B, genomic survey sequence. //3.1e-54:323:91//AQ219628

F-HEMBA1000569//M.musculus mRNA for GPI-anchored protein. //1.4e-19:440:61//X89571

F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces. //0.0016:557:57//AC005506

F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds. //1.7e-11:132:79//AF045573

F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein. //7.3e-43:228:97//AJ007509

F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence. //7.3e-07:68:94//AF046733

F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs. //8.7e-71:553:79//Z83822

F-HEMBA1000604//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE. //2.9e-21:158:75//AL021394

F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds. //1.1e-118:561:99//AB007925

F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence. //2.2e-28:426:70//AC004382

F-HEMBA1000636//Human CpG island sequence, clone Q28B8. //1.0e-15:274:68//D85773

F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds. //6.7e-137:639:99//AB014590

F-HEMBA1000655//, complete sequence. //5.1e-83:685:80//AC005815

F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds. //1.1e-91:597:84//U35776

F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.019:695:57//AC004907

F-HEMBA1000673//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE. //1.5e-48:325:85//Z86090

F-HEMBA1000682//Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence. //7.7e-61:615:74//L43411

F-HEMBA1000686

F-HEMBA1000702

F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.0037:569:57//AC005507

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F-HEMBA1000719//Streptomyces coelicolor cosmid IC2. //2.0e-09:483:62//AL031124

F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome. //0.00058:762:57//U87145

F-HEMBA1000726//H.sapiens HLA-DRB1*15 gene. //9.8e-49:189:89//X88791

F-HEMBA1000727//CIT-HSP-387P22. TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence. //0.0054:206:67//B60158

10 F-HEMBA1000747

F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //3.3e-05:124:75//AL024509

F-HEMBA1000752//Human Chromosome X, complete sequence. //5.9e-48:502:75//AC004073

F-HEMBA1000769//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.011:179:67//AC005043

F-HEMBA1000773//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE. //0.070:231:63//Z98870

F-HEMBA1000774//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence. //6.2e-40:385:75//AC004953

F-HEMBA1000791

F-HEMBA1000817//Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds. //0.99:244:58//U15678

F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island. //0.033:294:62//Z81370

F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome. //9.7e-05:463:58//AE001164

F-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence. //3.0e-153:732:98//AL022394

F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete

3161

cds. //1.6e-31:386:72//AF059273
 F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC
 14-617A9 (Roswell Park Cancer Institute Human PAC L
 ibrary) containing Arylsulfatase D and E genes, co
 mplete sequence. //8.5e-115:455:98//AC005295
 F-HEMBA1000867
 F-HEMBA1000869//Human DNA sequence from cosmid J13
 8017, between markers DXS6791 and DXS8038 on chromo
 some X contains EST CA repeat and an endogenous re
 troviral like element. //6.6e-41:424:75//Z72519
 F-HEMBA1000870//Gnamptodon pumilio cytochrome oxid
 ase II gene, partial cds; and tRNA-Asp, tRNA-His,
 and tRNA-Lys genes, complete sequence, mitochondri
 al genes for mitochondrial products. //0.0049:211:6
 6//AF034598
 F-HEMBA1000872//CIT-HSP-2355D20. TF CIT-HSP Homo sa
 piens genomic clone 2355D20, genomic survey sequen
 ce. //3.7e-33:180:98//AQ059583
 F-HEMBA1000876//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 473B4, WORKING DRAFT SE
 QUENCE. //5.6e-37:262:72//Z83826
 F-HEMBA1000908//Triticum aestivum low-affinity cat
 ion transporter (LCT1)mRNA, complete cds. //1.0:30
 4:59//AF015523
 F-HEMBA1000910//M.musculus necdin mRNA, complete c
 ds. //6.1e-08:256:61//M80840
 F-HEMBA1000918//Tetrahymena thermophila micronucle
 ar developmentally eliminated sequence region. //0.
 13:232:63//U88158
 F-HEMBA1000919//Gallus domesticus filamin mRNA, co
 mplete cds. //1.0:213:65//U00147
 F-HEMBA1000934//CIT-HSP-2053H24. TR CIT-HSP Homo sa
 piens genomic clone 2053H24, genomic survey sequen
 ce. //5.5e-11:275:64//B69224
 F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORK
 ING DRAFT SEQUENCE, 15unordered pieces. //9.7e-05:7
 8:83//AC004878
 F-HEMBA1000943//Homo sapiens chromosome 17, clone
 hRPK.640_I_15, complete sequence. //5.8e-140:661:99
 //AC005324
 F-HEMBA1000946
 F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORK
 ING DRAFT SEQUENCE, 12unordered pieces. //8.3e-16:1
 81:75//AC004967
 F-HEMBA1000968//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 69M21, WORKING DRAFT SE
 QUENCE. //4.4e-117:398:86//AL031735
 F-HEMBA1000971//H.sapiens CpG island DNA genomic M
 sel fragment, clone 182f4, forward read cpg182f4.f
 tla. //1.5e-20:126:96//Z57528

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F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3
 -p22 anti-oncogene of hepatocellular colorectal and
 non-small cell lung cancer, segment 1/11. //0.34:
 642:59//AB020858
 F-HEMBA1000974//Homo sapiens clone DA0091H08, comp
 lete sequence. //5.1e-183:865:98//AC004817
 F-HEMBA1000975//Orf virus homologue of retroviral
 pseudoprotease gene, complete cds. //0.00065:391:62
 //M30023
 10 F-HEMBA1000985//Human DNA sequence from clone 272E
 8 on chromosome Xp22.13-22.31. Contains a pseudoge
 ne similar to MDM2-Like P53-binding proteingene. C
 ontains STSs, GSSs and a CA repeat polymorphism, c
 omplete sequence. //3.4e-05:243:65//Z93929
 F-HEMBA1000986//Homo sapiens DNA from chromosome 1
 9-cosmid R31491, genomic sequence. //6.6e-06:508:61
 //AD000813
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complet
 e cds. //1.2e-22:193:84//D84064
 20 F-HEMBA1001007
 F-HEMBA1001008//Human DNA sequence from clone 3910
 22 on chromosome 6p21.2-21.31 Contains pseudogenes
 similar to ribosomal protein, ESTs, GSSs, complet
 e sequence. //7.8e-46:532:73//AL031577
 F-HEMBA1001009//Human mRNA for IgM heavy chain com
 plete sequence. //0.97:369:59//X17115
 F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 pro
 tein, complete cds. //4.4e-139:661:98//AB007937
 F-HEMBA1001019//Homo sapiens, clone hRPK.15_A_1, c
 omplete sequence. //1.6e-16:521:64//AC006213
 30 F-HEMBA1001020//Homo sapiens chromosome 17, clone
 hRPK.178_C_3, complete sequence. //3.8e-50:367:72//A
 C005702
 F-HEMBA1001022
 F-HEMBA1001024//Homo sapiens T-cell receptor alpha
 delta locus from bases 1 to 250529 (section 1 of
 5) of the Complete Nucleotide Sequence. //5.0e-23:3
 78:69//AE000658
 F-HEMBA1001026//Homo sapiens DNA sequence from PAC
 40 435D1 on chromosome Xq25. Contains ESTs and STS. /
 //7.6e-19:867:60//Z86064
 F-HEMBA1001043//HS_2219_B1_A10_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2219 Col=19 Row=B, genomic survey sequenc
 e. //3.0e-15:124:88//AQ301521
 F-HEMBA1001051//Human Chromosome X clone bWXD342,
 complete sequence. //4.8e-79:308:84//AC004072
 F-HEMBA1001052//Homo sapiens chromosome 17, clone
 hRPK.146_P_2, WORKING DRAFT SEQUENCE, 4 unordered p
 50 ieces. //0.53:384:61//AC005341

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F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084

F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.98:280:62//AC006079

F-HEMBA1001071//Human mRNA for pro alpha 1 (III) collagen C-terminal propeptide.//1.1e-31:181:96//X01742

F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 10 3951 nt].//3.6e-13:338:65//S78219

F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446

F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290121 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586

F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//I25863

F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from 7q22-q31.1, complete sequence.//2.4e-58:347:87//AC005250

F-HEMBA1001121//Human DNA sequence *** SEQUENCING 30 IN PROGRESS *** from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723

F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383

F-HEMBA1001123//Homo sapiens full length insert cDNA clone ZD38E12.//1.1e-11:231:68//AF086247

F-HEMBA1001133//Homo sapiens clone DJ0856024, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 pro 50

3164

tein, complete cds.//6.9e-72:527:77//AB018341

F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077

F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507

F-HEMBA1001174//R. norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604

F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815

F-HEMBA1001208//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410

F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917

F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered piece.//0.00010:557:57//AC006009

F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601_N_13, complete sequence.//0.0086:372:58//AC005389

F-HEMBA1001247//H.sapiens CpG island DNA genomic Msel fragment, clone 11b11, reverse read cpg11b11.rta.//2.0e-24:154:93//Z64441

F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:659:81//AF047020

F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205

F-HEMBA1001281

F-HEMBA1001286//B.taurus mRNA for RF-36-DNA-binding

3165

g protein.//7.7e-26:236:81//X15543
 F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.//5.5e-28:530:64//AC004131
 F-HEMBA1001294//Yeast mitochondrial aapl gene for ATPase subunit 8.//2.8e-15:722:60//X00960
 F-HEMBA1001299//Human DNA sequence from clone 422C23 on chromosome 6q24Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003
 F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260
 F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomicsequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505
 F-HEMBA1001310//HS_3252_B2_B12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic surveysequence.//1.2e-16:166:82//AQ217054
 F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408
 F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861
 F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with abeta-galucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences)and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368
 F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.012:152:65//AQ075713
 F-HEMBA1001330//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-103, complete sequence.//0.0037:254:62//AL010208
 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)mRNA, complete cds.//1.1e-103:516:97//AF057358
 F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, completesequence.//1.7e-150:706:99//AC006241
 F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505
 F-HEMBA1001377//HS_3020_B1_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl

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one Plate=3020 Col=23 Row=H, genomic surveysequence.//0.00022:63:77//AQ105297
 F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 ofthe complete sequence.//0.0035:317:60//AE001431
 F-HEMBA1001387//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035
 10 F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15unordered pieces.//4.2e-47:159:89//AC005073
 F-HEMBA1001391//Human DNA sequence from clone 409010 on chromosome 20q12Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256
 F-HEMBA1001398//H.sapiens CpG island DNA genomic Msel fragment, clone 70d11, forward read cpq70d11.f11b.//0.018:46:97//Z62591
 F-HEMBA1001405//Human DNA sequence *** SEQUENCING
 20 IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380
 F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645
 F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050
 F-HEMBA1001413
 F-HEMBA1001415//Human DNA sequence *** SEQUENCING
 30 IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732
 F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7unordered pieces.//8.0e-177:859:97//AC006146
 F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917
 F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63_A_1, completesequence.//1.2e-74:284:84//AC005670
 F-HEMBA1001442//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-66, complete sequence.//0.056:194:63//AL010138
 F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047
 F-HEMBA1001450
 F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB. ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115
 50 F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sap

3167

iens genomic clone 32J2, genomic survey sequence. /
/1.5e-05:223:65//B78859

F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652

F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144

F-HEMBA1001478//HS_2228_A2_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041

F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//7.7e-47:311:85//AL031133

F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:699:93//U89337

F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//AC005794

F-HEMBA1001517//Homo sapiens BAC clone RC459N13 from 7p15, complete sequence.//5.7e-162:769:98//AC004549

F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193

F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//0.31:120:69//Z98258

F-HEMBA1001533

F-HEMBA1001557//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136

F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FM02 and FM03 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase(N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FM0 II, FM0 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026

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F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044

F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//AC004453

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449

10 F-HEMBA1001581//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.30:484:59//AC004980

F-HEMBA1001585

F-HEMBA1001589//Human BAC clone RC317G18 from 7q31, complete sequence.//0.98:197:63//AC002432

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918

F-HEMBA1001608//RPCI11-72E2.TJ RPCI11 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131

20 F-HEMBA1001620//Oryza sativa RIN01 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107

F-HEMBA1001635//HS_3208_A1_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944

F-HEMBA1001636//Homo sapiens 12q24 PAC RPCI1-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//AC004216

30 F-HEMBA1001640//HS_3253_B2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058

F-HEMBA1001647//H. sapiens gene for plectin.//0.00052:629:61//Z54367

F-HEMBA1001651//Salmo salar DNA for a cryptic repeat.//7.9e-08:270:64//AJ012206

F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//AC005368

F-HEMBA1001658//M. musculus COL3A1 gene for collagen alpha-I.//2.4e-30:742:62//X52046

F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//AC005740

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//6.1e-152:725:98//AF072247

50 F-HEMBA1001675//RPCI11-54F8.TV RPCI11 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.

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3e-75:341:85//AQ082126
 F-HEMBA1001678//Homo sapiens Xp22 PAC RPCI1-167A22
 (from Roswell Park Cancer Center) complete sequen
 ce.//8.4e-54:551:74//AC002349
 F-HEMBA1001681
 F-HEMBA1001702//Plasmodium falciparum chromosome
 2, section 35 of 73 of the complete sequence.//0.9
 4:676:54//AE001398
 F-HEMBA1001709//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 702J19, WORKING DRAFT S 10
 EQUENCE.//0.74:659:58//AL033531
 F-HEMBA1001711//Lysiphlebus melandriicola NADH de
 hydrogenase 1 gene, mitochondrial gene encoding mit
 ochondrial protein, partial cds.//3.0e-07:413:60//
 AF069178
 F-HEMBA1001712//Homo sapiens BAC clone RG041H04 fr
 om 7q21-q22, complete sequence.//0.091:315:61//AC00
 4519
 F-HEMBA1001714//Rattus norvegicus mitochondrial AT
 Pase inhibitor gene, complete cds.//1.6e-28:218:75 20
 //U12250
 F-HEMBA1001718//HS_3056_A2_H08_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3056 Col=16 Row=0, genomic survey sequenc
 e.//2.0e-79:383:99//AQ106367
 F-HEMBA1001723//HS_2188_A2_D02_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2188 Col=4 Row=G, genomic survey sequenc
 e.//3.8e-28:174:94//AQ116793
 F-HEMBA1001731//HS_3021_A1_A11_T7 CIT Approved Hum 30
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3021 Col=21 Row=A, genomic survey sequenc
 e.//2.5e-11:420:62//AQ154658
 F-HEMBA1001734//Homo sapiens chromosome Y, clone 2
 64, M, 20, complete sequence.//0.00060:392:60//AC004
 617
 F-HEMBA1001744//HS_3194_A1_D05_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3194 Col=9 Row=G, genomic survey sequenc
 e.//5.8e-29:163:97//AQ252295
 F-HEMBA1001745//Homo sapiens chromosome 9q34, clon
 e 280C11, complete sequence.//0.66:627:59//AC00210
 2
 F-HEMBA1001746//HS_2163_B1_F04_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2163 Col=7 Row=L, genomic survey sequenc
 e.//1.4e-16:238:70//AQ085995
 F-HEMBA1001761//Genomic sequence from Mouse 9, com
 plete sequence.//3.5e-52:198:86//AC002109
 F-HEMBA1001781

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F-HEMBA1001784//Genomic sequence from Human 9q34,
 WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-
 13:296:65//AC002099
 F-HEMBA1001791//Homo sapiens DNA from chromosome 1
 9-cosmids R31158, R31874, and R28125, genomic sequ
 ence, complete sequence.//0.18:534:59//AF038458
 F-HEMBA1001800//CIT-HFP-2049N5.TF CIT-BSP Homo sap
 iens genomic clone 2049N5, genomic survey sequenc
 e.//2.2e-40:335:80//AQ009222
 F-HEMBA1001803//M.musculus (Balb/C) P/L01 mRNA.//
 1.7e-25:286:74//Z31360
 F-HEMBA1001804//Mouse interleukin 2 receptor (p55
 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0500.//7.8e-174:809:98//AB00
 7969
 F-HEMBA1001809//Bovine herpesvirus 1 complete geno
 me.//9.0e-09:639:57//AJ004801
 F-HEMBA1001815
 F-HEMBA1001819//HS_3079_B1_E04_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3079 Col=7 Row=J, genomic survey sequenc
 e.//1.4e-79:396:97//AQ186616
 F-HEMBA1001820//Homo sapiens BAC clone GS165L15 fr
 om 7p15, complete sequence.//0.00026:436:60//AC005
 013
 F-HEMBA1001822//Homo sapiens intersectin short for
 m mRNA, complete cds.//1.2e-40:510:65//AF064243
 F-HEMBA1001824//Homo sapiens expanded SCA7 CAG rep
 eat.//6.1e-20:344:68//AF020275
 F-HEMBA1001835//Homo sapiens BAC clone RG017K18 fr
 om 7q31, complete sequence.//0.0094:553:58//AC0051
 61
 F-HEMBA1001844//Homo sapiens chromosome Xp22-135-1
 36 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 un
 ordered pieces.//1.2e-22:316:70//AC005867
 F-HEMBA1001847//M.musculus Zfp-29 gene for zinc fi
 nger protein.//5.3e-27:397:69//X55126
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 pro
 tein, complete cds.//8.8e-184:865:98//AB014517
 F-HEMBA1001864//Arabidopsis thaliana chromosome II
 BAC F17H15 genomic sequence, complete sequence.//
 0.38:337:62//AC005395
 F-HEMBA1001866//Caenorhabditis elegans cosmid F48E
 3.//1.4e-10:224:63//U28735
 F-HEMBA1001869//Homo sapiens BAC clone RG114B19 fr
 om 7q31.1, complete sequence.//6.7e-98:288:91//AC0
 05065
 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone
 pDJ915f1 containing KvLQT1 gene, complete sequenc 50

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e.//4.9e-114:476:84//AC003693
 F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF026954
 F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC C clone h173, complete sequence.//0.90:221:63//AC003065
 F-HEMBA1001912//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732
 F-HEMBA1001913//Leishmania major chromosome 3 clone L4625 strain Friedlin, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00063:219:65//AC005766
 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//AB020873
 F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145
 F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310
 F-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-175:861:97//AC005629
 F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//0.097:107:71//AC006057
 F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934
 F-HEMBA1001950//H. sapiens CpG island DNA genomic Msel fragment, clone 15b5, forward read cpg15b5.ft1 q.//1.4e-27:168:95//Z54728
 F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha1 subunit.//0.010:108:71//AJ000390
 F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507
 F-HEMBA1001964
 F-HEMBA1001967//Human DNA sequence from clone 341E

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18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178
 F-HEMBA1001979//HS_3067_B1_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506
 F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551
 F-HEMBA1001991//HS_2237_A2_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283
 F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950nt].//2.7e-33:364:74//S90449
 F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948
 F-HEMBA1002018
 F-HEMBA1002022//Human p37NB mRNA, complete cds.//0.014:58:96//U32907
 F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:200:69//M17284
 F-HEMBA1002039//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053
 F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216
 F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422
 F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703
 F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943
 F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649
 F-HEMBA1002113//F. rubripes GSS sequence, clone 063 K10bB4, genomic survey sequence.//0.029:142:66//Z88840
 F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378
 F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds.//0.98:222:61//AF031815
 F-HEMBA1002139//Caenorhabditis elegans cosmid F55C

- 9, complete sequence.//0.0081:371:60//Z81549
 F-HEMBA1002144//*Saccharomyces cerevisiae* mitochondrion transfer RNA-Met(tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263
 F-HEMBA1002151
 F-HEMBA1002153//CITBI-E1-2519I20.TR CITBI-E1 Homo sapiens genomic clone2519I20, genomic survey sequence.//8.5e-61:334:94//AQ277613
 F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232
 F-HEMBA1002161//*Coturnix coturnix* slow myosin heavy chain 2 (qmyhc2) mRNA, partial cds.//2.1e-59:571:74//AF006829
 F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210
 F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (CTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712
 F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from 7q21-7q22, complete sequence.//2.5e-18:150:88//AC000066
 F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2unordered pieces.//0.00066:466:59//AC004825
 F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-23:176:77//AC005015
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589
 F-HEMBA1002199//Homo sapiens chromosome 4 clone B5 5B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150
 F-HEMBA1002204//HS_2055_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=0, genomic survey sequence.//1.2e-06:178:65//AQ235350
 F-HEMBA1002212//*S.cerevisiae* chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149
 F-HEMBA1002215//*M.musculus* mRNA for testin.//4.6e-80:504:87//X78989
 F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC R PCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035
 F-HEMBA1002229//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//2.6e-39:311:81 50
 //AC006044
 F-HEMBA1002237//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//1.6e-12:397:64//AC004861
 F-HEMBA1002241
 F-HEMBA1002253
 F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGK1) mRNA, complete cds.//3.5e-151:731:97//AF061936
 10 F-HEMBA1002265//Human DNA sequence from cosmid N28 H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183
 F-HEMBA1002267
 F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence.//0.069:495:58//AC006210
 F-HEMBA1002321//Homo sapiens PAC clone DJ0991023, complete sequence.//0.019:564:58//AC004944
 F-HEMBA1002328//CIT-HSP-2387N15.TF.1 CIT-HSP Homo sapiens genomic clone2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836
 F-HEMBA1002337//*Arabidopsis thaliana* genomic DNA, chromosome 5, Pl clone: MYN8, complete sequence.//0.84:547:57//AB020754
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314
 F-HEMBA1002348//CIT-HSP-2372K24.TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.//9.1e-33:230:75//AQ110676
 30 F-HEMBA1002349//*Plasmodium falciparum* histidine-rich protein II (HRP II) gene, complete cds.//9.4e-06:504:57//U69551
 F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:872:99//AF092563
 F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//2.1e-20:262:72//AB020868
 40 F-HEMBA1002389//*D.discoideum* spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546
 F-HEMBA1002417//*Canis familiaris* ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617
 F-HEMBA1002419//HS-1047-A1-F01-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 830 Col=1 Row=X, genomic survey sequence.//7.6e-06:111:76//B38165
 F-HEMBA1002430//HS_3137_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence

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e. //1.6e-56:367:88//AQ148697
 F-HEMBA1002439//Dictyostelium discoideum actin 8 g
 ene, 3' UTR. //0.67:129:64//M25216
 F-HEMBA1002458//Mus musculus REX-3 mRNA, complete
 cds. //1.1e-30:274:72//AF051347
 F-HEMBA1002460//Homo sapiens clone DJ1137M13, comp
 lete sequence. //4.0e-173:822:98//AC005378
 F-HEMBA1002462//Sequence 41 from patent US 570815
 7. //9.8e-51:519:73//I80067
 F-HEMBA1002469//Human mRNA for KIAA0122 gene, part 10
 ial cds. //4.0e-108:603:92//D50912
 F-HEMBA1002475//Streptomyces coelicolor cosmid 2H
 4. //0.0068:626:57//AL031514
 F-HEMBA1002477//Homo sapiens BAC clone NH0342K06 f
 rom 2, complete sequence. //1.5e-40:349:78//AC00503
 4
 F-HEMBA1002486
 F-HEMBA1002495//HS_3218_B1_A12_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3218 Col=23 Row=B, genomic surveysequenc 20
 e. //1.0:179:67//AQ181410
 F-HEMBA1002498//Homo sapiens full length insert cD
 NA clone ZD76B01. //1.4e-129:619:98//AF086404
 F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORK
 ING DRAFT SEQUENCE, 6unordered pieces. //1.9e-24:30
 6:68//AC004873
 F-HEMBA1002508//Homo sapiens chromosome 19, cosmid
 R33516, complete sequence. //2.9e-76:464:83//AC004
 799
 F-HEMBA1002513//Homo sapiens mRNA for histone deac 30
 etylase-like protein (JW21). //2.8e-157:738:98//AJ0
 11972
 F-HEMBA1002515//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 407F11, WORKING DRAFT S
 EQUENCE. //2.6e-07:307:64//AL022329
 F-HEMBA1002538//HS_2185_B2_B04_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2185 Col=8 Row=D, genomic survey sequenc
 e. //4.7e-37:339:78//AQ298315
 F-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Hum 40
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3197 Col=20 Row=D, genomic surveysequenc
 e. //3.2e-70:372:95//AQ188792
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA,
 partial cds. //3.5e-137:655:98//AF016903
 F-HEMBA1002552//Human Hep27 protein mRNA, complete
 cds. //8.8e-07:173:68//U31875
 F-HEMBA1002555//*** SEQUENCING IN PROGRESS *** Hom
 o sapiens chromosome 4, BAC clone C0190L06; HTGS p
 hase 1, WORKING DRAFT SEQUENCE, 21 unorderedpiece 50

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s. //2.2e-15:628:60//AC004670
 F-HEMBA1002558//Human Xp22 BAC CT-285I15 (from Cal
 Tech/Research Genetics), PAC RPC11-27C22 (from Ro
 swell Park Cancer Center), and Cosmid U35B5(from L
 awrence Livermore), complete sequence. //2.3e-41:35
 3:76//AC002366
 F-HEMBA1002561//Homo sapiens chromosome 17, clone
 HRPC29G21, complete sequence. //1.1e-39:538:66//AC0
 03687
 F-HEMBA1002569//Homo sapiens protein associated wi
 th Myc mRNA, completecds. //1.3e-140:457:99//AF0755
 87
 F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sap
 iens genomic clone 2321D3, genomic survey sequenc
 e. //5.1e-79:385:99//AQ038102
 F-HEMBA1002590//Homo sapiens chromosome 17, clone
 hRPK.167_N_20, complete sequence. //1.9e-35:430:70/
 /AC005940
 F-HEMBA1002592//Human genomic DNA sequence from cl
 one 30801 on chromosome Xp11.3-11.4. Contains EST,
 CA repeat, STS, GSS, CpG island. //4.4e-19:303:71/
 /Z93403
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 pro
 tein, partial cds. //4.4e-175:820:99//AB011169
 F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 f
 rom 7q21, complete sequence. //0.14:353:58//AC00441
 3
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808.pro
 tein, complete cds. //2.9e-187:632:97//AB018351
 F-HEMBA1002628//Plasmodium falciparum 3D7 chromoso
 me 12 PFYAC812 genomicsequence, WORKING DRAFT SEQU
 ENCE, 8 unordered pieces. //1.5e-05:792:58//AC00415
 3
 F-HEMBA1002629//Streptomyces coelicolor cosmid 1A
 9. //8.4e-08:576:58//AL034446
 F-HEMBA1002645//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 153G14, WORKING DRAFT S
 EQUENCE. //5.6e-47:222:86//AL031118
 F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 f
 rom 7p31, complete sequence. //3.8e-182:859:99//AC0
 04839
 F-HEMBA1002659//Z.mobilis alcohol dehydrogenase I
 (adhA) gene, completecds. //0.97:144:66//M32100
 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 f
 rom 7p21-p22, complete sequence. //1.3e-116:774:84//
 AC004535
 F-HEMBA1002666
 F-HEMBA1002678//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 1137F22, WORKING DRAFT
 SEQUENCE. //5.7e-156:750:98//AL034421

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F-HEMBA1002679//nbxb0002cc12r CUCI Rice BAC Library *Oryza sativa* genomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:58//AQ051621

F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complete genome.//8.3e-20:651:61//Z86099

F-HEMBA1002696//*Mus musculus* proteasome regulator PA28 beta subunit gene, complete cds.//7.6e-62:306:81//AF060195

F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds.//1.9e-10:327:62//AB007924

F-HEMBA1002712

F-HEMBA1002716//HS_3064_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, genomic survey sequence.//8.4e-97:491:96//AQ142980

F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence.//6.1e-21:217:77//AC004782

F-HEMBA1002730//Human platelet glycoprotein IIIa (GPIIIa) gene, exon 1.//0.57:125:67//M57481

F-HEMBA1002742//RPCI11-39J10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102

F-HEMBA1002746//*Mus musculus* chromosome 19, clone CIT282B21, complete sequence.//7.1e-70:303:82//AC03694

F-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732

F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89), complete sequence.//6.7e-40:232:70//AC004622

F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.0e-177:834:98//AB011126

F-HEMBA1002770//cDNA encoding novel rat protein TlP120 which is formed of complex with TBP (TATA binding protein).//1.3e-140:840:88//E12829

F-HEMBA1002777//*F. rubripes* GSS sequence, clone 189 C06dB12, genomic survey sequence.//1.1e-28:263:77//AL007965

F-HEMBA1002779//CIT-HSP-2333I1.TF CIT-HSP Homo sapiens genomic clone 2333I1, genomic survey sequence.//1.8e-32:180:98//AQ036891

F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, complete sequence.//7.0e-06:199:67//AC004592

F-HEMBA1002794//H. sapiens mRNA for protein kinase C mu.//0.00015:244:67//X75756

F-HEMBA1002801//*Plasmodium falciparum* MAL3P2, complete sequence.//0.0010:534:57//AL034558

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F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.1e-167:820:97//AF071185

F-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5unordered pieces.//3.1e-113:254:90//AC005043

F-HEMBA1002818//*Cricetulus griseus* H411 precursor (H411) mRNA, complete cds.//1.2e-122:760:86//AF046870

10 F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:65//AL022153

F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//1.4e-170:744:99//AC004707

F-HEMBA1002850//*Ephedrus persicae* NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//1.3e-05:334:59//AF069186

F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic clone 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419

F-HEMBA1002876//HS_2270_B1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, genomic survey sequence.//0.44:163:64//AQ164031

F-HEMBA1002886

F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793C5 (LBNL H58), complete sequence.//0.00015:277:61//AC005195

30 F-HEMBA1002921

F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic clone 2171H4, genomic survey sequence.//0.0016:175:66//B89715

F-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL031681

F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//4.9e-173:803:99//AB011148

F-HEMBA1002937//Human DNA sequence *** SEQUENCING

40 IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033531

F-HEMBA1002939//RPCI11-74014.TJ RPCI11 Homo sapiens genomic clone R-74014, genomic survey sequence.//1.7e-41:215:99//AQ266676

F-HEMBA1002944//RPCI11-55C2.TV RPCI11 Homo sapiens genomic clone R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240

F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complete sequence.//0.00074:683:58//AC005578

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F-HEMBA1002954//RPCI11-79F7.TV RPCI11 Homo sapiens genomic clone R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146

F-HEMBA1002968//HS_2262_B2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, genomic survey sequence.//0.99:270:60//AQ217059

F-HEMBA1002970//RPCI11-5L24.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5L24, genomic survey sequence.//1.4e-10:189:71//B49289

F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic clone 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ080538

F-HEMBA1002973//Rattus norvegicus Wistar 3', 5'-cyclic AMP phosphodiesterase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290

F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797

F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286

F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3unordered pieces.//7.5e-50:331:85//AC005484

F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A10-62B5, Pl clones DS02777, DS03222, DS02345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557

F-HEMBA1003034//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704

F-HEMBA1003035//Homo sapiens chromosome Y, clone 264, M, 20, complete sequence.//2.3e-05:591:57//AC004617

F-HEMBA1003037//RPCI11-88F2.TJ RPCI11 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677

F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983

F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182

F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505

F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783

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F-HEMBA1003071//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648

F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257

F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tensin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs.//9.4e-43:478:70//Z99297

F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673

F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548

20 F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//3.6e-11:734:58//AF001550

F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//I13750

F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308

F-HEMBA1003117//Mouse TIS11 primary response gene, complete cds.//0.00054:480:60//M58564

30 F-HEMBA1003129//HS_3139_B2_F05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635

F-HEMBA1003133//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259

F-HEMBA1003136

F-HEMBA1003142//Homo sapiens full length insert cDNA clone ZC39B06.//6.9e-121:563:100//AF086197

40 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670

F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 -complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302

F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882

F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one w

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ith homology to a worm protein. Contains ESTs, complete sequence. //5.4e-115:174:98//AL022325
 F-HEMBA1003197//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence. //1.1e-05:473:59//AC005824
 F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1. //1.6e-05:367:61//U09302
 F-HEMBA1003202//Homo sapiens BAC clone RC437L15 from 8q21, complete sequence. //9.0e-23:247:73//AC004003
 F-HEMBA1003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE. //4.7e-26:141:83//Z83824
 F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence. //1.9e-31:158:86//AC002037
 F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces. //3.4e-24:284:75//AC004150
 F-HEMBA1003222//RPC111-47P17.TJ RPC111 Homo sapiens genomic clone R-47P17, genomic survey sequence. //8.7e-39:202:99//AQ202885
 F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence. //0.86:227:62//AB019230
 F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence. //8.6e-05:372:61//AE001373
 F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 796 Col=3 Row=0, genomic survey sequence. //0.00032:57:96//B46142
 F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein. //2.2e-08:531:59//X64624
 F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA19H4. //0.070:267:64//Z78949
 F-HEMBA1003276//CIT-HSP-2301B4.TF CIT-HSP Homo sapiens genomic clone 2301B4, genomic survey sequence. //5.2e-08:295:63//AQ015073
 F-HEMBA1003278//HS_3075_A1_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence. //0.98:399:58//AQ120599
 F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces. //4.8e-101:277:97//AC005840
 F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyl transferase mRNA, complete cds. //9.0

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e-145:539:97//AF038662
 F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds. //5.0e-166:799:98//AB011109
 F-HEMBA1003296//CITBI-E1-2507M8.TR CITBI-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence. //1.9e-05:388:63//AQ262551
 F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene. //8.0e-05:388:62//L17343
 F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence. //0.0017:210:64//AF051177
 F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds. //4.6e-188:865:99//AB001872
 F-HEMBA1003322//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE. //2.4e-54:316:87//Z93015
 F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence. //8.4e-12:166:76//B67147
 F-HEMBA1003328//HS_2230_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence. //0.026:128:71//AQ153313
 F-HEMBA1003330//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds. //4.0e-160:745:99//AF045555
 F-HEMBA1003348//HS_3194_A1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence. //5.0e-79:381:99//AQ173779
 F-HEMBA1003369//H.vulgare GAA-satellite DNA. //0.12:89:71//Z50100
 F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence. //3.5e-32:199:80//AF024533
 F-HEMBA1003373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE. //0.019:117:71//AL034405
 F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence. //4.2e-30:196:85//U67229
 F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence. //4.6e-22:206:81//AL021528
 F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.00094:72:90//AC006026
 F-HEMBA1003395//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE. //0.00041:826:57//AL031744

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F-HEMBA1003402//CIT-HSP-2339K16. TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence. //2.4e-05:265:64//AQ056234

F-HEMBA1003403//Homo sapiens chromosome 4 clone B3 53C18 map 4q25, complete sequence. //4.3e-135:780:90//AC004066

F-HEMBA1003408

F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence. //1.9e-41:239:95//AL031321

F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3' UTR and trinucleotide repeat microsatellites. //2.2e-06:247:64//U08273

F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds. //1.4e-149:697:99//AF051334

F-HEMBA1003447//Homo sapiens chromosome 4 clone B3 53C18 map 4q25, complete sequence. //1.7e-77:461:90//AC004066

F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, FliI (fliI) and FliJ (fliJ) genes, complete cds. //8.6e-08:752:58//U31090

F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence. //0.089:172:68//AC004098

F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence. //4.5e-150:562:97//AC005041

F-HEMBA1003528//Streptomyces fradiae gene for tryptophan precursor, complete cds. //4.7e-09:433:60//D16687

F-HEMBA1003531//Homo sapiens PAC clone DJ1185107 from 7q11.23-q21, complete sequence. //2.3e-48:297:90//AC004990

F-HEMBA1003538//Human complement C1r mRNA, complete cds. //4.3e-22:474:63//M14058

F-HEMBA1003545//Rattus norvegicus (clone 1.6kb) islet-2 mRNA, complete cds. //3.5e-143:805:91//L35571

F-HEMBA1003548

F-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447E6, WORKING DRAFT SEQUENCE. //3.4e-58:331:83//AL031724

F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence. //6.0e-99:703:84//AC005913

F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds. //1.3e-99:587:89//J05071

F-HEMBA1003568//HS_3149_A1_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence. //4.1e-05:389:57//AQ166810

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e. //4.1e-05:389:57//AQ166810

F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence. //1.6e-102:669:85//AC005539

F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds. //0.00033:649:58//U60170

F-HEMBA1003579//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE. //0.00034:623:56//AL031744

10 F-HEMBA1003581//Mouse mRNA for talin. //3.3e-41:181:86//X56123

F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPC1-11_192K18, complete sequence. //4.4e-70:273:94//AC006075

F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence. //6.0e-17:768:58//AE001395

F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence. //4.0e-09:777:56//AE001398

F-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence. //1.3e-146:692:98//AC005153

F-HEMBA1003615//HS_2010_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence. //1.1e-22:137:97//AQ226592

F-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds. //2.4e-169:501:97//AB015344

30 F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds. //4.7e-37:165:92//AF034080

F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.0024:514:58//AC005139

F-HEMBA1003630//CIT-HSP-2168N15. TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence. //6.5e-15:358:63//B92984

F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //5.0e-21:238:76//AC005077

F-HEMBA1003640//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE. //2.3e-15:371:63//Z85987

F-HEMBA1003645//A. thaliana 81kb genomic sequence. //1.0:529:57//X98130

F-HEMBA1003646

F-HEMBA1003656

F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence. //1.6e-175:824:98//AC005746

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F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.1e-24:190:87//AC004765
 F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065
 F-HEMBA1003680//H. sapiens DNA sequence.//7.3e-22:172:87//Z22322
 F-HEMBA1003684//H. sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723
 F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691
 F-HEMBA1003692
 F-HEMBA1003711//Homo sapiens chromosome 17, clone HRPC41C23, complete sequence.//0.55:450:60//AC003101
 F-HEMBA1003714
 F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-16:316:68//AL023575
 F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056
 F-HEMBA1003725//CIT-HSP-2351H9.TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence.//1.1e-112:532:99//AQ079348
 F-HEMBA1003729//HS_3043_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345
 F-HEMBA1003733//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.7e-104:761:82//AC006213
 F-HEMBA1003742//HS_3027_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731
 F-HEMBA1003758//CIT-HSP-2379D18.TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513
 F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194
 F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139
 F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496
 F-HEMBA1003784//Caenorhabditis elegans cosmid C55B

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6.//0.054:463:58//U88181
 F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DGCR Region, complete sequence.//1.9e-44:425:76//AC000070
 F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178
 F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-138:275:99//AC004596
 F-HEMBA1003805//Mus musculus quaking type I (QKI) mRNA, complete cds.//6.6e-148:753:95//U44940
 F-HEMBA1003807//HS-1068-B1-C06-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 278 Col=11 Row=N, genomic survey sequence.//6.7e-07:241:67//B47212
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516
 F-HEMBA1003836//S.cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125
 F-HEMBA1003838//CIT-HSP-384J15.TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810
 F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT987SK-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875
 F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300
 F-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds.//5.9e-81:853:71//AF030430
 F-HEMBA1003879//H. sapiens CBP80 mRNA.//2.0e-08:87:95//X80030
 F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036
 F-HEMBA1003885//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079
 F-HEMBA1003893//H. sapiens CpG island DNA genomic Msel fragment, clone 11b6, forward read cpg11b6.ft1a.//3.6e-32:173:99//Z59012
 F-HEMBA1003902//RPCI11-26W20.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-26W20, genomic survey sequence.//8.2e-12:422:61//AQ003455
 F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:468:58//AE001401
 F-HEMBA1003926//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.//3.6e-27:278:76//AL031658

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F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region. //1.4e-55:315:81//AF109718
 F-HEMBA1003939//HS-1047-A1-G04-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence. //6.1e-09:413:63//B38195
 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.42:205:65//AC005140
 F-HEMBA1003950//M. capricolum DNA for CONTIG MC072. //0.029:458:58//Z33058
 F-HEMBA1003953//HS_2268_A1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence. //9.0e-07:239:64//AQ085098
 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence. //2.8e-57:424:74//AC004894
 F-HEMBA1003959//RPCI11-78E8.TV RPCI11 Homo sapiens genomic clone R-78E8, genomic survey sequence. //4.3e-86:441:96//AQ285498
 F-HEMBA1003976//HS_3146_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=0, genomic survey sequence. //6.3e-10:129:80//AQ141146
 F-HEMBA1003978
 F-HEMBA1003985//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5, WORKING DRAFT SEQUENCE. //1.0:258:60//Z98855
 F-HEMBA1003987
 F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9. //0.40:238:61//AL034446
 F-HEMBA1004000//Rattus norvegicus satellite sequence d0Mco2. //2.0e-07:116:70//U19354
 F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces. //0.098:286:60//AC004710
 F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence. //2.8e-185:896:97//AC005670
 F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence. //6.3e-68:417:80//AC005411
 F-HEMBA1004024//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence. //2.0e-47:418:77//AC005859
 F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE. //1.6e-51:564:74//AP000052

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F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence. //1.2e-05:636:55//AE001398
 F-HEMBA1004045//Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence. //1.9e-31:373:76//AC002252
 F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2. //0.039:234:63//D63393
 F-HEMBA1004049//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence. //4.8e-135:780:89//AC003106
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence. //4.7e-09:457:58//L13435
 F-HEMBA1004056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE. //3.3e-25:246:77//AL021977
 F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence. //7.8e-24:233:76//B68555
 F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds. //4.5e-08:614:59//U49822
 F-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds. //5.9e-121:502:85//AF091234
 F-HEMBA1004111//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14; HTGS p-hase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces. //2.0e-36:317:80//AC006160
 F-HEMBA1004131//Mus musculus clone OST2067, genomic survey sequence. //8.7e-24:320:71//AF046393
 F-HEMBA1004132//HS_3226_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence. //9.7e-13:232:71//AQ182017
 F-HEMBA1004133
 F-HEMBA1004138//HS_3036_B1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence. //0.0035:165:64//AQ294763
 F-HEMBA1004143
 F-HEMBA1004146
 F-HEMBA1004150//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS. //0.0011:618:60//Z96811
 F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence. //2.9e-30:454:68//AC005913

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F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-133:649:97//AF067855
 F-HEMBA1004199
 F-HEMBA1004200//HS_2015_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957
 F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.//7.8e-59:216:83//AC004807
 F-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15unordered pieces.//6.3e-98:173:98//AC005488
 F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748
 F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424
 F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927
 F-HEMBA1004238
 F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708
 F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and CDSs, complete sequence.//6.1e-21:254:77//AL031010
 F-HEMBA1004248//Rattus rattus insulin-induced growth-respons protein (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619
 F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693
 F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//3.1e-78:335:87//AC004707
 F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-118OD12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-176:856:97//AC005831
 F-HEMBA1004274//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993
 F-HEMBA1004275//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051

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F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795
 F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence.//1.0:387:59//AB013395
 10 F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment RP11-3A.//7.8e-06:92:89//AB012254
 F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897
 F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.//0.28:522:57//AJ235271
 F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130
 20 F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720
 F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094
 F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4unordered pieces.//7.0e-168:895:93//AC004995
 F-HEMBA1004334//Homo sapiens Xp22.BAC 620F15 (Genome Systems BAC library) complete sequence.//4.6e-73:713:75//AC002980
 30 F-HEMBA1004335//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL024498
 F-HEMBA1004341
 F-HEMBA1004353//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571
 F-HEMBA1004354//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.1e-45:190:92//U75968
 F-HEMBA1004356
 40 F-HEMBA1004366//P.falciparum complete gene map of plastid-like DNA (IR-A).//2.2e-07:736:57//X95275
 F-HEMBA1004372//H.sapiens dystrophin gene intron 4.4.//1.0:129:62//X77644
 F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//4.7e-42:237:94//M21977
 F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//5.2e-05:519:59//AE001402
 F-HEMBA1004396//Human BAC clone RC302F04 from 7q31, complete sequence.//4.0e-32:261:76//AC002463

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F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:58//AC005507

F-HEMBA1004408//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-69:195:100//AC005037

F-HEMBA1004429//HS_3193_A1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942

F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//3.2e-27:242:82//AC002554

F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.7e-75:590:81//AC004846

F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence.//0.045:215:66//AL034407

F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//AF060194

F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//6.8e-17:791:59//AC005505

F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//4.4e-125:251:94//AC004686

F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.012:635:57//AC004709

F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:88//AC004453

F-HEMBA1004507

F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14(ESSAII project).//1.0e-13:244:67//AL021712

F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (ABP-280).//1.6e-72:678:74//X53416

F-HEMBA1004538//Sequence 1 from patent US 5612190.//0.00015:416:59//I36871

F-HEMBA1004542//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.95:202:64//AC005038

F-HEMBA1004554//Arabidopsis thaliana BAC T26D22.//0.45:624:56//AF058826

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F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//9.1e-10:173:70//D87457

F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence.//6.1e-23:134:73//AC002542

F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J2, complete sequence.//1.6e-15:190:77//AC004525

F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-31:388:76//AC004895

F-HEMBA1004596//RPCI11-81021.TJ RPCI11 Homo sapiens genomic clone R-81021, genomic survey sequence.//2.2e-90:458:90//AQ285136

F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.//8.6e-105:699:84//AF071316

F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//5.4e-20:267:72//AC004983

20 F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey sequence.//6.2e-26:147:99//AQ034944

F-HEMBA1004629//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.6e-06:766:56//AC005504

F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//4.7e-73:412:92//Z83843

30 F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHV1 ORF 46, VZV ORF 44.//0.92:181:61//X90418

F-HEMBA1004637//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//7.8e-47:784:65//X74904

F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds.//6.4e-06:458:61//AF004431

F-HEMBA1004666//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.30:733:55//Z98865

F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-3

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6.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence. //7.5e-136:521:98//AL031432

F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence. //0.43:365:59//AC000045

F-HEMBA1004672

F-HEMBA1004693//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.096:651:54//AC005308

F-HEMBA1004697//CIT-HSP-2326C13. TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence. //0.23:238:65//AQ040642

F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell Park Cancer Center) complete sequence. //2.1e-27:375:72//AC0002357

F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence. //1.6e-36:191:91//AC006210

F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence. //1.1e-133:639:99//AC005562

F-HEMBA1004725//RPC111-75O13. TJ RPC111 Homo sapiens genomic clone R-75O13, genomic survey sequence. //6.2e-32:169:100//AQ266512

F-HEMBA1004730//Human BAC clone RG035E18 from 7q3

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1, complete sequence. //8.0e-68:732:72//AC004029

F-HEMBA1004733//CIT-HSP-2305M23. TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence. //4.9e-18:209:69//AQ017556

10 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds. //1.8e-13:451:62//AF028340

F-HEMBA1004736//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinosis (X-linked, juvenile) 1 (XLR1). Contains ESTs, an STS and GSSs, complete sequence. //5.0e-87:646:78//Z94056

20 F-HEMBA1004748//Human BAC clone RG204I16 from 7q31, complete sequence. //0.24:526:57//AC002461

F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces. //1.4e-25:268:76//AC004913

F-HEMBA1004752//R. norvegicus mRNA for leucocyte common antigen-related protein (3941 bp). //1.1e-07:503:61//X83546

F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence. //4.5e-38:314:81//AC000028

30 F-HEMBA1004756//Homo sapiens, complete sequence. //1.4e-111:326:84//AC005854

F-HEMBA1004758//Sequence 29 from patent US 5534410. //3.9e-135:769:91//I23472

F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds. //3.6e-47:404:79//U75285

F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence. //6.7e-107:890:78//AC004941

40 F-HEMBA1004770//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //7.9e-09:806:59//AC004709

F-HEMBA1004771//G. muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA. //0.69:239:61//X65063

F-HEMBA1004776

F-HEMBA1004778

F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DAKAP550 mRNA, partial cds. //3.4e-46:778:64//AF003622

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F-HEMBA1004803//Homo sapiens chromosome Y, clone 264, M, 20, complete sequence. //4.3e-82:580:82//AC004617

F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence. //5.4e-07:642:59//AC005083

F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3. //1.4e-46:171:92//L01042

F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14. //3.5e-31:546:66//M86257

F-HEMBA1004820//C.botulinum progenitor toxin complex genes. //0.0014:343:62//X87972

F-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68). //1.5e-85:512:88//X53744

F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBRI) gene, exon 1. //0.0065:284:61//AF054590

F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence. //0.92:250:59//AC000400

F-HEMBA1004864

F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence. //3.6e-12:214:72//AL031120

F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence. //1.1e-08:255:69//AC004020

F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds. //0.062:155:69//U32943

F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence. //0.00055:323:60//L12043

F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence. //9.6e-16:166:80//AC003051

F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial. //0.81:146:65//M94003

F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543, , and F15613 containing ZNF gene family member, genomic sequence, complete sequence. //1.4e-36:338:78//AC003006

F-HEMBA1004929//CIT-HSP-2373I16. TR CIT-HSP Homo sapiens genomic clone 2373I16, genomic survey sequence. //2.4e-86:443:96//AQ108676

F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence. //4.6e-20:219:73//AC004109

F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Ge

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omic Sperm Library CHomo sapiens genomic clone Plate=CT 497 Col=19 Row=I, genomic survey sequence. //1.4e-28:216:85//B30726

F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267010, complete sequence. //0.53:222:61//AF042091

F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5unordered pieces. //1.2e-58:509:78//AC005482

F-HEMBA1004954//HS_2033_A2_A08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence. //3.7e-47:243:99//AQ229758

F-HEMBA1004956//P.falciparum complete gene map of plastid-like DNA (IR-B). //0.048:421:58//X95276

F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8. //0.89:333:58//Z97343

F-HEMBA1004972

F-HEMBA1004973//RPCI11-66P8.TK RPCI11 Homo sapiens genomic clone R-66P8, genomic survey sequence. //3.5e-22:245:77//AQ238471

F-HEMBA1004977//Homo sapiens full length insert cDNA clone YZ83B08. //9.0e-11:84:98//AF086080

F-HEMBA1004978//CIT-HSP-2354E10. TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence. //0.0021:152:66//AQ075713

F-HEMBA1004980//HS_3018_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=I, genomic survey sequence. //1.9e-77:392:97//AQ071873

F-HEMBA1004983//Albinaria corrugata isolate cor.Pr n1.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence. //0.0030:276:61//AF031680

F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 306E6 (LANL), complete sequence. //4.2e-138:640:99//AC005590

F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence. //6.8e-20:160:88//U52077

F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds. //2.0e-144:668:99//AF041474

F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds. //1.4e-146:693:98//AB014548

F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24(L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H41KE (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/

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k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, CDSs and genomic marker D6S464, complete sequence. //2.2e-115:668:90//AL009179

F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence. //4.6e-138:591:98//AC004596

F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence. //3.7e-61:271:88//AQ055486

F-HEMBA1005047//Mus musculus mRNA for Rab24 protein. //3.8e-17:218:73//Z22819 F-HEMBA1005050//Human Tis11d gene, complete cds. //0.079:251:63//U07802

F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.018:560:56//AC004688

F-HEMBA1005066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE. //3.4e-97:432:84//AL034410

F-HEMBA1005075//H. sapiens DNA 3' flanking simple sequence region clone wg2c3. //6.9e-07:176:68//X76589

F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence. //2.1e-48:274:93//AQ038720

F-HEMBA1005083//HS_2248_B1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence. //3.4e-06:230:64//AQ129575

F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds. //1.3e-161:762:98//AF080561

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F-HEMBA1005113//L. esculentum microsatellite repeat DNA region. //0.0038:742:57//X90770

F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces. //9.6e-83:479:78//AC004854

F-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE. //3.9e-24:576:64//AL023808

F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence. //4.7e-36:283:80//AC004542

F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces. //5.0e-10:332:64//AC004469

F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE. //4.0e-10:734:58//AP000023

F-HEMBA1005185//H. sapiens CpG island DNA genomic Msel fragment, clone 91b2, forward read cpg91b2.ft1a. //2.2e-14:93:100//Z63847

F-HEMBA1005201//Drosophila melanogaster cosmid 152A3. //4.7e-35:679:64//AL009194

F-HEMBA1005202//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68). //6.7e-138:778:90//X53744

F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene. //7.1e-12:376:62//AJ011320

F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds. //7.1e-05:411:60//AB007914

F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence. //3.5e-06:212:66//AC004542

50 F-HEMBA1005232//Plasmodium falciparum 3D7 chromoso

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me 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //3.7e-07:625:57//AC005308

F-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence. //8.7e-45:567:72//AC005154

F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence. //0.96:298:62//AC002365

F-HEMBA1005251

F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence. //4.5e-160:392:99//AC005837

F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence. //2.3e-05:496:60//AF069291

F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence. //5.7e-05:220:64//AL033521

F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds. //2.4e-20:338:65//U97018

F-HEMBA1005296

F-HEMBA1005304//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence. //1.6e-51:381:78//AL031012

F-HEMBA1005311

F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE. //0.94:226:63//AP000031

F-HEMBA1005315//Homo sapiens BAC810, complete sequence. //9.5e-15:684:62//U85198

F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone. //2.6e-05:472:59//Z83823

F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence. //3.3e-90:300:90//AC005803

F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial. //1.4e-151:740:97//AJ007581

F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence. //2.1e-86:438:97//AQ016145

F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds. //1.8e-98:500:88//U09414

F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds. //8.3e-72:577:73//AF047714

F-HEMBA1005372//Human DNA sequence from PAC 293E14 50

3200

contains ESTs, STS. //1.3e-07:274:66//Z82900

F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces. //1.9e-48:611:69//AC004813

F-HEMBA1005382//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence. //1.6e-27:154:98//AQ103204

F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence. //4.0e-07:443:61//M23175

F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence. //7.6e-17:225:71//AQ076749

F-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //4.5e-131:278:98//AL034379

F-HEMBA1005408//HS_3007_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence. //8.0e-06:218:66//AQ294366

F-HEMBA1005410//Human DNA sequence from cosmid cU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS. //1.5e-41:432:76//Z73496

F-HEMBA1005411

F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)mRNA, complete cds. //1.0e-169:537:99//AF041248

F-HEMBA1005426

30 F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence. //7.1e-37:260:76//AC006130

F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence. //5.0e-133:631:98//B93234

F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence. //1.5e-118:868:83//AL022576

F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence. //1.2e-179:838:99//AC005212

F-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE. //3.4e-20:187:74//AL031985

F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE. //4.1e-22:445:65//AP000041

50 F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sa

3201

piens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941
 F-HEMBA1005497//HS_3097_A2_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic surveysequence.//1.4e-66:345:96//AQ103810
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:98//AC004957
 F-HEMBA1005506//Mus musculus (clone 0EBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147
 F-HEMBA1005508//Homo sapiens, clone hRPK.1_A_1, complete sequence.//0.00012:455:60//AC006196
 F-HEMBA1005511//Homo sapiens MHC class 1 region.//3.3e-43:421:77//AF055066
 F-HEMBA1005513//Drosophila melanogaster males-abse-
 nt on the first (mof) gene, complete cds.//2.3e-20:352:69//U71219
 F-HEMBA1005517//Homo sapiens DNA for (CGG)_n trinucleotide repeat region, isolate E7.//2.5e-08:431:62//AJ001216
 F-HEMBA1005518//M. musculus mRNA for paladin gene.//8.2e-90:651:81//X99384
 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.8e-167:755:99//AC004913
 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//2.4e-42:475:73//AC006241
 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855
 F-HEMBA1005530
 F-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE.//9.4e-87:422:99//AL034431
 F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//6.1e-41:486:68//AC004743
 F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377
 F-HEMBA1005568//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153
 F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407
 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932

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F-HEMBA1005577//HS-1004-A1-E11-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 498 Col=21 Row=I, genomic survey sequence.//0.00034:254:64//B30971
 F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531
 F-HEMBA1005582//HS_3242_A1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic surveysequence.//1.1e-13:91:98//AQ211275
 F-HEMBA1005583
 F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025
 F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.3e-158:748:99//AC005746
 F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527
 F-HEMBA1005606//CIT-HSP-2326I6.TR CIT-HSP Homo sapiens genomic clone 2326I6, genomic survey sequence.//0.0014:132:70//AQ041484
 F-HEMBA1005609//Homo sapiens clone RC315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089
 F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome Xq21.1-Xq21.3. rab proteins geranylgeranyltransferase component A 1 (rabescort protein 1) (REP-1) (choroideraemia protein) (TCD protein).//6.5e-29:279:69//AL009175
 F-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731
 F-HEMBA1005627//RPCI11-34P9.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110
 F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004460
 F-HEMBA1005632
 F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33. Contains ESTs.//6.6e-38:452:67//Z98036
 F-HEMBA1005666
 F-HEMBA1005670//Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.//5.1e-59:687:74//AC004850
 F-HEMBA1005679//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478

- F-HEMBA1005680
- F-HEMBA1005685//RPCI11-23D19.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742
- F-HEMBA1005699//Human ligand for eph-related receptor tyrosine kinases (EPLG8) mRNA, complete cds.//1.4e-72:406:92//U57001
- F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513
- F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348
- F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697
- F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from 7q21-q22, complete sequence.//5.6e-15:157:79//AC005156
- F-HEMBA1005746//RPCI11-63N8.TK RPCI11 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535
- F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181
- F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196
- F-HEMBA1005780//RPCI11-74E19.TJ RPCI11 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432
- F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//0.14:326:61//AC004079
- F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523
- F-HEMBA1005822//Mouse Bac 291G16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020
- F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 Fosmid Clone f39e1 In DGCR Region, complete sequence.//8.8e-42:370:79//AC000094
- F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577
- F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//A
- L018749
- F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone 2289L23, genomic survey sequence.//2.2e-68:333:99//B98952
- F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL H191), complete sequence.//1.9e-57:331:87//AC005351
- F-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945
- F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086
- F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FM02 and FM03 genes for Flavin-containing Monooxygenase2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase(N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026
- F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584
- F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.3e-41:431:77//AC005666
- F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPCI4-761J14, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086
- F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974
- F-HEMBA1005962//RPCI11-17015.TV RPCI-11 Homo sapiens genomic clone RPCI-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821
- F-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=I, genomic survey sequence.//9.3e-73:372:97//AQ147357
- F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516
- F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of the complete sequence.//6.3e-07:423:60//AE001408
- F-HEMBA1005999//Homo sapiens chromosome 4 clone CO026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599

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F-HEMBA1006002
 F-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405
 F-HEMBA1006031
 F-HEMBA1006035
 F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009
 F-HEMBA1006042//Homo sapiens chromosome 10 clone C1T987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:70//AC005386
 F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153
 F-HEMBA1006081
 F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500
 F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098
 F-HEMBA1006100//Homo sapiens chromosome 10 clone C1T987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880
 F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(I V). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177
 F-HEMBA1006121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 691N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL031672
 F-HEMBA1006124//CIT-HSP-2355B17.TF CIT-HSP Homo sapiens genomic clone 2355B17, genomic survey sequence.//0.044:225:61//AQ058966
 F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085
 F-HEMBA1006138//Homo sapiens DNA sequence from PAC454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162
 F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500
 F-HEMBA1006155//H.sapiens CpG island DNA genomic Msel fragment, clone 119b6, forward read cpg119b6.f1a.//1.0:85:72//Z64428

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F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693
 F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400
 F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PA C clone pDJ105119, complete sequence.//1.4e-22:194:74//AC005318
 10 F-HEMBA1006198
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557
 F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074
 F-HEMBA1006252//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664
 F-HEMBA1006253
 F-HEMBA1006259//HS_2231_A1_D10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722
 F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673
 F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791
 F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134
 30 F-HEMBA1006283
 F-HEMBA1006284//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289
 F-HEMBA1006291//HS_2208_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804
 F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415
 40 F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070
 F-HEMBA1006310//Rattus norvegicus cytosolic sortin g protein PACS-1a (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183
 F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splice s), complete cds.//1.5e-46:485:73//L29074
 F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//

0.0032:61:91//B40563
 F-HEMBA1006344//HS-1009-A2-B02-WF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420
 F-HEMBA1006347//Drosophila melanogaster males-abse nt on the first (mof)gene, complete cds.//1.6e-31:484:68//U71219
 F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671
 F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244
 F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413
 F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327
 F-HEMBA1006380//CIT-HSP-2172K18.TF CIT-HSP Homo sapiens genomic clone 2172K18, genomic survey sequence.//1.3e-110:525:99//B92570
 F-HEMBA1006381//HS-1045-B2-F10-WF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813
 F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC11-36 OE11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806
 F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//3.7e-15:157:78//AC005179
 F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unknown putative gene, a pseudogene with high similarity to part of anti gen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165
 F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.//2.4e-41:438:76//AF107885
 F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein ho

molog). Contains ESTs, STSs and GSSs, complete sequence.//0.027:293:64//AL031781
 F-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930
 F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465
 F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088
 F-HEMBA1006446//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749
 F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560
 F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.0:293:59//AC006120
 F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709
 F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247
 F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBNL H167), complete sequence.//2.9e-48:286:84//AC004752
 F-HEMBA1006485//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence.//0.96:283:59//AC006031
 F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577
 F-HEMBA1006489//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283
 F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//6.0e-122:337:100//AC005828
 F-HEMBA1006494//Homo sapiens chromosome 7qtel0 BAC E3, complete sequence.//3.8e-23:459:68//AF093117
 F-HEMBA1006497//HS_3023_B2_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequenc

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e. //2.3e-81:433:95//AQ093846
 F-HEMBA1006502//H.sapiens 7SL repeat (clones 2-19 b). //1.6e-13:86:87//X62364
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds. //2.3e-139:470:98//AB014566
 F-HEMBA1006521//Human BAC clone RC167B05 from 7q21, complete sequence. //4.3e-27:406:71//AC003991
 F-HEMBA1006530//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE. //2.9e-27:408:65//AL031650
 F-HEMBA1006535//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE. //0.028:599:60//AL034557
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds. //1.4e-171:654:98//AF093419
 F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene. //3.8e-104:811:80//Z73986
 F-HEMBA1006559//Mus musculus PRAJA1 (Prajai) mRNA, complete cds. //4.8e-99:386:82//U06944
 F-HEMBA1006562//Human fructose-1,6-bisphosphatase (FBP1) gene, exon 1. //0.012:322:60//U21925
 F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.0026:580:58//AC005504
 F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds. //6.3e-08:231:70//U39357
 F-HEMBA1006579//CIT-HSP-2380A22. TR CIT-HSP Homo sapiens genomic clone 2380A22, genomic survey sequence. //0.036:250:62//AQ197107
 F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. //1.0:225:63//AL021841
 F-HEMBA1006595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE. //3.6e-50:689:69//AL022156
 F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces. //1.9e-42:253:84//AC004166
 F-HEMBA1006612//RPC111-88F20.TJ RPC111 Homo sapiens genomic clone R-88F20, genomic survey sequence. //1.1e-51:266:98//AQ286726
 F-HEMBA1006617//HS_2193_B2_H07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence. //1.1e-59:413:85//AQ299685
 F-HEMBA1006624//Human DNA sequence from clone 406A

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7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and CSSs, complete sequence. //1.4e-35:257:89//AL023284
 F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ356d6, complete sequence. //9.6e-112:800:83//AC002036
 F-HEMBA1006635//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE. //0.15:393:58//AL031745
 F-HEMBA1006639//Petromyzon marinus polyadenylate binding protein (PABP)mRNA, complete cds. //9.6e-15:318:68//AF032896
 F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces. //0.58:254:65//AC006148
 F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds. //1.5e-37:108:88//U94479
 F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence. //1.3e-154:671:96//AC005601
 F-HEMBA1006653
 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence. //5.2e-110:254:93//AC005189
 F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence. //1.4e-14:177:76//AC004554
 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56. //5.5e-15:122:90//Y12065
 F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence. //0.098:218:63//AC004755
 F-HEMBA1006682//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE. //1.4e-05:719:57//AL034346
 F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence. //3.1e-22:151:78//AC006011
 F-HEMBA1006696//CITBI-E1-2522D16.TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence. //5.6e-17:324:66//AQ280738
 F-HEMBA1006708
 F-HEMBA1006709
 F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces. //3.3e-08:136:79//AC005537
 F-HEMBA1006737//Homo sapiens chromosome 17, clone

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hRPK.269_G_24, complete sequence.//5.8e-162:497:98//AC005828
 F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//7.4e-48:320:87//AC004796
 F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBC) genes, ESTs and STSs.//4.1e-129:804:85//Z83850
 F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//2.2e-162:766:99//AC005752
 F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOX NC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465
 F-HEMBA1006779//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, CSS, complete sequence.//1.4e-103:355:87//AL022727
 F-HEMBA1006780//CIT-HSP-2359P7.TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208
 F-HEMBA1006789//nbxb0037I13r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0037I13r, genomic survey sequence.//0.00011:288:63//AQ290474
 F-HEMBA1006795//CIT-HSP-2307E3.TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298
 F-HEMBA1006807//Homo sapiens mRNA for SPOP.//1.2e-66:651:73//AJ000644
 F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_0_9, complete sequence.//6.0e-116:541:99//AC004797
 F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262
 F-HEMBA1006832//Homo sapiens (subclone 3_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196
 F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.//0.15:403:60//AB020872
 F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.20:472:57//AE001369
 F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:76//AF046757

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F-HEMBA1006885//HS_2208_B2_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-18:206:76//AQ089246
 F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, CSS, complete sequence.//5.4e-07:298:65//AL031321
 F-HEMBA1006914//S.pombe chromosome II cosmid c16H5.//0.00040:194:66//AL022104
 10 F-HEMBA1006921//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//1.1e-174:813:99//AC006027
 F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704
 F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275
 F-HEMBA1006936
 F-HEMBA1006938//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MALIP4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747
 20 F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841
 F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X, contains STS and polymorphic CA repeat.//0.67:217:62//Z82205
 F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828
 F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058
 30 F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071
 F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209
 F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence.//0.99:388:58//AC002328
 40 F-HEMBA1007017//Sequence 3 from Patent W09416067.//0.96:220:62//A39358
 F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088
 F-HEMBA1007045
 F-HEMBA1007051//Caenorhabditis elegans cosmid Y57C11C, complete sequence.//0.17:343:60//Z99281
 F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056
 F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572
 50 F-HEMBA1007066//HS_3116_A2_A03_T7 CIT Approved Hum

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an Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467

F-HEMBA1007073//Homo sapiens 12q13 PAC RPC11-316M2 4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.3e-54:519:68//AC004242

F-HEMBA1007078//CIT-HSP-2318N6.TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076

F-HEMBA1007080

F-HEMBA1007085//Streptomyces coelicolor cosmid 7A 1.//3.5e-06:496:59//AL034447

F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:56//Z98551

F-HEMBA1007112//HS_2171_A1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865

F-HEMBA1007113//Human DNA sequence from clone 1044 017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875

F-HEMBA1007121//Caenorhabditis elegans cosmid ZK43 0.//1.4e-08:265:64//U42833

F-HEMBA1007129//CITBI-E1-2504A5.TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence.//0.97:267:62//AQ264035

F-HEMBA1007147//HS_3208_A2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=8 Row=E, genomic survey sequence.//9.1e-90:466:95//AQ176696

F-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//6.0e-138:524:98//AC005239

F-HEMBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780

F-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//2.0e-62:318:97//AF062085

F-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC005911

F-HEMBA1007194//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492

F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//D86987

F-HEMBA1007206//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//0.024:342:63//AC004223

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F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340

F-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68//J00060

F-HEMBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//V00899

F-HEMBA1007256//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240

10 F-HEMBA1007267//HS_3218_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence.//2.9e-62:393:87//AQ181128

F-HEMBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//1.1e-63:314:99//B95401

F-HEMBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//3.1e-31:401:72//AC004638

20 F-HEMBA1007281//HS_3115_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence.//5.0e-70:372:96//AQ186691

F-HEMBA1007288//Human DNA sequence from clone 422G 23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98//AL031003

F-HEMBA1007300//Canis familiaris PDE5 mRNA for 3', 5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467

30 F-HEMBA1007301//COL1A1=type I collagen pro alpha 1 (I) chain propeptide {3' region} [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 85 5 nt].//1.7e-08:388:61//S64596

F-HEMBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-84:390:75//AC000399

F-HEMBA1007320

F-HEMBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence.//0.091:260:64//AC004485

F-HEMBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140

F-HEMBA1007341//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-18:408:64//AC006120

F-HEMBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//8.7e-25:50

50 0:62//AC005377

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F-HEMBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete sequence.//0.75:269:61//AC005738

F-HEMBA1000005//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//5.0e-05:441:60//AC004617

F-HEMBA1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491

F-HEMBA1000018//HS_2179_B2_E04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250

F-HEMBA1000024//Human DNA sequence from PAC 106I20 on chromosome 22q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369

F-HEMBA1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.96:198:62//AQ062938

F-HEMBA1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173

F-HEMBA1000036//H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857

F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928

F-HEMBA1000039//HS_2167_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404

F-HEMBA1000044//Borrelia burgdorferi (section 50 of f 70) of the complete genome.//1.0e-07:486:61//AE001164

F-HEMBA1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507

F-HEMBA1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseudo?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170

F-HEMBA1000054//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349

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F-HEMBA1000055//Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880

F-HEMBA1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096

F-HEMBA1000083

F-HEMBA1000089//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.0036:679:56//AL031744

F-HEMBA1000099//Homo sapiens chromosome 18 BAC RPC111-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909

F-HEMBA1000103//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210

F-HEMBA1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450

F-HEMBA1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521

F-HEMBA1000136//Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.//0.59:217:66//Z74697

F-HEMBA1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid f14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090

F-HEMBA1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542

F-HEMBA1000173//Homo sapiens 12q24 BAC RPC11-162P23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.4e-160:562:93//AC002996

F-HEMBA1000175

F-HEMBA1000198//HS_3071_A2_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388

F-HEMBA1000215//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839

F-HEMBA1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808

F-HEMBA1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792

F-HEMBA1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ES

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Ts and CpG island.//1.7e-90:175:92//Z69890
 F-HEM BB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918
 F-HEM BB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7unordered pieces.//4.8e-08:355:63//AC005522
 F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587
 F-HEM BB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M98818
 F-HEM BB1000264//Human clone C3 CHL1 protein (CHLR1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968
 F-HEM BB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems HumanBAC library) complete sequence.//3.8e-16:176:78//AC004470
 F-HEM BB1000272//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.011:379:58//AE001369
 F-HEM BB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project).//0.92:272:61//AL022580
 F-HEM BB1000284//Human Xp22 BAC CT-285I15 (from Cal Tech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366
 F-HEM BB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like; zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745
 F-HEM BB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007
 F-HEM BB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic survey sequence.//0.00033:173:65//AL026242
 F-HEM BB1000318//HS_3244_B2_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951
 F-HEM BB1000335//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence.//0.63:285:61//AC005968
 F-HEM BB1000336
 F-HEM BB1000337//Homo sapiens chromosome 4 clone B208C5 map 4q25, complete sequence.//0.0014:309:64//AC004051

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F-HEM BB1000338//HS_3108_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356
 F-HEM BB1000339//Homo sapiens 12q24 PAC RPCI1-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351
 F-HEM BB1000341
 F-HEM BB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547
 F-HEM BB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989
 F-HEM BB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090
 F-HEM BB1000374//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409
 F-HEM BB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//3.5e-54:352:88//AL034377
 F-HEM BB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982
 F-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838
 F-HEM BB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//7.7e-15:466:63//AC002368
 F-HEM BB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714
 F-HEM BB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D11S1 through D11S25, complete sequence.//0.013:399:62//AC001228
 F-HEM BB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263
 F-HEM BB1000438//RPCI11-21E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21E14, genomic survey sequence.//0.0030:295:63//B83110
 F-HEM BB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone 1147g11, complete sequence.//2.5e-33:372:72//AC000035
 F-HEM BB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c oxidase, delta-aminolevulinate synthase (erythroid); 5-aminolevulin

- inic acid synthase. (EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.10 5, EC 3.1.3.46), ESTs and STS. //1.3e-51:534:72//Z83821
- F-HEM BB1000455//*Saccharomyces cerevisiae* mitochondrion origin of replication (ori6) and oli1 gene, complete cds. //0.016:522:58//L36899
- F-HEM BB1000472
- F-HEM BB1000480
- F-HEM BB1000487//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12803, WORKING DRAFT SEQUENCE. //0.00013:314:64//Z98742
- F-HEM BB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE. //4.1e-110:529:98//AL034423
- F-HEM BB1000491//*Plasmodium falciparum* chromosome 2, section 25 of 73 of the complete sequence. //0.10:187:65//AE001388
- F-HEM BB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //3.7e-06:637:58//AL022577
- F-HEM BB1000510//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence. //3.1e-96:737:81//AC005553
- F-HEM BB1000518//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces. //0.00014:163:68//AC004676
- F-HEM BB1000523//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence. //0.41:349:56//AL010212
- F-HEM BB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus. //6.6e-37:138:96//Y11710
- F-HEM BB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //3.9e-56:683:71//AB020860
- F-HEM BB1000554//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE. //2.2e-51:282:84//AJ011929
- F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds. //6.1e-32:537:65//AB018293
- F-HEM BB1000564
- F-HEM BB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //8.2e-33:26 50
- 8:73//AC005077
- F-HEM BB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence. //5.8e-47:734:66//AL022476
- F-HEM BB1000586//H.sapiens highly polymorphic microsatellite DNA. //0.030:147:67//X79883
- F-HEM BB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence. //6.3e-41:278:83//AC002300
- F-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence. //1.1e-182:871:98//AC005184
- F-HEM BB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19. //0.012:185:64//AF009074
- F-HEM BB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence. //1.2e-131:353:93//AF053356
- F-HEM BB1000598//Homo sapiens 12p13.3 BAC RPC13-488B23 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //9.1e-58:600:72//AC006207
- F-HEM BB1000623//cDNA encoding *Coliolum manganese* peroxidase. //0.89:284:62//E12284
- F-HEM BB1000630//*Mus musculus* clone NSAT47 non satellite RNA sequence. //1.9e-15:129:87//U26231
- F-HEM BB1000631//Sequence 26 from patent US 5708157. //3.2e-27:180:88//I80057
- F-HEM BB1000632//Human mRNA for KIAA0351 gene, complete cds. //1.6e-48:811:65//AB002349
- F-HEM BB1000637//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE, 5 unordered pieces. //4.1e-58:649:73//AC005478
- F-HEM BB1000638//HS_3051_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence. //0.0032:497:56//AQ155234
- F-HEM BB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //2.4e-50:791:68//AC005077
- F-HEM BB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence. //5.2e-64:775:69//AC003009
- F-HEM BB1000652//Homo sapiens chromosome 10 clone CRI-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces. //2.7e-52:334:89//AC006186
- F-HEM BB1000665//Human DNA sequence from clone 452M

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16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493

F-HEM BB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island.//9.6e-95:399:78//Z84488

F-HEM BB1000673//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic surveysequence.//3.8e-50:293:92//AQ155121

F-HEM BB1000684//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65:282:83//Z93241

F-HEM BB1000693//Homo sapiens neuroan1 mRNA, complete cds.//1.6e-118:575:97//AF040723

F-HEM BB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:61//ACO05507

F-HEM BB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118

F-HEM BB1000709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554

F-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475

F-HEM BB1000726//Human Chromosome 16 BAC clone CIT9 87SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321

F-HEM BB1000738//Human Xq28 cosmids U126C1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889

F-HEM BB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//6.2e-46:262:89//ACO05849

F-HEM BB1000763//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//1.6e-99:316:98//AL034405

F-HEM BB1000770//Human DNA sequence from clone 80I19 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//0.044:325:60//AL022727

F-HEM BB1000774

F-HEM BB1000781//Sequence 3 from patent US 5753446.//1.2e-92:599:86//ARO08277

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F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds.//9.3e-64:672:71//AB014577

F-HEM BB1000790//Homo sapiens 12q13.1 PAC RPC11-228 P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.4e-41:460:74//AC004801

F-HEM BB1000794//HS_3034_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic surveysequence.//1.8e-74:378:97//AQ117099

10 F-HEM BB1000807//H. sapiens CpG island DNA genomic Msel fragment, clone 39d7, reverse read cpg39d7.rtl a.//8.5e-14:95:97//Z58412

F-HEM BB1000810//H. sapiens chromosome 22 CpG island DNA genomic Msel fragment, clone 303a8, complete read.//3.2e-05:138:71//Z79983

F-HEM BB1000821//HS_2168_B1_A12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic surveysequence.//0.85:208:60//AQ086361

20 F-HEM BB1000822//Human BAC clone GS113H23 from 5p15.2, complete sequence.//3.0e-06:361:60//AC003015

F-HEM BB1000826//Human BAC clone RG180F08 from 7q31, complete sequence.//1.1e-27:360:69//AC002431

F-HEM BB1000827

F-HEM BB1000831

F-HEM BB1000835//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//0.00098:234:63//AL023581

30 F-HEM BB1000840//Human Chromosome 11 Cosmid cSRL97a 6, complete sequence.//4.5e-61:328:79//U73649

F-HEM BB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//9.7e-144:809:87//AL021068

40 F-HEM BB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.12:492:58//AC004157

F-HEM BB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0024:212:67//AC004157

F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial cds.//1.5e-32:200:94//AF085351

50 F-HEM BB1000883//HS_3065_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl

- one Plate=3065 Col=8 Row=F, genomic survey sequence.//0.0017:152:66//AQ137687
 F-HEM BB1000887
 F-HEM BB1000888//CIT-HSP-2329A10. TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey sequence.//1.5e-31:172:98//AQ044369
 F-HEM BB1000890
 F-HEM BB1000893//Plasmodium falciparum MAL3P2, complete sequence.//9.5e-06:768:56//AL034558
 F-HEM BB1000908//Homo sapiens clone DJ1119N05, complete sequence.//4.5e-21:199:82//AC004968
 F-HEM BB1000910//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL4P1, WORKING DRAFT SEQUENCE.//0.72:366:59//AL034557
 F-HEM BB1000913//HS_3078_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//9.9e-12:221:63//AQ144507
 F-HEM BB1000915//Homo sapiens DNA for (CGC)_n trinucleotide repeat region, isolate P4.//1.2e-49:252:99//AJ001215
 F-HEM BB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H62), complete sequence.//2.3e-42:316:76//AC006077
 F-HEM BB1000927//Human BDR-2 mRNA for hippocalcin, complete cds.//3.6e-30:528:65//D16593
 F-HEM BB1000947//CpG0856B CpIOWAgDNA1 Cryptosporidium parvum genomic, genomic survey sequence.//0.81:262:62//AQ254493
 F-HEM BB1000959//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//1.2e-43:454:75//Z84487
 F-HEM BB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds.//8.3e-42:458:72//AF099973
 F-HEM BB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence.//0.98:196:63//AB005234
 F-HEM BB1000981
 F-HEM BB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//2.9e-06:566:57//AC004476
 F-HEM BB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//0.099:391:57//Z98753
 F-HEM BB1000996//Human DNA sequence from BAC 999D10 on chromosome 22q13.3. Contains two BAC end-sequences (GSSs).//6.2e-33:227:80//Z94802
 F-HEM BB1001004
 F-HEM BB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence.//4.0e-13:164:79/ 50
 /AC002551
 F-HEM BB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//7.5e-13:229:69//AC002310
 F-HEM BB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LANL), complete sequence.//0.32:474:58//AC005751
 F-HEM BB1001020//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.6e-39:218:80//AF069291
 F-HEM BB1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//5.3e-05:656:59//AF070717
 F-HEM BB1001037//CIT-HSP-2358K16. TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence.//6.6e-05:228:64//AQ080539
 F-HEM BB1001047//Homo sapiens cosmid Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence.//4.0e-27:385:71//U82671
 F-HEM BB1001051//H. sapiens mRNA for FAN protein.//1.2e-27:160:98//X96586
 F-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5unordered pieces.//2.3e-89:180:91//AC006014
 F-HEM BB1001058//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-41:468:74//AC006060
 F-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.3e-122:785:86//U49973
 F-HEM BB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING DRAFT SEQUENCE.//7.1e-162:770:99//AL034375
 F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//3.1e-146:736:95//AF034803
 F-HEM BB1001096//Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon(atpCDG AHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds.//0.00088:690:57//AF008210
 F-HEM BB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//2.1e-76:368:99//AF049612
 F-HEM BB1001105//CIT-HSP-2185N1. TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence.//1.0e-09:136:76//AQ002987
 F-HEM BB1001112//Rattus rattus sec61 homologue mRNA, complete cds.//1.0e-108:909:76//M96630

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F-HEM BB1001114//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//7.2e-07:459:59//AC005284

F-HEM BB1001117//HS_2178_B1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence.//7.8e-50:331:86//AQ068244

F-HEM BB1001119//Human collagen type XII alpha-1 precursor (COL12A1) mRNA, complete cds.//1.6e-25:150:98//U73778

F-HEM BB1001126

F-HEM BB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//2.8e-24:228:80//AC004673

F-HEM BB1001137

F-HEM BB1001142//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//1.0e-40:231:76//AC004617

F-HEM BB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.9e-47:640:67//AF015264

F-HEM BB1001153//CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.//0.76:136:67//AQ075724

F-HEM BB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat.//9.9e-63:259:79//AL008712

F-HEM BB1001175//Human mRNA for ankyrin motif, complete cds.//2.2e-34:509:66//D78334

F-HEM BB1001177//CIT-HSP-2321I17.TR CIT-HSP Homo sapiens genomic clone 2321I17, genomic survey sequence.//5.9e-27:320:75//AQ036473

F-HEM BB1001182//RPCI11-30J5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30J5, genomic survey sequence.//5.7e-06:62:96//B85188

F-HEM BB1001199

F-HEM BB1001208//HS_2026_B1_C07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237

F-HEM BB1001209//CITBI-E1-2521F23.TF CITBI-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357

F-HEM BB1001210//HS_3102_A2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196

F-HEM BB1001218//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT S

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SEQUENCE.//1.0e-31:315:72//AL031291

F-HEM BB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504

F-HEM BB1001234//H.sapiens CpG island DNA genomic Msel fragment, clone 39f9, forward read cpg39f9.ft1e.//4.0e-30:171:97//Z65435

F-HEM BB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754

F-HEM BB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087

F-HEM BB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032

F-HEM BB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173

F-HEM BB1001267//Homo sapiens chromosome 17, clone hRPK.488_L_1, complete sequence.//3.5e-30:236:78//AC005303

F-HEM BB1001271//HS_3011_A1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217

F-HEM BB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20, genomic survey sequence.//1.8e-16:109:97//AQ060969

F-HEM BB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366

F-HEM BB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387

F-HEM BB1001294//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035

F-HEM BB1001302

F-HEM BB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence.//2.2e-07:370:61//B69144

F-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:663:85//U92703

F-HEM BB1001315//Homo sapiens chromosome 10 clone L A10NC01_40_G_3 map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096

F-HEM BB1001317//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete se

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quence.//1.4e-122:680:91//AC006210
 F-HEM BB1001326//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//AC004129
 F-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//3.7e-56:458:79//D63850
 F-HEM BB1001335//HS_3055_A1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=0, genomic survey sequence.//1.0:222:63//AQ147384
 F-HEM BB1001337//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.0e-74:319:85//AC003983
 F-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//U85056
 F-HEM BB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871
 F-HEM BB1001348//Homo sapiens BAC clone NB0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//AC006041
 F-HEM BB1001356//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:386:59//AC005079
 F-HEM BB1001364//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//0.97:349:61//AC004662
 F-HEM BB1001366//Homo sapiens chromosome 10 clone CIT987SK-118815 map 10p11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876
 F-HEM BB1001367//Homo sapiens chromosome 17, clone hRPC.906_A_24, complete sequence.//3.0e-55:510:76//AC004408
 F-HEM BB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//AC005192
 F-HEM BB1001380//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:78//AC006204
 F-HEM BB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//AF071314
 F-HEM BB1001387//Leishmania tarentolae mitochondria 12S ribosomal RNA gene.//7.1e-05:546:58//X02354
 F-HEM BB1001394//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//4.0e-129:788:88//AC005023
 F-HEM BB1001410//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555
 F-HEM BB1001424//Mus musculus Chromosome 4 BAC clone

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e BacB6, complete sequence.//0.0012:435:59//AC003019
 F-HEM BB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.8e-17:360:64//AC005482
 F-HEM BB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367
 F-HEM BB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
 F-HEM BB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//L18966
 F-HEM BB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:385:62//AC004768
 F-HEM BB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790
 F-HEM BB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382
 F-HEM BB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:59//AF001549
 F-HEM BB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320
 F-HEM BB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564
 F-HEM BB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873
 F-HEM BB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080
 F-HEM BB1001527
 F-HEM BB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h In DGCRRegion, complete sequence.//1.3e-79:696:79//AC000089
 F-HEM BB1001535//O. aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268
 F-HEM BB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548
 F-HEM BB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262
 F-HEM BB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605

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F-HEM BB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041

F-HEM BB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989

F-HEM BB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003

F-HEM BB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-166:816:97//AL031677

F-HEM BB1001586

F-HEM BB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261

F-HEM BB1001603

F-HEM BB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289

F-HEM BB1001619//HS_3079_B1_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388

F-HEM BB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089

F-HEM BB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559

F-HEM BB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANF precursor (Atrial Natriuretic peptide ANP, Prepronatriodilatin), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155

F-HEM BB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MP012, complete sequence.//0.00097:721:58//AB006702

F-HEM BB1001653//Homo sapiens chromosome 2 clone 10

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1B6 map 2p11, complete sequence.//0.15:276:63//AC002038

F-HEM BB1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320

F-HEM BB1001668//F16C15-T7 ICF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308

F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546

F-HEM BB1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//I86429

F-HEM BB1001685//CIT-HSP-228709.TF CIT-HSP Homo sapiens genomic clone 228709, genomic survey sequence.//2.3e-34:191:97//B99261

F-HEM BB1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178

F-HEM BB1001704//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575

F-HEM BB1001706

F-HEM BB1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543

F-HEM BB1001717//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.1e-13:723:58//AJ223323

F-HEM BB1001735//Human PAC clone DJ0596009 from 7p15, complete sequence.//1.3e-36:427:73//AC003074

F-HEM BB1001736//S.pombe chromosome II cosmid c4B4.//0.0085:479:57//AL023706

F-HEM BB1001747//Homo sapiens PAC clone DJ1002N02 from 7p21-p22, complete sequence.//4.0e-112:532:84//AC005376

F-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.3e-98:395:82//AC005829

F-HEM BB1001753//S.maximus repeat region, 342bp.//4.2e-11:69:85//Z78099

F-HEM BB1001756//Homo sapiens full length insert cDNA clone ZD86A11.//0.0015:302:62//AF088064

F-HEM BB1001760//P.falciparum complete gene map of

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plastid-like DNA (IR-A).//0.011:615:56//X95275
 F-HEMBB1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184
 F-HEMBB1001785//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746
 F-HEMBB1001797//Human heterogenous nuclear RNA W16 W.//0.00012:83:86//X17272
 F-HEMBB1001802//Plasmodium falciparum MAL3P7, complete sequence.//1.8e-11:538:60//AL034559
 F-HEMBB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882
 F-HEMBB1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204
 F-HEMBB1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209
 F-HEMBB1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291012, genomic survey sequence.//7.6e-08:73:94//AQ004168
 F-HEMBB1001836//Homo sapiens 12q13.1 PAC RPC11-228 P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801
 F-HEMBB1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073
 F-HEMBB1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0027:812:58//AC005504
 F-HEMBB1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581
 F-HEMBB1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563
 F-HEMBB1001868//Rattus norvegicus clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with CGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145
 F-HEMBB1001869//Homo sapiens full length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974
 F-HEMBB1001872
 F-HEMBB1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000
 F-HEMBB1001875//Human DNA sequence from clone J428

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A131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209
 F-HEMBB1001880//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403
 F-HEMBB1001899//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 4-10, complete sequence.//0.0038:425:58//AL010216
 F-HEMBB1001905//S.pombe chromosome III cosmid c33 0.//1.1e-23:520:62//AL031603
 F-HEMBB1001906
 F-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//3.7e-82:672:81//U47742
 F-HEMBB1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505
 F-HEMBB1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705
 F-HEMBB1001915//Caenorhabditis elegans cosmid T05H 10, complete sequence.//1.2e-16:283:67//Z47812
 F-HEMBB1001921//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//3.4e-07:803:58//AC003950
 F-HEMBB1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391
 F-HEMBB1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181
 F-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//3.2e-158:745:99//AB020867
 F-HEMBB1001944//, complete sequence.//4.1e-60:638:73//AC005815
 F-HEMBB1001945//HS_3185_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882
 F-HEMBB1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390
 F-HEMBB1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899
 F-HEMBB1001952//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341
 F-HEMBB1001953//Homo sapiens chromosome 17, clone

- hRPK.795_F_17, complete sequence.//0.11:589:58//AC005284
- F-HEM BB1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941
- F-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.//2.8e-147:727:97//AC005736
- F-HEM BB1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963
- F-HEM BB1001973//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844
- F-HEM BB1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071
- F-HEM BB1001988//D.polychroa microsatellite sequence (clone Dp 1C e12).//4.5e-07:337:62//X92189
- F-HEM BB1001990//HS_3234_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ024689
- F-HEM BB1001996//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507
- F-HEM BB1001997//Homo sapiens clone RC140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069
- F-HEM BB1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153
- F-HEM BB1002005//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685
- F-HEM BB1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00033:790:56//AC005506
- F-HEM BB1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056
- F-HEM BB1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012
- F-HEM BB1002043
- F-HEM BB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//3.0e-16
- 7:809:97//AC005740
- F-HEM BB1002045
- F-HEM BB1002049//Homo sapiens chromosome 17, clone hRPC.161_P_9, complete sequence.//0.87:177:65//AC006237
- F-HEM BB1002050//Streptomyces coelicolor cosmid D7 8.//8.5e-08:644:58//AL034355
- F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512
- 10 F-HEM BB1002069
- F-HEM BB1002092//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064
- F-HEM BB1002094//Homo sapiens genomic DNA, 21q region, clone: 125H6N2, genomic survey sequence.//2.9e-49:302:83//AG001476
- F-HEM BB1002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence.//0.00023:542:61//AC004035
- 20 F-HEM BB1002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3e-43:533:70//U43843
- F-HEM BB1002139//HS-1048-A2-B02-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714
- F-HEM BB1002142//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748
- 30 F-HEM BB1002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421
- F-HEM BB1002189//Homo sapiens cosmid ICRFc104I0935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998
- F-HEM BB1002190//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140
- 40 F-HEM BB1002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I80846
- F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10.//1.2e-23:405:67//X52332
- F-HEM BB1002218//HS_2056_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711
- F-HEM BB1002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648
- 50 F-HEM BB1002247

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F-HEM BB1002249//Homo sapiens DNA sequence from BAC 3418 on chromosome 6p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fl1-2, rat helix destabilizing protein, mouse Topoisomerase-inhibitor suppressed gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIKE pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene 1) genes. Contains ESTs, STSs and GSSs, complete sequence. //4.1e-45:327:83//AL021918

F-HEM BB1002254//Human chromosome 16 BAC clone LANCOSMID-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces. //9.8e-40:315:82//AC002506

F-HEM BB1002255//Plasmodium falciparum MAL3P3, complete sequence. //0.0035:312:62//Z98547

F-HEM BB1002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.013:469:59//AC005504

F-HEM BB1002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence. //5.3e-18:527:61//AC004682

F-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence. //8.6e-139:818:88//U73642

F-HEM BB1002306//HS_3109_A2_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=0, genomic survey sequence. //1.3e-75:371:98//AQ148164

F-HEM BB1002327//HS_3235_B2_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=N, genomic survey sequence. //3.3e-83:418:97//AQ209752

F-HEM BB1002329//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence. //3.3e-31:220:88//AQ263402

F-HEM BB1002340

F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein. //4.1e-154:724:98//AJ010841

F-HEM BB1002358//Human thymidylate kinase (CDC8) mRNA, complete cds. //3.3e-36:192:98//L16991

F-HEM BB1002359//Human Rev interacting protein Rip1 mRNA, complete cds. //1.8e-13:96:96//U55766

F-HEM BB1002364//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 376D21, WORKING DRAFT SEQUENCE. //7.5e-24:202:71//Z98946

F-HEM BB1002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //1.9e-06:674:56//AC004153

F-HEM BB1002381//Homo sapiens chromosome 16, cosmid 50

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clone RT163 (LANL), complete sequence. //0.34:238:61//AC005222

F-HEM BB1002383

F-HEM BB1002387//CIT-HSP-2173E20.TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence. //5.2e-17:434:66//B91052

F-HEM BB1002409//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (CTR2-2), ESTs and CA repeat. //1.2e-56:324:88//AL008712

F-HEM BB1002415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE. //8.9e-35:334:75//AL031319

F-HEM BB1002425//Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence. //1.0e-36:317:76//U62317

F-HEM BB1002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds. //4.3e-88:296:92//U92010

F-HEM BB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE. //2.7e-43:419:78//AL034349

F-HEM BB1002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.3e-27:542:68//AC005534

F-HEM BB1002458//HS_3246_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey sequence. //3.2e-51:257:99//AQ217993

F-HEM BB1002477//Human Grb2-associated binder-1 mRNA A, complete cds. //1.9e-87:493:92//U43885

F-HEM BB1002489

F-HEM BB1002492//Arabidopsis thaliana BAC T15B16. //0.028:516:57//AF104919

F-HEM BB1002495//Homo sapiens chromosome 17, clone hRPK.421_E14, complete sequence. //1.1e-16:297:68//AC006141

F-HEM BB1002502//Homo sapiens clone DJ1163L11, complete sequence. //1.1e-91:675:82//AC005230

F-HEM BB1002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence. //2.7e-11:648:60//AC004605

F-HEM BB1002510//HS_3236_B1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey sequence. //1.2e-06:67:94//AQ205992

F-HEM BB1002520//Homo sapiens BAC clone NH0004N07 from Y, complete sequence. //1.2e-70:580:72//AC006152

F-HEM BB1002522//Homo sapiens Xp22 bin 150 clone GS HB-223P11 (Genome Systems Human BAC library) complete

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ete sequence.//5.6e-22:516:64//AC004553

F-HEM BB1002531

F-HEM BB1002534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346

F-HEM BB1002545//Human BAC clone RG128M16 from 7q21-7q22, complete sequence.//2.7e-44:200:82//AC000059

F-HEM BB1002550//Homo sapiens PAC clone DJ0910117 from 7q11.21-q11.23, complete sequence.//0.22:161:68//AC004927

F-HEM BB1002556//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//7.5e-43:306:77//AC004861

F-HEM BB1002579

F-HEM BB1002582//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520

F-HEM BB1002590//Yeast (*S.cerevisiae*) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471

F-HEM BB1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639

F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749

F-HEM BB1002601//Human BAC clone RG020D02 from 7q22, complete sequence.//1.5e-07:416:60//AC002381

F-HEM BB1002603//Human BAC clone GS552A01 from 7q21-q22, complete sequence.//0.40:341:60//AC002454

F-HEM BB1002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (*Hmx1*) gene, complete cds.//0.0042:460:60//AF009614

F-HEM BB1002610//Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:63//AC003029

F-HEM BB1002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//AC000025

F-HEM BB1002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:324:56//AE001417

F-HEM BB1002617//Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.//2.1e-07:441:60//AF001550

F-HEM BB1002623//*C.hyalina* microsatellite marker DNA (1d ATCC4).//0.57:106:66//Z95304

F-HEM BB1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//U348

19

F-HEM BB1002664//HS_2265_A1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=11 Row=0, genomic survey sequence.//0.54:115:67//AQ101557

F-HEM BB1002677//Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774

F-HEM BB1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492

F-HEM BB1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748

F-HEM BB1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077

F-HEM BB1002692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525

F-HEM BB1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955

F-HEM BB1002699//Mus musculus D6Mm5e protein (D6Mm5e) and DOK protein (Dok) genes, complete cds; and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363

F-HEM BB1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720

F-HEM BB1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151

F-HEM BB1002712//Human DNA sequence from cosmid cU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71

40 187

F-MAMMA1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117

F-MAMMA1000019

F-MAMMA1000020//H. sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//2.0e-40:185:97//Z47553

F-MAMMA1000025//Homo sapiens PAC clone DJ0806A17 from 7p13-p14, complete sequence.//1.0:211:65//AC005483

F-MAMMA1000043//Human angiotensin I-converting enz

3239

yme (ACE) gene, intron12.//0.075:204:65//M73275
 F-MAMMA1000045//Human DNA sequence from clone 142F
 18 on chromosome Xq26.3-27.2 Contains part of a ge
 ne similar to melanoma-associated antigen, EST, GS
 S and an inverted repeat, complete sequence.//4.1e
 -122:495:79//AL031073
 F-MAMMA1000055//M.musculus mRNA for testin.//2.1e-
 35:559:66//X78989
 F-MAMMA1000057//Homo sapiens chromosome 17, clone
 hRPK.259_G_18, complete sequence.//5.5e-121:703:89 10
 //AC005829
 F-MAMMA1000069//Homo sapiens minisatellite ceb1 re
 peat region.//0.00013:329:60//AF048727
 F-MAMMA1000084//Homo sapiens DNA sequence from PAC
 958B3 on chromosome Xp22.11-Xp22.22. Contains EST
 s STS and CpG island.//2.1e-53:445:79//Z93023
 F-MAMMA1000085//Caenorhabditis elegans cosmid Y23E
 5A.//0.0017:164:64//AF077541
 F-MAMMA1000092//Homo sapiens BAC clone GS465N13 fr
 om 7p15-p21, complete sequence.//1.2e-70:598:78//AC 20
 004744
 F-MAMMA1000103//Homo sapiens chromosome 17, clone
 hCIT.91_J_4, complete sequence.//1.1e-156:857:92//A
 C003976
 F-MAMMA1000117//HS_3223_B2_D08_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3223 Col=16 Row=H, genomic survey sequenc
 e.//5.4e-100:527:94//AQ221160
 F-MAMMA1000129//ryanodine receptor.//0.055:492:59/
 /A20359
 F-MAMMA1000133
 F-MAMMA1000134//HS_3078_B1_C02_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3078 Col=3 Row=F, genomic survey sequenc
 e.//2.1e-93:462:97//AQ144362
 F-MAMMA1000139//Homo sapiens Xp22 PAC RPCI1-5G11
 (from Roswell Park Cancer Center) complete sequenc
 e.//3.3e-14:322:65//AC002369
 F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 pro
 tein, complete cds.//6.9e-25:148:97//AB014585 40
 F-MAMMA1000155//Homo sapiens homeobox transcriptio
 n factor barx2 (BARX2)mRNA, complete cds.//1.0e-2
 9:219:87//AF031924
 F-MAMMA1000163
 F-MAMMA1000171//Homo sapiens chromosome 19, CIT-HS
 P BAC 470n8, complete sequence.//6.3e-14:92:88//AC0
 05393
 F-MAMMA1000173//Mus musculus SH3-containing protei
 n SH3P7 mRNA, complete cds. similar to Human Drebri
 n.//2.2e-114:698:87//U58884

3240

F-MAMMA1000175//HS_3050_B1_B03_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3050 Col=5 Row=D, genomic survey sequenc
 e.//6.2e-73:357:99//AQ102678
 F-MAMMA1000183//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone Y313F4, WORKING DRAFT S
 EQUENCE.//4.6e-94:904:73//AL023808
 F-MAMMA1000198//Z.diploperennis repetitive DNA (cl
 one ZEAR 266).//0.18:152:70//X53610
 F-MAMMA1000221//Human Chromosome 15q11-q13 PAC clo
 ne pDJ778a2, complete sequence.//0.017:99:75//AC004
 583
 F-MAMMA1000227//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 467K16, WORKING DRAFT S
 EQUENCE.//0.36:312:62//AL031283
 F-MAMMA1000241//HS_3217_B1_B02_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3217 Col=3 Row=D, genomic survey sequenc
 e.//1.9e-94:456:98//AQ193401
 F-MAMMA1000251//Homo sapiens NF2 gene.//0.00092:27
 0:64//Y18000
 F-MAMMA1000254//Plasmodium falciparum 3D7 chromoso
 me 12 PFYACB8-420 genomic sequence, WORKING DRAFT
 SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC0
 05140
 F-MAMMA1000257//Homo sapiens DNA sequence from PAC
 201D7 on chromosome 6p22.1-22.3. Contains EST and
 STS.//0.00036:230:65//AL022717
 F-MAMMA1000264//Homo sapiens (subclone 9_f5 from P
 30 1 H17) DNA sequence, complete sequence.//1.5e-30:4
 99:68//L81612
 F-MAMMA1000266//Bacillus lyncceorum strain pMEL12 B
 ag320 satellite DNA.//0.28:218:64//AF034430
 F-MAMMA1000270//Human Chromosome 16 BAC clone CIT9
 87SK-A-270G1, complete sequence.//1.4e-157:788:96//
 AF001549
 F-MAMMA1000277//Mycobacterium tuberculosis H37Rv c
 omplete genome; segment 48/162.//0.70:320:61//AL02
 1897
 F-MAMMA1000278//Sequence 23 from patent US 570815
 7.//9.3e-103:540:95//180055
 F-MAMMA1000279//Human DNA sequence from clone 769D
 20 on chromosome Xp21.1-21.3 Contains EST, STS, GS
 S, complete sequence.//2.4e-49:262:77//AL031643
 F-MAMMA1000284//cSRL-165E12-u cSRL flow sorted Chr
 omosome 11 specific cosmid Homo sapiens genomic cl
 one cSRL-165E12, genomic survey sequence.//1.1e-3
 0:324:75//B03004
 F-MAMMA1000287//Homo sapiens, clone hRPK.15_A_1, c
 omplete sequence.//2.7e-54:401:83//AC006213 50

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F-MAMMA1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541
 F-MAMMA1000307//Homo sapiens chromosome 12p13.3 clone RPC15-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces.//0.15:449:59//AC006205
 F-MAMMA1000309//cDNA coding human apolipoprotein E 3.//0.00010:691:58//E00359
 F-MAMMA1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 798A17, WORKING DRAFT SEQUENCE.//0.27:301:60//AL031274
 F-MAMMA1000313
 F-MAMMA1000331//Human Chromosome 16 BAC clone CIT9 87SK-A-735G6, complete sequence.//9.8e-06:151:71//AC002400
 F-MAMMA1000339
 F-MAMMA1000340//HS_2181_B2_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288
 F-MAMMA1000348//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence.//5.3e-30:575:66//AC004139
 F-MAMMA1000356//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-52:264:76//AC005052
 F-MAMMA1000360//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.//6.5e-91:569:88//AC004879
 F-MAMMA1000361//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950
 F-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.9e-114:516:89//AL022345
 F-MAMMA1000385//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//6.9e-26:377:71//AQ279944
 F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:98//AB015132
 F-MAMMA1000395
 F-MAMMA1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-115:845:85//AC005999
 F-MAMMA1000410//HS_3245_A1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768
 F-MAMMA1000413//HS_3223_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl

3242

one Plate=3223 Col=2 Row=L, genomic survey sequence.//1.6e-48:318:89//AQ188456
 F-MAMMA1000414//HS_2027_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369
 F-MAMMA1000416//Drosophila melanogaster DNA sequence (Pls DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004640
 10 F-MAMMA1000421//Homo sapiens clone DJ1129D05, complete sequence.//3.3e-29:223:84//AC005630
 F-MAMMA1000422
 F-MAMMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240
 F-MAMMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973
 F-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//8.0e-99:545:92//AF062484
 20 F-MAMMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283
 F-MAMMA1000444//Human DNA sequence from clone 714B7 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z99755
 F-MAMMA1000446
 F-MAMMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620
 30 F-MAMMA1000468//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017
 F-MAMMA1000472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543
 F-MAMMA1000478//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:369:77//AC005081
 F-MAMMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//3.6e-34:332:77//AC004381
 F-MAMMA1000490//Homo sapiens 12q13.1 PAC RPC11-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:822:87//AC003686
 F-MAMMA1000500//CIT-HSP-231905.TF CIT-HSP Homo sapiens genomic clone 231905, genomic survey sequence.//4.8e-29:175:94//AQ044812
 F-MAMMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gen

3243

e. Contains GSSs and an STS, complete sequence.//
5.7e-45:334:82//AL022336

F-MAMMA1000516//Human DNA sequence from PAC 50A13
on chromosome Xp11. Contains ATP SYNTHASE LIPID BI
NDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G
2, ATP5G3) like pseudogene, ESTs and STSs. Contain
s polymorphic CA repeat.//2.9e-43:529:69//Z92545

F-MAMMA1000522//Human DNA sequence from clone 20J2
3 on chromosome Xq26.2-27.2 Contains ras-related C
3 botulinum toxin substrate 1 (P21-RAC1) (ras-like
protein TC25) EST, CA repeat, STS, CpG island, co
mplete sequence.//2.0e-14:380:63//AL022576

F-MAMMA1000524//Homo sapiens chromosome 10 clone C
IT-HSP-1338F24 map 10p11.2-10p12.1, complete seque
nce.//1.4e-22:420:66//AC006101

F-MAMMA1000559//Human HepG2 3' region cDNA, clone
hmd3f08.//5.4e-29:168:97//D16922

F-MAMMA1000565//RPCI11-61K6.TJ RPCI11 Homo sapiens
genomic clone R-61K6, genomic survey sequence.//1.
7e-120:561:100//AQ194238

F-MAMMA1000567//Human DNA sequence from PAC 179D3,
between markers DXS6791 and DXS8038 on chromosome
X contains S10 GTP-binding protein, ESTs and CpG
island.//3.1e-43:387:80//Z81370 F-MAMMA10
00576//Homo sapiens BAC c
lone RG442F18 from 2, com
plete sequence.//1.2e-30:
237:75//AC005104

F-MAMMA1000583//RPCI11-60
M22. TJ RPCI11 Homo sapien
s genomic clone R-60M22,
genomic survey sequence.//
9.6e-102:487:99//AQ19809
1

F-MAMMA1000585//Homo sapi
ens clone UWGC:djs14 from
7p14-15, complete sequen
ce.//5.2e-39:370:78//AC00
6195

F-MAMMA1000594//Homo sapi
ens chromosome 19, cosmid
R31646, complete sequenc
e.//3.9e-43:328:83//AC005
338

F-MAMMA1000597//Homo sapi
ens chromosome 17, clone
hRPK.481_C_4, complete seq
uence.//1.5e-32:259:82//A
C005839

F-MAMMA1000605//Human DNA 50

3244

sequence *** SEQUENCING
IN PROGRESS *** from clon
e 97P20, WORKING DRAFT SE
QUENCE.//2.4e-59:318:83//
AL031297

F-MAMMA1000612//HS_2188_A
2_D02_MF CIT Approved Hum
an Genomic Sperm Library
D Homo sapiens genomic cl
one Plate=2188 Col=4 Row=
G, genomic survey sequenc
e.//4.8e-30:171:96//AQ116
793

F-MAMMA1000616//HS_3176_A
1_E06_T7 CIT Approved Hum
an Genomic Sperm Library
D Homo sapiens genomic cl
one Plate=3176 Col=11 Row
=I, genomic survey sequenc
e.//4.7e-28:287:79//AQ300
310

F-MAMMA1000621//Human DNA
sequence *** SEQUENCING
IN PROGRESS *** from clon
e 273F20, WORKING DRAFT S
EQUENCE.//0.015:478:58//A
L034371

F-MAMMA1000623

F-MAMMA1000625//DNA encod
ing Hepatitis C virus ant
igen.//0.93:196:61//E0689
8

F-MAMMA1000643//Homo sapi
ens nephrocystin (NPHP1)
mRNA, partial cds.//0.95:
365:59//AF023674

F-MAMMA1000664//HS_3096_B
1_C02_MR CIT Approved Hum
an Genomic Sperm Library
D Homo sapiens genomic cl
one Plate=3096 Col=3 Row=
F, genomic survey sequenc
e.//2.7e-51:257:99//AQ145
137

F-MAMMA1000669//Homo sapi
ens chromosome 19, cosmid
R26908, complete sequenc
e.//2.0e-66:586:67//AC004
785

F-MAMMA1000670//HS_2243_B

3245

2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=B, genomic survey sequence. //8.7e-05:94:80//AQ153650

F-MAMMA1000672//Mus musculus clone OST8270, genomic survey sequence. //3.9e-64:471:81//AF046705

F-MAMMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds. //1.2e-07:186:67//U27489

F-MAMMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2; neurofibromatosis 1 (NF1) exons 28-49; ecotropic viral integration site 2B (EVI2B) exons 1-2; ecotropic viral integration site 2A (EVI2A) exons 1-2; adenylate kinase (AK3) exons 1-2. //3.0e-53:653:70//L05367

F-MAMMA1000707//CIT-HSP-2302019. TR CIT-HSP Homo sapiens genomic clone 2302019, genomic survey sequence. //1.8e-08:131:77//AQ017947

F-MAMMA1000713//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats. //0.062:134:67//U00762

F-MAMMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end. //1.0:266:61//X15028

F-MAMMA1000718//CIT-HSP-2171B10. TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence. //10.0:266:61//X15028

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ce. //3.6e-05:289:60//B95401

F-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence. //4.4e-184:842:98//AC005781

F-MAMMA1000723//Homo sapiens clone DJ0892G19, complete sequence. //8.8e-05:430:60//AC004917

F-MAMMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence. //3.8e-55:796:66//AC004274

F-MAMMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a. //6.6e-77:555:74//AF064859

F-MAMMA1000733//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE. //0.98:479:58//AL031749

F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds. //7.3e-168:802:98//AF100141

F-MAMMA1000738//S. cerevisiae chromosome XIV reading frame ORF YNL132w. //8.6e-31:626:63//Z71408

F-MAMMA1000744//Gorilla Alu-repetitive sequence in beta-globin gene cluster. //2.7e-54:410:82//X06123

F-MAMMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10F4, complete sequence. //3.7e-109:779:83//AC004158

F-MAMMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unor

3247

dered pieces. //1. 2e-20:44
4:63//AC005075
F-MAMMA1000760//Homo sapi
ens clone RG015P03, compl
ete sequence. //1. 5e-44:40
3:79//AC005048
F-MAMMA1000761//Homo sapi
ens Chromosome 7 BAC Clon
e 239c10, WORKING DRAFT S
EQUENCE, 9 unordered piec 10
es. //2. 3e-22:159:81//AC00
4166
F-MAMMA1000775//Homo sapi
ens chromosome 17, clone
hRPK. 849_N_15, complete s
equence. //1. 3e-51:789:68/
/AC005703
F-MAMMA1000776//Human DNA
sequence from BAC 57G9 o
n chromosome 22q12.1 Cont 20
ains ESTs, CA repeat, GS
S. //5. 7e-40:238:78//Z9511
6
F-MAMMA1000778//Human DNA
sequence *** SEQUENCING
IN PROGRESS *** from clon
e 153G14, WORKING DRAFT S
EQUENCE. //7. 6e-29:222:84/
/AL031118
F-MAMMA1000782//Human 2, 4 30
-dienoyl-CoA reductase ge
ne, exon 9. //0. 90:137:62/
/U94987
F-MAMMA1000798//*** SEQUE
NCING IN PROGRESS *** EPM
1/APECED region of chromo
some 21, clones A68E8, B1
27P21, B173L3, B23N8, C12
42C9, C579E2, A70B6, B159
G9, B175D10, B52C10, C124 40
G1 Note: Sequencing in th
is region has been discon
tinued by the Stanford Hu
man Genome Center, WORKIN
G DRAFT SEQUENCE, 50 unor
dered pieces. //0. 00058:16
3:71//AC003656
F-MAMMA1000802//Homo sapi
ens chromosome 19, cosmid
R33729, complete sequenc 50

3248

e. //6. 3e-151:714:99//AC00
5339
F-MAMMA1000824//Homo sapi
ens 12p13.3 BAC RPC111-54
3P15 (Roswell Park Cancer
Institute Human BAC Libr
ary) complete sequence. //4.
2e-104:503:99//AC005912
F-MAMMA1000831//Homo sapi
ens clone UWGC:g1211a139,
complete sequence. //0. 7
6:302:58//AC005502
F-MAMMA1000839//Human BAC
clone RG013L03 from 7q2
1, complete sequence. //1.
9e-54:322:68//AC002456
F-MAMMA1000841//Human DNA
sequence *** SEQUENCING
IN PROGRESS *** from clon
e 968D22, WORKING DRAFT S
EQUENCE. //6. 7e-140:647:92
//AL023755.
F-MAMMA1000842//, complet
e sequence. //0. 0068:499:5
9//AC005817
F-MAMMA1000843//Plasmodiu
m falciparum 3D7 chromoso
me 12 PFYAC588 genomicseq
uence, WORKING DRAFT SEQU
ENCE, 2 unordered pieces.
//0. 13:439:59//AC004710
F-MAMMA1000845//Plasmodiu
m falciparum DNA *** SEQU
ENCING IN PROGRESS ***fro
m MAL4P1, WORKING DRAFT S
EQUENCE. //2. 2e-05:208:64/
/AL034557
F-MAMMA1000851//Gallus do
mesticus filamin gene 5'
region, partial cds. //0. 8
6:193:63//U00146
F-MAMMA1000855//Human min
isatellite region detecte
d by myoglobin 33-repeat
probe, clone lambda 33.1
0. //0. 081:229:62//M30549
F-MAMMA1000856//B. taurus
microsatellite marker ETH
8 (D6S3) DNA. //0. 0024:25
3:60//Z22747

3249

F-MAMMA1000859//Sequence
6 from Patent WO9722695. /
/2.3e-79:533:82//A63553
F-MAMMA1000862
F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE. //1.0e-28:439:64//AP000050
F-MAMMA1000865
F-MAMMA1000867//CIT-HSP-2385J8. TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence. //0.00017:158:70//AQ240906
F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232G24 on chromosome Xq27.1-q27.3. Contains two exons similar to MAGE gene family, EST, CA repeat, STS, complete sequence. //1.0:121:68//AL022152
F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence. //8.4e-41:185:90//AF015152
F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence. //8.3e-57:522:75//AL022336
F-MAMMA1000880//Homo sapiens full length insert cDNA clone ZD54A10. //5.2e-26:143:100//AF086327
F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence. //0.99:225:63//AL023801
F-MAMMA1000897//R.norvegicus mRNA for plasma protein. //4.8e-07:479:58//Y11283
F-MAMMA1000905//F26L5TRB IGF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence. //0.94:115:66//B61433
F-MAMMA1000906//HS_3110_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence. //2.5e-63:548:78//AQ182819
F-MAMMA1000908//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE. //5.2e-80:480:90//AL033397
F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence. //7.6e-09:596:58//AL034560
F-MAMMA1000921//CIT-HSP-2171D8. TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence. //6.6e-07:249:66//B89575
F-MAMMA1000931//Homo sapiens clone DJ0892G19, complete sequence. //2.9e-43:415:66//AC004917
F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Ge

3250

omic Sperm Library CHomo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence. //6.1e-44:235:78//B47296
F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 -complete genomic sequence, complete sequence. //9.4e-48:443:75//AC002299
F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence. //1.8e-14:175:76//AL031117
F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.0082:684:56//AC005308
F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence. //3.3e-30:530:67//AC004643
F-MAMMA1000957//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence. //1.3e-72:390:94//AQ155121
F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces. //1.8e-58:318:86//AC006001
F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence. //1.4e-18:396:65//AL022394
F-MAMMA1000975//Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence. //1.4e-79:690:77//AL024458
F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence. //0.089:214:66//AC004991
F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence. //1.1e-58:458:82//AC000114
F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat. //1.1e-05:439:62//AL021406
F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase com

3251

ponent A 1, Choroideraemia protein, Tapetochoroida
l Dystrophy (TCD) protein). Contains ESTs and an S
TS, complete sequence.//0.24:166:68//AL022401

F-MAMMA1001008//Homo sapiens *** SEQUENCING IN PRO
GRESS *** WORKING DRAFT SEQUENCE.//1.6e-103:139:9
9//AJ011929

F-MAMMA1001021//Homo sapiens clone 24544 beta-dyst
robrevin mRNA, partial cds.//6.5e-48:465:76//AF0705
67

F-MAMMA1001024//CITBI-E1-2501L21.TF.1 CITBI-E1 Hom
o sapiens genomic clone 2501L21, genomic survey se
quence.//1.0:175:62//AQ241701

F-MAMMA1001030//Homo sapiens G protein-coupled rec
eptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:75
3:61//AF061444

F-MAMMA1001035//Human Chromosome 16 BAC clone CIT9
87SK-A-1000D7, complete sequence.//7.9e-24:256:76/
/AC002990

F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sa
piens genomic clone 2284N21, genomic survey sequen
ce.//0.96:78:75//AQ000903

F-MAMMA1001041//Chicken mRNA for alpha-actinin, co
mplete cds.//2.8e-09:355:63//D26597

F-MAMMA1001050//Homo sapiens BAC clone RG060P12 fr
om 7q21, complete sequence.//2.6e-40:378:76//AC002
457

F-MAMMA1001059//Mouse RNA helicase and RNA-depende
nt ATPase from the DEAD box family mRNA, complete
cds.//4.8e-97:661:83//L25125

F-MAMMA1001067//Homo sapiens genomic intron breakp
oint sequence of MLL rearrangement, 285 bp.//2.8e-
18:110:100//AJ000169

F-MAMMA1001073//HS_3046_A2_G08_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3046 Col=16 Row=M, genomic survey sequenc
e.//1.0:142:68//AQ098420

F-MAMMA1001074//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 455J7, WORKING DRAFT SE
QUENCE.//1.2e-23:386:70//AL031733

F-MAMMA1001075//Homo sapiens (clone F4) transmembr
ane protein mRNA sequence.//1.1e-27:559:65//L09749

F-MAMMA1001078//Homo sapiens chromosome 17, clone
hRPK.346_K_10, complete sequence.//2.0e-22:334:69/
/AC006120

F-MAMMA1001080//Human immunoglobulin heavy chain v
ariable region (VH III family) from IgM rheumatoid
factor.//6.4e-58:327:92//L29155

F-MAMMA1001082//Homo sapiens Xp22 CSHB-314C4 (Geno
me Systems Human BAC library) complete sequence.//
3.8e-87:695:77//AC004087

3252

F-MAMMA1001091//Homo sapiens chromosome 19, cosmid
F21967, complete sequence.//7.0e-05:594:60//AC005
256

F-MAMMA1001092//Human DNA sequence from PAC 49C23
on chromosome X contains malate dehydrogenase pseu
dogene and STS.//1.6e-91:174:87//Z93019

F-MAMMA1001105//Homo sapiens OV0-like 1 binding pr
oteins (OVOL1) mRNA, complete cds.//6.4e-23:507:66/
/AF016045

F-MAMMA1001110//Homo sapiens chromosome 19, cosmid
F16815, complete sequence.//0.77:316:60//AC004637

F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1
locus, complete sequence.//3.3e-21:237:73//AF0478
25

F-MAMMA1001133//Human DNA sequence from BAC 57G9 o
n chromosome 22q12.1 Contains ESTs, CA repeat, GS
S.//0.97:202:63//Z95116

F-MAMMA1001139//tricarboxylate carrier [rats, live
r, mRNA Partial, 2986nt].//1.6e-84:406:82//S70011

F-MAMMA1001143//Homo sapiens DNA sequence from cos
mid N75B3 on chromosome 22 Contains EST, exon tra
p, complete sequence.//1.3e-14:182:76//AL022339

F-MAMMA1001145//Human DNA sequence from cosmid cU1
15G11, between markers DXS6791 and DXS8038 on chrom
osome X contains ESTs and STS.//5.2e-87:714:78//Z7
1187

F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sa
piens genomic clone 2341D13, genomic survey sequen
ce.//0.00051:249:61//AQ055735

F-MAMMA1001161//Homo sapiens chromosome 14, BAC CI
TB-135H17 containing the RAD51L1 gene, complete se
quence.//2.2e-30:410:70//AC004518

F-MAMMA1001162//Homo sapiens full length insert cD
NA clone ZA79C01.//2.4e-13:87:100//AF086123

F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, p
artial cds.//9.3e-15:432:60//U31629

F-MAMMA1001186//Homo sapiens chromosome 17, clone
hRPK.74_E_22, complete sequence.//6.8e-57:670:72/
/AC005696

F-MAMMA1001191

F-MAMMA1001198//Mus musculus eps15R mRNA, complete
cds.//1.5e-117:759:84//U29156

F-MAMMA1001202

F-MAMMA1001203//Homo sapiens chromosome 17, clone
hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pi
eces.//1.5e-161:764:98//AC005412

F-MAMMA1001206//Homo sapiens chromosome 17, clone
HCIT421K24, complete sequence.//5.1e-30:535:65//AC
004099

50 F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HS

3253

P BAC 470n8, complete sequence. //8.4e-182:860:98//A
C005393

F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 f
rom 7q31, complete sequence. //7.7e-58:690:70//AC00
4875

F-MAMMA1001222//Mouse lorocrin mRNA, complete cds.
//2.7e-07:624:58//M34398

F-MAMMA1001243//Homo sapiens chromosome 17, clone
hrPK.192_H_23, complete sequence. //0.91:177:66//A
C005726

F-MAMMA1001244

F-MAMMA1001249//Human 28S ribosomal RNA psuedogene
s and alu repeat region sequence. //6.7e-09:502:58/
/U67616

F-MAMMA1001256//Human DNA sequence from clone 441J
1 on chromosome 6p24 Contains STS, GSS, complete s
equence. //5.0e-37:342:80//Z99495

F-MAMMA1001259

F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 pro
tein, complete cds. //8.7e-40:659:64//AB014561

F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 f
rom 7p12-p13, complete sequence. //4.9e-43:265:81//A
C004453

F-MAMMA1001271//Salmo salar DNA for a cryptic repe
at. //2.6e-06:311:63//AJ012206

F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORK
ING DRAFT SEQUENCE, 12unordered pieces. //6.6e-70:3
27:83//AC004840

F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC R
PCI1-122K4 (Roswell Park Cancer Institute Human PA
C Library) complete sequence. //1.0e-05:276:66//AC0
03035

F-MAMMA1001292//Human DNA sequence from clone 1170
K4 on chromosome 22q12.2-13.1. Contains three nove
l genes, one of which codes for a Trypsin family p
rotein with class A LDL receptor domains, and the
IL2RB gene for Interleukin 2 Receptor, Beta (IL-2
Receptor, CD122 antigen). Contains a putative CpG
island, ESTs, and GSSs, complete sequence. //3.6e-9
8:199:98//AL022314

F-MAMMA1001296//RPCI11-38B4.TV RPCI-11 Homo sapien
s genomic clone RPCI-11-38B4, genomic survey seque
nce. //4.7e-33:292:71//AQ030084

F-MAMMA1001298//Homo sapiens chromosome 17, clone
hrPK.849_N_15, complete sequence. //1.6e-182:860:98
//AC005703

F-MAMMA1001305//Human DNA sequence from clone 116F
5 on chromosome 22q13. Contains part of an unknown
gene and part of a RhoGAP (CDC42 GTPase Activating
Protein) LIKE gene. Contains ESTs, STSs, GSSs, ge

3254

nomie marker D22S1168 and a CA repeat polymorphis
m, complete sequence. //1.9e-70:163:97//Z93244

F-MAMMA1001322//Human DNA sequence from clone 774I
24 on chromosome 1q24.1-24.3 Contains protein simi
lar to pregnancy-associated plasma protein Aprecur
sor neuronal migration protein astrotactin, ESTs,
STS and GSS, complete sequence. //2.6e-19:379:68//A
L031290

F-MAMMA1001324//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 197L1, WORKING DRAFT SE
QUENCE. //4.5e-131:751:90//AL031390

F-MAMMA1001330

F-MAMMA1001341//Sus scrofa. //1.6e-36:420:73//Z4690
6

F-MAMMA1001343//Plasmodium falciparum DNA *** SEQU
ENCING IN PROGRESS ***from MAL1P1, WORKING DRAFT S
EQUENCE. //1.1e-05:818:58//AL031744

F-MAMMA1001346

F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUEN
CE, 52 unordered pieces. //2.0e-44:505:74//AC004086

F-MAMMA1001388//Human IGF binding protein complex
acid-labile subunit amRNA, complete cds. //1.5e-07:
415:58//M86826

F-MAMMA1001397//Human DNA sequence from clone 462D
8 on chromosome 22q11.21-12.1 Contains EST, STS an
d GSS, complete sequence. //1.6e-23:209:75//AL02233
2

F-MAMMA1001408//HS_3242_A1_H11_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3242 Col=21 Row=0, genomic surveysequenc
e. //2.7e-07:181:69//AQ207300

F-MAMMA1001411//Homo sapiens autosomal dominant po
lycystic kidney disease type II protein (PKD2) gen
e, exon 14. //0.98:120:68//AF004872

F-MAMMA1001419//HS_2053_B1_F12_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2053 Col=23 Row=L, genomic surveysequenc
e. //1.9e-75:424:93//AQ244585

F-MAMMA1001420//Homo sapiens chromosome 4 clone B2
03C23 map 4q25, complete sequence. //2.4e-09:199:70
//AC004049

F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BA
C clone CIT987SK-201104, WORKING DRAFT SEQUENCE, 4
unordered pieces. //5.1e-42:558:69//AC004529

F-MAMMA1001442//Plasmodium falciparum chromosome
2, section 37 of 73 of the complete sequence. //0.00
19:516:56//AE001400

F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5
(Genome Systems Human BAC library) complete sequen
ce. //3.6e-42:486:70//AC003684

3255

F-MAMMA1001452//RPCI11-48022.TJ RPCI11 Homo sapiens genomic clone R-48022, genomic survey sequence.//5.3e-87:423:98//AQ199294

F-MAMMA1001465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543

F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783

F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12unordered pieces.//1.0e-13:158:77//AC005486

F-MAMMA1001501//Human mRNA for calcium activated neutral protease largesubunit (muCANP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366

F-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714

F-MAMMA1001510//Human PAC clone DJ43804 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378

F-MAMMA1001522

F-MAMMA1001547

F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931

F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548

F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//M61764

F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949

F-MAMMA1001600//HS_3022_A2_H01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=0, genomic survey sequence.//1.6e-66:405:90//AQ163791

F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Nenin like sequence, complete sequence.//0.00043:715:58//AL008626

F-MAMMA1001606//jd114 Trypanosome Shotgun M13 genomic Trypanosoma bruceibrucei genomic clone 2G6, genomic survey sequence.//0.19:266:62//B13685

F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630

F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//M29833

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F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKINGDRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412

F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796

F-MAMMA1001635//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118

F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577

F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284

F-MAMMA1001663//CIT-HSP-2165E16.TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491

F-MAMMA1001670//HS_3136_A1_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779

F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614

F-MAMMA1001679//HS_3054_A1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=0, genomic survey sequence.//1.0:89:70//AQ106118

F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970

F-MAMMA1001686//HS_3219_B1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=B, genomic survey sequence.//0.00072:180:65//AQ180345

F-MAMMA1001692//HS_3047_B1_B10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228

F-MAMMA1001711//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7unordered pieces.//1.2e-42:316:82//AC004845

F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125

F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, p

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artial cds.//1.8e-133:646:97//AF095687
 F-MAMMA1001735//chicken brain tubulin beta chain m
 rna.//3.5e-110:740:84//J00913
 F-MAMMA1001740//Human DNA sequence from PAC 136017
 on chromosome X contains ESTs and STS.//0.98:416:
 57//Z72001
 F-MAMMA1001743//Homo sapiens clone DJ0981007, comp
 lete sequence.//3.2e-16:194:75//AC006017
 F-MAMMA1001744//Homo sapiens DNA sequence from clo
 ne 46618 on chromosomeXq11.1-13.2. Contains an unk
 nown gene similar to Coagulation Factor V (Activat
 ed Protein C Cofactor), Coagulation Factor VIII (P
 rocoagulant Component) and Ceruloplasmin (EC 1.16.
 3.1, Ferroxidase). Contains ESTs andan STS, comple
 te sequence.//0.0036:181:66//AL030998
 F-MAMMA1001745//Homo sapiens BAC clone 529F11 from
 8q21, complete sequence.//1.2e-60:822:68//AF07071
 8
 F-MAMMA1001751//Human potassium channel KCN01 mRN
 A, complete cds.//1.2e-35:583:65//U90065
 F-MAMMA1001754//Bos taurus vacuolar proton pump su
 bunit SFD alpha isoform (SFD) mRNA, complete cds./
 /8.4e-102:627:87//AF041338
 F-MAMMA1001757//HS_2058_B2_C04_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2058 Col=8 Row=F, genomic survey sequenc
 e.//1.7e-24:173:88//AQ243865
 F-MAMMA1001760//Human DNA sequence from clone 354N
 19 on chromosome 6q22. Contains the 3' part of the
 gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannos
 idase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a
 Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) ps
 eudogene and a pseudogene similar to60S Ribosomal
 Protein L13A. Contains genomic markers D6S287 and
 D6S1696, ESTs, STSs, GSSs and two CA repeat polymor
 phisms, complete sequence.//6.6e-76:349:87//AL0227
 22
 F-MAMMA1001764//Saccharomyces douglasii mitochondr
 ial cytochrome c oxidase subunit I (COXI) gene, co
 mplete cds.//0.23:633:57//M97514
 F-MAMMA1001768//Bovine herpesvirus 1 complete geno
 me.//2.3e-11:547:60//AJ004801
 F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPCI1-228
 P16 (Roswell Park Cancer Institute Human PAC Libra
 ry) complete sequence.//1.1e-76:509:78//AC004801
 F-MAMMA1001771//M.musculus mRNA for semaphorin B./
 /2.7e-106:744:82//X85991
 F-MAMMA1001783//Human PAC clone 127H14 from 12q, c
 omplete sequence.//6.0e-20:228:75//AC002563
 F-MAMMA1001785

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F-MAMMA1001788//Human DNA sequence from clone 425C
 14 on chromosome 6q22Contains the HSF2 gene for He
 at Shock Factor 2 (Heat Shock TranscriptionFactor
 2, HSTF 2) and an unknown gene similar to the plac
 ental proteinD1FF33 gene. Contains ESTs, STSs and
 GSSs, complete sequence.//5.0e-05:152:74//Z99129
 F-MAMMA1001790//Homo sapiens chromosome 12p13.3 cl
 one RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unord
 ered pieces.//4.5e-53:318:80//AC005845
 10 F-MAMMA1001806//Homo sapiens chromosome 19, cosmid
 R29368, complete sequence.//1.0:131:67//AC004262
 F-MAMMA1001812//Human Chromosome X clone bWXd187,
 complete sequence.//3.0e-34:257:83//AC004383
 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 f
 rom 7q21.2-q22, complete sequence.//5.2e-61:516:79
 //AC004128
 F-MAMMA1001817//Homo sapiens 12q24 PAC RPCI1-261P5
 (Roswell Park CancerInstitute Human PAC library)
 complete sequence.//3.1e-32:295:78//AC004031
 20 F-MAMMA1001818//Homo sapiens chromosome 21q22.3, P
 AC clones 314N7, 225L15, BAC clone 7B7, complete s
 equence bases 1..333303.//0.71:179:67//AJ011930
 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608
 gene.//3.0e-91:726:79//Y13148
 F-MAMMA1001824//HS_3108_A1_G12_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3108 Col=23 Row=M, genomic surveysequenc
 e.//3.4e-05:119:74//AQ107508
 F-MAMMA1001836//Homo sapiens chromosome 18, clone
 30 hRPK.537_E_1, completesequence.//3.4e-45:312:85//A
 C006211
 F-MAMMA1001837//Rattus norvegicus zinc finger prot
 ein Y1 (RLZF-Y) mRNA,complete cds.//4.5e-51:480:75
 //AF052042
 F-MAMMA1001848//CITBI-E1-2516P17.TF CITBI-E1 Homo
 sapiens genomic clone2516P17, genomic survey seque
 nce.//1.0e-100:486:98//AQ279620
 F-MAMMA1001851//Human DNA from overlapping chromos
 ome 19-specific cosmids R30072 and R28588, genomic
 40 sequence, complete sequence.//5.1e-07:197:67//AC0
 02390
 F-MAMMA1001854
 F-MAMMA1001858//RPCI11-11L22.TP RPCI-11 Homo sapie
 ns genomic clone RPCI-11-11L22, genomic survey seq
 uence.//0.091:161:65//B75631
 F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq2
 3, complete sequence.//2.6e-09:397:61//AC003013
 F-MAMMA1001868//HS_2196_B2_A12_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2196 Col=24 Row=B, genomic surveysequenc
 50

3259

e.//5.8e-13:86:100//AQ032455
 F-MAMMA1001874//H.sapiens CpG island DNA genomic M
 sel fragment, clone 63h5, reverse read cp63h5.rt1
 a.//1.0:127:63//Z62129
 F-MAMMA1001878//Human DNA sequence from BAC 999D10
 on chromosome 22q13.3. Contains two BAC end-sequen
 ces (GSSs).//1.7e-19:372:67//Z94802
 F-MAMMA1001880//RPCI11-90K3.TJ RPCI11 Homo sapiens
 genomic clone R-90K3, genomic survey sequence.//6.
 6e-11:362:62//AQ283465
 F-MAMMA1001890//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 508115, WORKING DRAFT S
 EQUENCE.//1.8e-45:317:86//AL021707
 F-MAMMA1001907//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 424J12, WORKING DRAFT S
 EQUENCE.//2.7e-23:255:77//Z82207
 F-MAMMA1001908//HS_2225_A1_A03_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2225 Col=5 Row=A, genomic survey sequenc
 e.//5.4e-08:264:62//AQ301597
 F-MAMMA1001931//HS_3049_B2_D09_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3049 Col=18 Row=H, genomic surveysequenc
 e.//1.7e-47:295:90//AQ100157
 F-MAMMA1001956//H.sapiens DNA sequence.//0.056:23
 3:66//Z22493
 F-MAMMA1001963//Homo sapiens adenylosuccinate lyas
 e gene, complete cds.//0.99:173:68//AF106656
 F-MAMMA1001969//Human DNA sequence from cosmid 232
 L22, between markers DXS366 and DXS87 on chromosom
 e X contains ESTs glycerol kinase pseudogene.//5.3
 e-63:479:78//Z73986
 F-MAMMA1001970//Homo sapiens BAC clone BK085E05 fr
 om 22q12.1-qter, complete sequence.//1.4e-126:699:
 93//AC003071
 F-MAMMA1001992//HS_3078_A1_A09_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3078 Col=17 Row=A, genomic surveysequenc
 e.//3.3e-08:257:65//AQ143646
 F-MAMMA1002009//Homo sapiens chromosome 17, clone
 hRPK.214_0_1, complete sequence.//1.5e-07:244:62//A
 C005224
 F-MAMMA1002011//HS_3252_B1_B05_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3252 Col=9 Row=D, genomic survey sequenc
 e.//1.3e-07:170:69//AQ304711
 F-MAMMA1002032//Homo sapiens chromosome 12p13.3, W
 ORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-3
 4:315:79//AC004803
 F-MAMMA1002033//HS_3023_A2_G04_T7 CIT Approved Hum

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an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3023 Col=8 Row=M, genomic survey sequenc
 e.//4.3e-69:366:94//AQ105493
 F-MAMMA1002041//Genomic sequence from Human 9q34,
 complete sequence.//5.3e-85:439:82//AC001227
 F-MAMMA1002042//Homo sapiens chromosome 3, clone h
 RPK.165_I_16, complete sequence.//1.4e-20:314:70//A
 C005669
 F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPCI11-42
 9A20 (Roswell Park Cancer Institute Human BAC Libr
 ary) complete sequence.//6.8e-14:526:62//AC005906
 F-MAMMA1002056//Human DNA sequence from clone 1189
 B24 on chromosome Xq25-26.3. Contains NADH-Ubiquin
 one Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.
 6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene
 Tyrosine-proteinKinase FER (EC 2.7.1.112, P94-FER,
 C-FER, TYK3) pseudogenes, and part of a novel gen
 e similar to hypothetical proteins S. pombe C22F3.
 14C and C. elegans C16A3.8. Contains ESTs, an STS
 and GSSs, complete sequence.//1.1e-47:648:71//AL03
 0996
 F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 f
 rom 7p11.2-p13, complete sequence.//2.4e-19:256:74
 //AC004869
 F-MAMMA1002068//Homo sapiens, clone hRPK.2_A_1, co
 mplete sequence.//5.4e-41:407:78//AC006197
 F-MAMMA1002078//Human DNA sequence from PAC 106120
 on chromosome 22q12 Contains ESTs and STS, comple
 te sequence.//0.021:333:64//Z81313
 F-MAMMA1002082
 F-MAMMA1002084//Caenorhabditis elegans cosmid F28C
 12, complete sequence.//0.032:469:58//Z93380
 F-MAMMA1002093//HS_3050_B1_F06_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3050 Col=11 Row=L, genomic surveysequenc
 e.//1.0:77:71//AQ105997
 F-MAMMA1002108//Homo sapiens anion exchanger 3 gen
 e, exons 1 and 2 and complete 5' UTR.//8.3e-10:464:
 60//AF017308
 F-MAMMA1002118
 F-MAMMA1002125//Homo sapiens chromosome 17, clone
 HCIT217L10, complete sequence.//1.0e-35:619:68//AC
 003962
 F-MAMMA1002132//RPCI11-78F11.TJ RPCI11 Homo sapien
 s genomic clone R-78F11, genomic survey sequence.//
 1.0e-90:357:97//AQ286460
 F-MAMMA1002140//Homo sapiens 12q24 PAC RPCI1-66E7
 (Roswell Park Cancer Institute Human PAC library)
 complete sequence.//1.6e-45:583:64//AC004216
 F-MAMMA1002143//Human serum constituent protein (M

3261

SE55) mRNA, complete cds.//6.0e-11:192:70//M88338
F-MAMMA1002145//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 102D24, WORKING DRAFT S
EQUENCE.//0.0028:570:59//AL021391

F-MAMMA1002153//HS_3005_A1_D04_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3005 Col=7 Row=G, genomic survey sequenc
e.//4.9e-41:213:99//AQ132213

F-MAMMA1002155//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 462023, WORKING DRAFT S 10
EQUENCE.//1.2e-45:303:78//AL031431

F-MAMMA1002156

F-MAMMA1002158//CITBI-E1-2508P18.TR CITBI-E1 Homo
sapiens genomic clone2508P18, genomic survey seque
nce.//7.1e-42:255:92//AQ266165

F-MAMMA1002170//Homo sapiens chromosome 17, clone
HCIT187M2, complete sequence.//2.0e-81:604:81//AC0
04448

F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 fr
om 6p21, complete sequence.//3.2e-43:333:83//AC004 20
212

F-MAMMA1002198//H.sapiens thiol-specific antioxi
da nt protein mRNA.//1.0e-34:121:98//Z22548

F-MAMMA1002209//HS_2197_B1_E07_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2197 Col=13 Row=J, genomic surveysequenc
e.//9.6e-18:163:84//AQ210058

F-MAMMA1002215//Homo sapiens anion exchanger 3 gen
e, exons 1 and 2 and complete 5'UTR.//6.3e-08:435:
60//AF017308

F-MAMMA1002219//Rattus norvegicus rexo70 mRNA, com
plete cds.//1.8e-124:752:87//AF032667

F-MAMMA1002230//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC588 genomicsequence, WORKING DRAFT SEQU
ENCE, 2 unordered pieces.//0.67:356:59//AC004710

F-MAMMA1002236//Rattus norvegicus initiation facto
r eIF-2B gamma subunit(eIF-2B gamma) mRNA, complet
e cds.//9.3e-140:836:87//U38253

F-MAMMA1002243//Homo sapiens chromosome 17, clone
hRPK.112_H_10, complete sequence.//1.4e-145:691:98 40
//AC005666

F-MAMMA1002250//Homo sapiens chromosome 16, P1 clo
ne 109-9G (LANL), complete sequence.//6.0e-138:66
0:98//AC005600

F-MAMMA1002267//Homo sapiens chromosome 2, P1 clon
e 777H5 (LBNL H27), complete sequence.//0.066:333:
60//AC003676

F-MAMMA1002268//Mus musculus sphingosine kinase (S
PHK1a) mRNA, partial cds.//1.1e-39:404:74//AF06874

8

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F-MAMMA1002269//HS_3163_B1_D03_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3163 Col=5 Row=H, genomic survey sequenc
e.//1.0:150:63//AQ171576

F-MAMMA1002282//Human Chromosome 16 BAC clone CIT9
87SK-327024, complete sequence.//1.5e-22:315:67//AC
003108

F-MAMMA1002292//B.garinii (strain TIs1) p83/100 ge
ne (partial).//0.73:200:64//X81533

F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORK
ING DRAFT SEQUENCE, 25unordered pieces.//1.6e-56:4
08:75//AC006023

F-MAMMA1002294//Sequence 2 from Patent W09516779./
/1.8e-06:401:62//A45258

F-MAMMA1002297

F-MAMMA1002298//Homo sapiens DNA from chromosome 1
9, cosmid R29144, complete sequence.//0.0056:525:6
1//AC004221

F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sap
iens genomic clone 2345B2, genomic survey sequenc
e.//1.2e-90:446:98//AQ053994

F-MAMMA1002308//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 850H21, WORKING DRAFT S
EQUENCE.//1.3e-35:329:78//AL031680

F-MAMMA1002310//Human gastric (H+ + K+)-ATPase gen
e, complete cds.//0.0060:301:60//J05451

F-MAMMA1002311//Human Chromosome 15q11-q13 clone p
DJ276c12 from the Prader-Willi/Angelman syndrome r
egion, WORKING DRAFT SEQUENCE, 3 unordered pieces. 30
//8.6e-50:327:69//AC004737

F-MAMMA1002312//Homo sapiens DNA sequence from PAC
435D1 on chromosome Xq25. Contains ESTs and STS./
/1.3e-09:741:58//Z86064

F-MAMMA1002317

F-MAMMA1002319//Homo sapiens chromosome 19, fosmid
39347, complete sequence.//1.9e-158:746:99//AC005
756

F-MAMMA1002322//Homo sapiens Chromosome 11p14.3 PA
C clone pDJ1034g4, complete sequence.//5.3e-52:61
7:70//AC004796

F-MAMMA1002329//Homo sapiens RaP2 interacting prot
ein 8 (RPIP8) mRNA, complete cds.//0.22:143:67//U9
3871

F-MAMMA1002332//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQ
UENCE.//1.6e-31:287:74//AL034402

F-MAMMA1002333//Mycobacterium tuberculosis H37Rv c
omplete genome; segment 148/162.//2.5e-09:674:59//
AL022022

50 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, c

3263

osmid clone Q4H9 complete sequence bases 1..41604.
//2.1e-57:522:77//AJ011932

F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence. //2.0e-14:258:69//AC004129

F-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE. //7.8e-132:723:91//AL022100

F-MAMMA1002352//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12803, WORKING DRAFT SEQUENCE. //5.8e-17:326:70//Z98742

F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces. //1.1e-14:399:63//AC004825

F-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE. //3.7e-43:420:75//AL023879

F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.0022:534:59//AC004153

F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPCI5-118 OD12 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //5.3e-18:156:75//AC005831

F-MAMMA1002360//Human DNA sequence from cosmid L21 F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST. //4.9e-43:353:69//Z68885

F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence. //1.8e-22:282:74//AL008719

F-MAMMA1002362//Platemys spixii CR1-like LINE, partial sequence. //0.00058:83:79//D82938

F-MAMMA1002380//CIT-HSP-2383K24.TF CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence. //4.4e-10:85:92//AQ196889

F-MAMMA1002384//RPCI11-80J20.TV RPCI11 Homo sapiens genomic clone R-80J20, genomic survey sequence. //2.7e-56:286:98//AQ284134

F-MAMMA1002385//CIT-HSP-2328G13.TF CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence. //5.5e-46:335:84//AQ043985

F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence. //8.5e-29:273:78//AC004888

F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence. //8.2e-09:287:63//AL023875

F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds. //9.6e-08:730:57//L40608

F-MAMMA1002417//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE. //4.1e-06:181:72//AL034402

F-MAMMA1002427//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces. //1.3e-51:593:72//AC004604

F-MAMMA1002428

F-MAMMA1002434//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island. //7.3e-56:388:81//Z93023

F-MAMMA1002446//CIT-HSP-2324022.TR CIT-HSP Homo sapiens genomic clone 2324022, genomic survey sequence. //2.3e-56:302:95//AQ027479

F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence. //1.1e-54:190:94//AC005229

F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds. //0.00045:457:60//U14005

20 F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205. //9.7e-33:709:60//U10556

F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPCI3-340 I3 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //0.092:506:58//AC004671

F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //0.025:100:76//AC005077

F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds. //2.9e-118:560:98//AF055460

30 F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence. //1.5e-22:297:73//AC005913

F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence. //7.2e-10:330:64//AC002477

F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon. //0.0080:124:72//L49359

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds. //1.4e-160:775:97//AF065214

40 F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence. //1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17.TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence. //1.7e-07:76:90//AQ006579

50 F-MAMMA1002573//Homo sapiens DNA, trinucleotide re

3265

peats region, clone GAA C27. //2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence. //2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE. //1.3e-34:550:69//AL034548

F-MAMMA1002598//H. sapiens mRNA for ribosomal protein L7. //1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence. //0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence. //2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces. //0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPC IP704E14135Q2. //9.5e-71:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds. //1.5e-20:157:90//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence. //8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING DRAFT SEQUENCE. //1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RC385F02 from 7p15, complete sequence. //4.8e-85:478:78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds. //5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds. //3.6e-115:785:82//AF055666

F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence. //1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds. //6.6e-06:61:59//L41919

F-MAMMA1002655//HS_2003_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence. //9.0e-15:198:74//AQ224233

F-MAMMA1002662

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F-MAMMA1002665//Homo sapiens BAC clone GS588C18 from 7p12-p14, complete sequence. //1.4e-37:235:84//AC005029

F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds. //0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds. //3.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING DRAFT SEQUENCE. //6.2e-45:510:70//AL023585

F-MAMMA1002698//HS_3024_B1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence. //1.7e-10:155:75//AQ072214

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds. //5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-6, complete cds. //1.2e-159:749:99//AB011399

F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence. //3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence. //3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350H5.TR CIT-HSP Homo sapiens genomic clone 2350H5, genomic survey sequence. //1.4e-06:265:63//AQ061245

F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence. //0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome c oxidase, delta-aminolevulinic acid synthase (erythroid); 5-aminolevulinic acid synthase. (EC 2.3.1.37). 6-phosphofructose-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS. //3.2e-05:362:63//Z83821

F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence. //0.0010:535:58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence. //1.2e-182:880:97//AC005856

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F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPC I4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone bW XD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166 a1, complete sequence.//5.2e-49:355:81//U73636

F-MAMMA1002765//RPCI11-20A22.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1.TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//5.6e-105:179:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS_3213_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D, genomic survey sequence.//0.00018:219:63//AQ175845

F-MAMMA1002796

F-MAMMA1002807//Human Chromosome X PAC RPCI1-290C9 from the Pieter de Jong Human PAC library; complete sequence.//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035

F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529I10, complete sequence.//1.0e-64:320:83//AC002553

F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875

F-MAMMA1002835

F-MAMMA1002838//A-916H10.TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462

F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353

F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana 50

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genomic clone F1707, genomic survey sequence.//6.7e-17:383:66//B11616

F-MAMMA1002858

F-MAMMA1002868//RPCI11-54F9.TJ RPCI11 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566

F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//I25863

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388

F-MAMMA1002880//RPCI11-23M23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518

F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027

F-MAMMA1002886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653

F-MAMMA1002887//HS_3238_B2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814

F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds; Bf, C2, C9A, NG22, C9, HSP70, HSP70, HSC70t, and smRNP genes, complete cds; C7A gene, partial cds; and unknown genes.//4.6e-35:136:73//AF109906

F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096

F-MAMMA1002895//H.sapiens CpG island DNA genomic Msel fragment, clone 46b6, forward read cpg46b6.ft1a.//3.7e-36:190:100//Z58616

F-MAMMA1002908//Panaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828

F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402

F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems HumanBAC library) complete sequence.//0.25:260:62//AC004467

F-MAMMA1002937//H.sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623

F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193:910:98//AB014598

F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-CGT Region, complete sequence.//2.7e-23:174:77//AC004032

F-MAMMA1002947//Rhodobacter capsulatus strain SB1003, partial genome.//1.3e-09:475:61//AF010496

F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, exon 5.//0.0029:314:60//AF019366

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F-MAMMA1002970//Human DNA sequence from PAC 436H11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinosis (X-linked, juvenile) 1 (XLR1). Contains ESTs, an STS and GSSs, complete sequence. //4.0e-10:194:71//Z94056

F-MAMMA1002972//H.sapiens CpG island DNA genomic MseI fragment, clone 2g10, forward read cp2g10.ft1 aa. //0.38:156:66//Z55272

F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence. //2.9e-41:234:79//AC005919
F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3. //1.7e-05:322:63//AL022098

F-MAMMA1002987//CITBI-E1-2514J12. TR CITBI-E1 Homo sapiens genomic clone 2514J12, genomic survey sequence. //0.0064:135:66//AQ275871

F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence. //2.8e-31:201:89//B01998

F-MAMMA1003004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y237C10, WORKING DRAFT SEQUENCE. //1.6e-10:180:73//AL031601

F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleotide repeat polymorphism at the D11S488 locus. //3.5e-12:435:61//L04732

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds. //2.3e-50:734:67//U79139

F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, complete sequence. //1.2e-86:341:79//AC003694

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nce. //1.2e-86:341:79//AC003694

F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M7, complete sequence. //2.6e-13:443:61//AC003661

F-MAMMA1003019//HS_3221_A1_A01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, genomic survey sequence. //2.8e-51:299:92//AQ184271

F-MAMMA1003026

F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence. //0.0037:134:73//AC005214

F-MAMMA1003035//RPCI11-11P4. TP RPCI-11 Homo sapiens genomic clone RPCI-11-11P4, genomic survey sequence. //1.1e-07:66:100//B74936

F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPCI3-34013 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //2.1e-19:220:76//AC004671

F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p35-36.2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus. //9.5e-91:469:78//Z98257

F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence. //0.21:289:61//AL031321

F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds. //1.7e-139:663:98//AF077952

F-MAMMA1003049

F-MAMMA1003055//HS_3014_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, genomic survey sequence. //4.2e-05:215:64//AQ164940

F-MAMMA1003056//HS_3221_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl

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one Plate=3221 Col=24 Row=H, genomic survey sequence. //1.4e-16:206:74//AQ302772
 F-MAMMA1003057//M.domesticus MD6 mRNA. //8.5e-128:654:94//X54352
 F-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE. //1.0:142:71//AL034371
 F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence. //1.7e-42:373:78//AC004796
 F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds. //2.6e-42:288:88//AF042166
 F-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds. //1.6e-12:477:64//U72634
 F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds. //3.4e-121:789:85//AF071316
 F-MAMMA1003127//R.norvegicus MYR1 mRNA for myosin I heavy chain. //9.4e-58:423:83//X68199
 F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP)mRNA, complete cds. //0.62:676:58//U67916
 F-MAMMA1003140
 F-MAMMA1003146//Homo sapiens mRNA for GALT3 protein. //2.2e-80:397:97//Y15062
 F-MAMMA1003150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE. //7.3e-123:266:88//AL021579
 F-MAMMA1003166//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE. //1.6e-33:143:82//Z99716
 F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence. //0.50:216:61//Z95400
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds. //4.8e-65:385:92//D31886
 F-NT2RM1000032
 F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating protein (SCAP) mRNA, complete cds. //6.3e-135:565:84//U67060
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds. //1.1e-106:542:95//AB014590
 F-NT2RM1000039//Mouse genetic suppressor element mRNA. //0.080:239:60//L27155
 F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds. //8.4e-96:535:91//D87671
 F-NT2RM1000059//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE. //1.0:257:59//AL031600

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F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds. //0.54:306:63//U37520
 F-NT2RM1000080//Sequence 2 from patent US 5763589. //1.5e-115:566:97//AR012692
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds. //1.8e-114:550:97//AB014561
 F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complete sequence. //0.63:180:65//AC005594
 10 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds. //0.027:126:70//AF007155
 F-NT2RM1000119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE. //0.022:644:58//Z97630
 F-NT2RM1000127//RPC111-44E5.TJ RPC111 Homo sapiens genomic clone R-44E5, genomic survey sequence. //1.6e-45:254:94//AQ195884
 F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds. //5.5e-153:778:95//AB018335
 20 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. //1.1e-90:448:97//AF044959
 F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence. //5.9e-07:66:96//U49890
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds. //0.025:126:70//AF007155
 F-NT2RM1000187//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence. //1.1e-05:56:98//AQ261184
 30 F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds. //1.6e-38:711:65//D64009
 F-NT2RM1000242
 F-NT2RM1000244//HS_2229_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, genomic survey sequence. //2.0e-13:95:95//AQ298474
 F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206_C_20, complete sequence. //0.023:225:61//AC006070
 F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequence. //8.5e-24:473:64//Z68336
 F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds. //6.4e-69:455:85//AF035940
 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds. //6.5e-57:460:80//D50920
 F-NT2RM1000271
 F-NT2RM1000272
 50 F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit

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it D (VATD) mRNA, complete cds.//6.7e-97:430:92//U11927

F-NT2RM1000300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097

F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e-127:708:92//D63880

F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, complete cds.//5.7e-34:182:99//D79205

F-NT2RM1000341//Homo sapiens full length insert cDNA clone YP11F06.//1.3e-100:504:97//AF085879

F-NT2RM1000354//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//1.6e-11:201:73//AQ218494

F-NT2RM1000355//Mus musculus E25B protein mRNA, complete cds.//1.8e-77:578:82//U76253

F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5unordered pieces.//9.4e-113:367:97//AC004821

F-NT2RM1000377//H.sapiens mRNA for MAP kinase phosphatase 4.//6.1e-14:362:62//Y08302

F-NT2RM1000388//Azospirillum brasilense lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679

F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979

F-NT2RM1000399

F-NT2RM1000421//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737

F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928

F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989

F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//4.6e-73:533:83//AC004993

F-NT2RM1000553

F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:555:97//AF070542

F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6unordered pieces.//1.3e-123:477:100//AC004873

F-NT2RM1000623//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737

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F-NT2RM1000648//Halobium cutirubrum L11, L1, L10 and L12 equivalent ribosomal protein gene cluster.//1.3e-06:414:61//X15078

F-NT2RM1000661//Homo sapiens cap-binding protein 4 EHP mRNA, complete cds.//9.3e-54:275:97//AF047695

F-NT2RM1000666//HS_2016_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865

F-NT2RM1000669//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133

F-NT2RM1000672

20 F-NT2RM1000691//Homo sapiens HRIHFB2060 mRNA, partial cds.//2.2e-119:582:98//AB015348

F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627

F-NT2RM1000702//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514

F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832

40 F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139

F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208

F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete s

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equence bases 1..333303. /
 /0.92:395:58//AJ011930
 F-NT2RM1000770//Homo sapi
 ens inosine monophosphate
 dehydrogenase type I gene,
 complete cds.//2.1e-7
 0:407:92//L39210
 F-NT2RM1000772//Human Chr
 omosome 3 pac pDJ70i11, W
 ORKING DRAFT SEQUENCE, 2 u
 nordered pieces.//6.6e-3
 6:98:93//AC000380
 F-NT2RM1000780//Human DNA
 for 5' terminal region o
 f LINE-1 transposable elem
 ent clone CGL1-4.//9.3e-2
 2:126:99//X52233
 F-NT2RM1000781//Plasmodiu
 m falciparum 3D7 chromoso
 me 12 PFYAC812 genomic seq
 uence, WORKING DRAFT SEQU
 ENCE, 8 unordered pieces.
 //7.1e-09:540:59//AC00415
 3
 F-NT2RM1000800//Mus muscu
 lus mRNA for B-IND1 prote
 in.//4.0e-81:497:88//Z972
 07
 F-NT2RM1000802
 F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, c
 omplete cds.//3.7e-63:490:84//AF027208
 F-NT2RM1000826//Homo sapiens clone 24514 unknown m
 RNA.//7.2e-153:749:96//AF070542
 F-NT2RM1000829//HS_3047_A1_A05_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3047 Col=9 Row=A, genomic survey sequenc
 e.//0.74:215:67//AQ099134
 F-NT2RM1000833//Canis familiaris sec61 homologue m
 RNA, complete cds.//5.1e-114:683:88//M96629
 F-NT2RM1000850//F.rubripes GSS sequence, clone 163
 A22aF11, genomic survey sequence.//1.1e-26:279:74/
 /AL018762
 F-NT2RM1000852//Homo sapiens mRNA for ATP-dependen
 t RNA helicase, partial.//9.3e-148:726:97//AJ01084
 0
 F-NT2RM1000857//Rattus norvegicus gene for cytochr
 ome P450/6 beta B, exon 2.//0.97:124:65//AB008378
 F-NT2RM1000867//H.sapiens DNA sequence surrounding
 NotI site, clone NRLA143D.//1.2e-31:172:98//X9583

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F-NT2RM1000874//Homo sapiens KE05 protein mRNA, co
 mplete cds.//2.8e-131:632:97//AF064605
 F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PA
 C clone pDJ519o13 containing human gene for ferrit
 in heavy chain (FTH), complete sequence.//1.2e-98:
 214:99//AC004228
 F-NT2RM1000883//Homo sapiens I-1 receptor candidat
 e protein mRNA, complete cds.//2.7e-156:762:97//AF
 082516
 10 F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 pro
 tein, complete cds.//2.0e-17:310:67//AB014561
 F-NT2RM1000894//Mus musculus second largest subuni
 t of RNA polymerase I (RPA2) mRNA, complete cds.//
 3.2e-95:469:83//U58280
 F-NT2RM1000898
 F-NT2RM1000905//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 466N1, WORKING DRAFT SE
 QUENCE.//1.8e-74:188:98//Z97630
 F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORK
 20 ING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:6
 01:98//AC004873
 F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORK
 ING DRAFT SEQUENCE, 21 unordered pieces.//0.071:39
 2:60//AC004846
 F-NT2RM1000962//H.sapiens CpG island DNA genomic M
 sel fragment, clone 140d1, forward read cpg140d1.f
 t1a.//4.1e-35:187:99//Z56803
 F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23
 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered piece
 s.//1.1e-23:266:77//AC005959
 30 F-NT2RM1001003//Homo sapiens alpha-catenin-like pr
 otein mRNA, complete cds.//4.0e-160:760:98//U97067
 F-NT2RM1001008//Kaposi's sarcoma-associated herpes
 -like virus ORF73 homolog gene, complete cds.//1.7
 e-11:602:61//U52064
 F-NT2RM1001043//Human DNA sequence from PAC 27K14
 on chromosome Xp11.3-Xp11.4. Contains monoamine ox
 idase B (MAOB), ESTs and polymorphic CA repeats.//
 3.9e-93:645:86//Z95125
 40 F-NT2RM1001044//S.pombe chromosome III cosmid c32
 0.//0.90:128:66//AL022245
 F-NT2RM1001059//Homo sapiens chromosome 5, Bac clo
 ne 58g14 (LBNL H76), complete sequence.//3.8e-53:2
 61:80//AC005915
 F-NT2RM1001066//CIT-HSP-2172N17.TF CIT-HSP Homo sa
 piens genomic clone 2172N17, genomic survey sequen
 ce.//0.64:285:59//B94391
 F-NT2RM1001072//HS_3115_B1_D07_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3115 Col=13 Row=H, genomic survey sequenc

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e. //7.3e-23:140:95//AQ147905
 F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence. //5.0e-50:186:98//AC005263
 F-NT2RM1001082//Sequence 1 from Patent W09718303. //2.1e-144:736:95//A62731
 F-NT2RM1001085//CIT-HSP-2310F21. TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence. //8.8e-45:235:97//AQ020757
 F-NT2RM1001092//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence. //1.1e-89:471:95//AQ155489
 F-NT2RM1001102//Human HEM45 mRNA, complete cds. //1.2e-28:482:63//U88964
 F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5' UTR). //0.0014:349:61//Z95973
 F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence. //0.060:429:58//AC004678
 F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds. //0.93:156:62//AF024624
 F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence. //1.2e-10:466:59//AC004755
 F-NT2RM2000006//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE. //5.3e-150:724:98//AL031291
 F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit. //1.5e-58:749:69//X58826
 F-NT2RM2000030//Homo sapiens clone DJ0708P22, WORKING DRAFT SEQUENCE, 11unordered pieces. //2.1e-97:270:77//AC004863
 F-NT2RM2000032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //1.9e-25:172:76//AL034379
 F-NT2RM2000042//Human DNA sequence from cosmid U55E4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs. //5.0e-05:325:65//Z73418
 F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism. //0.63:117:68//L12269
 F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes. //0.38:312:62//AF109905
 F-NT2RM2000101

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F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subunit mRNA, complete cds. //3.8e-58:297:97//M12303
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds. //3.8e-138:653:98//AF067224
 F-NT2RM2000192//CIT-HSP-2172B3. TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence. //2.2e-33:191:95//B93289
 F-NT2RM2000239//F.rubripes GSS sequence, clone 156P04aG12, genomic survey sequence. //8.9e-44:445:69//AL018549
 F-ntnnnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds. //0.00020:380:61//AF075292
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds. //3.1e-128:615:98//AB011162
 F-NT2RM2000259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE. //0.0013:305:63//AL031658
 F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence. //3.0e-14:645:61//AF073934
 F-NT2RM2000287//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces. //1.3e-11:96:86//AC003656
 F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence. //8.5e-115:233:97//AL031864
 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds. //8.8e-175:805:99//AB011132
 F-NT2RM2000363//RPC111-90B10. TJ RPC111 Homo sapiens genomic clone R-90B10, genomic survey sequence. //6.7e-15:96:98//AQ285300
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds. //1.2e-94:599:86//U48251
 F-NT2RM2000371//RPC111-57I4. TJ RPC111 Homo sapiens genomic clone R-57I4, genomic survey sequence. //1.1e-52:312:91//AQ083343
 F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene. //6.7e-31:196:91//X70514
 F-NT2RM2000395//Leishmania major chromosome 1, complete sequence. //0.99:345:58//AE001274

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F-NT2RM2000402//*Arabidopsis thaliana* BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973
 F-NT2RM2000407//*Mus musculus* semaphorin VIa mRNA, complete cds.//1.4e-131:439:88//AF030430
 F-NT2RM2000420//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204
 F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022
 F-NT2RM2000452//HS_3009_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794
 F-NT2RM2000469//HS_2019_A1_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290
 F-NT2RM2000502
 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243
 F-NT2RM2000522
 F-NT2RM2000540
 F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPCI5-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466
 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132
 F-NT2RM2000567//*Pseudomonas aeruginosa* enoyl-CoA hydratase gene, partial cds; pilin biosynthetic protein (fimL) gene, complete cds; and unknown gene.//3.0e-06:664:58//AF083252
 F-NT2RM2000569//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031681
 F-NT2RM2000577//RPCI11-43G22.TJ RPCI11 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987
 F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPCI5-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466
 F-NT2RM2000594//*Mus musculus* DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626
 F-NT2RM2000599//*O. sativa* osr40g3 gene.//0.30:585:56//Y08988

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F-NT2RM2000609
 F-NT2RM2000612//*Rattus norvegicus* ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776
 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952
 F-NT2RM2000624
 2.9e-06:231:64//Z82061
 10 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272
 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558
 F-NT2RM2000639//RPCI11-69E5.TJ RPCI11 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576
 F-NT2RM2000669
 20 F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984
 F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244
 F-NT2RM2000740//*Mus musculus* lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691
 30 F-NT2RM2000795//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING DRAFT SEQUENCE.//1.0e-78:723:76//AL021392
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228
 F-NT2RM2000837//Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.//1.1e-05:361:62//AC005017
 40 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046
 F-NT2RM2000952
 F-NT2RM2000984//*Mus musculus* major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//7.6e-41:239:76//AF109905
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey sequence.//1.1e-11:298:66//AQ035862
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F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//AF071314
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6unordered pieces.//2.3e-145:614:99//AC004873
 F-NT2RM2001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.7e-95:461:99//AL034380
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-24:726:62//U52064
 F-NT2RM2001141
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.98:300:62//AL022401
 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15unordered pieces.//1.2e-147:741:96//AC005488
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds.//0.026:408:59//U66829
 F-NT2RM2001196//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5unordered pieces.//2.2e-135:627:98//AC004987
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
 F-NT2RM2001221//Chimpanzee (P. paniscus) involucrin, complete cds.//0.53:670:55//M26514
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150
 F-NT2RM2001243
 F-NT2RM2001247//CITBI-E1-2521M18. TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey sequence.//0.0011:274:59//AQ276184
 F-NT2RM2001256//M. musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169
 F-NT2RM2001291//CIT-HSP-2010I15. TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.//4.6e-09:156:72//B57734
 F-NT2RM2001306//RPCI11-2815. TP RPCI-11 Homo sapiens genomic clone RPCI-11-2815, genomic survey sequence.//0.069:234:64//B84850
 F-NT2RM2001312//Homo sapiens chromosome 17, clone

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hrPK.142_H_19, complete sequence.//1.1e-22:111:81//AC005919
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the complete genome.//0.99:340:58//AE001118
 F-NT2RM2001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING DRAFT SEQUENCE.//3.7e-44:340:85//Z84465
 F-NT2RM2001345//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.042:290:58//AQ089514
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-60:365:87//U56429
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815D20 from 7p11-p13, complete sequence.//0.98:415:58//AC004899
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PA C Clone p_m11 In BCRL2-GGT Region, complete sequence.//4.0e-54:394:75//AC004033
 F-NT2RM2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033520
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.1e-96:453:99//AJ007509
 F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.//7.1e-91:601:83//AB000113
 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complete sequence.//0.81:200:69//AC005624
 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2.//3.8e-16:316:65//Z99708
 F-NT2RM2001544
 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//3.3e-24:318:67//AL032657
 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//2.1e-26:582:64//M34551
 F-NT2RM2001582//M. musculus red-1 gene.//1.4e-102:581:90//X92750
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:282:65//AB007902
 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6e-131:736:90//AF032667
 F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nalm-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431
 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA A, complete cds.//8.6e-118:779:85//M96630

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F-NT2RM2001632//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. //1.5e-50:561:71//AC004691

F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds. //9.2e-153:740:98//AB014518

F-NT2RM2001637//F. rubripes GSS sequence, clone 155 D22bD8, genomic survey sequence. //2.5e-13:224:64//Z91020

F-NT2RM2001641//CIT-HSP-2347F23. TF CIT-HSP Homo sapiens genomic clone 2347F23, genomic survey sequence. //1.3e-67:340:98//AQ060913

F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cds. //1.4e-110:459:89//M96629

F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (ARF-GEF1) mRNA, complete cds. //1.2e-153:807:93//AF023451

F-NT2RM2001659//nbxb0002cE07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002J13f, genomic survey sequence. //1.0:485:56//AQ051653

F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds. //3.7e-172:802:99//AF044195

F-NT2RM2001668

F-NT2RM2001670//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease. //3.2e-18:279:70//AJ003147

F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein-3 mRNA, complete cds. //1.6e-137:683:94//U21157

F-NT2RM2001675//RPC111-51J16.TJ RPC111 Homo sapiens genomic clone R-51J16, genomic survey sequence. //1.0:394:58//AQ053677

F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T805 (ESSAII project). //0.87:220:61//AL021890

F-NT2RM2001688//B. paraptussis bvg locus (transcription regulators of virulence factors) with bvgA and bvgS genes. //1.0:286:62//X52948

F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, genomic survey sequence. //3.2e-53:241:82//B59854

F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment 2, clone Mu2. //1.2e-05:306:58//M10668

F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence. //6.0e-06:548:59//AL021920

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F-NT2RM2001699//HS_3195_B2_D01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, genomic survey sequence. //2.7e-07:322:61//AQ189056

F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome; segment 109/162. //7.8e-05:354:58//Z95556

F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces. //7.5e-42:335:81//AC004469

F-NT2RM2001716

F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence. //4.2e-08:536:58//AC004290

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence. //1.4e-26:163:95//AF052123

F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds. //6.2e-111:530:98//AB007931

F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPC IP704E14135Q2. //3.1e-102:248:95//AJ010598

F-NT2RM2001743

F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequence. //0.11:138:66//Z68117

F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cds. //9.4e-100:418:88//M96629

F-NT2RM2001768//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence. //3.1e-28:153:100//AQ136993

F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence. //1.3e-66:680:72//AC006116

F-NT2RM2001782

F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb). //0.027:384:60//Z48053

F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence. //1.6e-18:229:65//AC004770

F-NT2RM2001797//HS_3045_A1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, genomic survey sequence. //1.4e-74:381:97//AQ129456

F-NT2RM2001800

F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds. //8.3e-178:827:99//AF044195

F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein kinase (LRPKm1) gene, 5' flanking region and 5' UTR. //1.0:290:58//AF053126

F-NT2RM2001813//CIT-HSP-2169F21.TR CIT-HSP Homo sa

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piens genomic clone 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870
 F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//5.8e-62:819:68//AC004274
 F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds.//3.6e-131:738:90//AF013759
 F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.1e-57:422:79//AC002347
 F-NT2RM2001855//HS_3224_A1_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=0, genomic survey sequence.//0.00012:68:91//AQ205285
 F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(I V). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.068:102:70//AL031177
 F-NT2RM2001879//Human DNA sequence from cosmid cu72E5, between markers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328
 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//1.9e-187:866:97//AB014610
 F-NT2RM2001896//S.cerevisiae chromosome III complete DNA sequence.//8.6e-30:613:63//X59720
 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.9e-176:859:97//AB007931
 F-NT2RM2001930//M.musculus mRNA for semaphorin G.//4.7e-117:730:85//X97818
 F-NT2RM2001935//Sequence 11 from Patent W09610637.//1.0:356:60//A50028
 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence.//6.9e-138:653:98//AF091080
 F-NT2RM2001950//RPCI11-24L12.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
 F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24121 genomic sequence, complete sequence.//0.42:179:65//AC005825
 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRNA, complete cds.//3.8e-20:123:98//AF089816
 F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981
 F-NT2RM2001997//Human HepG2 partial cDNA, clone hm

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dlb08m5.//9.6e-25:160:95//D16955
 F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151
 F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407
 F-NT2RM2002014
 F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//1.5e-89:822:74//U00932
 F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132
 F-NT2RM2002055
 F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936
 F-NT2RM2002091//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380
 F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840
 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435
 F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152
 F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121
 F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928
 F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936
 F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423
 F-NT2RM4000024//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826
 F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429
 F-NT2RM4000030//H.sapiens CpG island DNA genomic Msel fragment, clone 56h10, forward read cpg56h10.ftla.//9.3e-22:127:100//Z55685
 F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059
 F-NT2RM4000061

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F-NT2RM4000085//B.taurus mRNA for nuclear DNA heli case II. //1.9e-10:485:59//X82829
 F-NT2RM4000086
 F-NT2RM4000104//Homo sapiens chromosome 16 zinc fi nger protein ZNF210 (ZNF210) mRNA, complete cds.// 4.2e-23:345:69//AF060865
 F-NT2RM4000139//R.norvegicus trg mRNA. //1.4e-56:70 8:69//X68101
 F-NT2RM4000155//CIT-HSP-2282N15. TR CIT-HSP Homo sa piens genomic clone 2282N15, genomic survey sequen ce. //3.0e-09:88:90//AQ000070
 F-NT2RM4000156//H.sapiens HPBRII-7 gene. //2.0e-21: 586:60//X67336
 F-NT2RM4000167//Mouse kif4 mRNA for microtubule-ba sed motor protein KIF4, complete cds. //2.7e-143:81 0:90//D12646
 F-NT2RM4000169//Plasmodium falciparum 3D7 chromoso me 12 PFYAC293 genomicsequence, WORKING DRAFT SEQU ENCE, 9 unordered pieces. //0.0054:746:57//AC004157
 F-NT2RM4000191//Mus musculus cathepsin S (CatS) ge ne, promoter region and exons 1 and 2. //0.00018:46 8:60//AF051726
 F-NT2RM4000197
 F-NT2RM4000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT S EQUENCE. //0.67:461:60//AL031667
 F-NT2RM4000200
 F-NT2RM4000202//H.sapiens CpG island DNA genomic M sel fragment, clone 34c2, forward read cpg34c2.ft1 a. //1.7e-27:190:90//Z65361
 F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 pro tein, complete cds. //1.4e-182:856:98//AB018255
 F-NT2RM4000215//S.cerevisiae MAK16 protein gene, c omplete cds, and LTEIprotein gene, 3' end. //3.1e-3 1:731:62//J03852
 F-NT2RM4000229//Homo sapiens chromosome 10 clone C IT987SK-1144G6 map 10q25.1, complete sequence. //4. 6e-102:233:94//AC005383
 F-NT2RM4000233//Mus musculus semaphorin VIa mRNA, complete cds. //1.6e-135:835:86//AF030430
 F-NT2RM4000244//RPCI11-24P15. TV RPCI-11 Homo sapie ns genomic clone RPCI-11-24P15, genomic survey seq uence. //5.5e-08:422:62//B86757
 F-NT2RM4000251//Mus musculus clone UWGC:mbac92 fro m 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence. //0.98:207:60//AC005855
 F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PA C clone pDJ1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence. //5.2e-41:70 7:65//AC003689

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F-NT2RM4000290//Human transducin-like enhancer pro tein (TLE3) mRNA, complete cds. //7.9e-153:609:93// M99438
 F-NT2RM4000324
 F-NT2RM4000327//Rattus norvegicus guanine nucleoti de binding protein beta 4 subunit mRNA, partial cd s. //3.9e-44:727:68//AF022085
 F-NT2RM4000344//Mus musculus ATP-dependent metallo protease FtsH1 mRNA, complete cds. //1.0e-143:801:9 0//AF090430
 F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence. //6.1e-80:503:86//AF046700
 F-NT2RM4000354//HS_2221_A2_C07_MF CIT Approved Hum an Genomic Sperm Library D Homo sapiens genomic cl one Plate=2221 Col=14 Row=E, genomic surveysequenc e. //1.0e-20:180:83//AQ253449
 F-NT2RM4000356
 F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 pro tein, partial cds. //1.6e-133:628:99//AB014542
 F-NT2RM4000368//RPCI11-91B5. TJ RPCI11 Homo sapiens genomic clone R-91B5, genomic survey sequence. //5. 0e-12:431:61//AQ283217
 F-NT2RM4000386//Mus musculus DOC4 (Doc4) mRNA, com plete cds. //7.4e-86:845:72//AF059485
 F-NT2RM4000395//Saccharomyces cerevisiae chromosom e VI cosmid 9965. //2.5e-34:767:61//D44597
 F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulok inase, complete cds. //1.5e-15:114:94//AB015046
 F-NT2RM4000421
 F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence. //1.5e-37:295:82/ /AC005921
 F-NT2RM4000433//Mus musculus retinoic acid-respons ive protein (Stra6) mRNA, complete cds. //3.9e-94:7 40:78//AF062476
 F-NT2RM4000457//CIT-HSP-2346B17. TR CIT-HSP Homo sa piens genomic clone 2346B17, genomic survey sequen ce. //1.5e-22:149:92//AQ062111
 F-NT2RM4000471//Homo sapiens mRNA for putative tRN A splicing protein, partial. //1.3e-76:386:97//AJ01 0952
 F-NT2RM4000486//Homo sapiens mRNA, complete cds, c lone: RES4-22A. //1.1e-22:356:67//AB000459
 F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPCI11-47 6M19 (Roswell Park Cancer Institute Human BAC Libr ary) complete sequence. //0.53:198:70//AC005908
 F-NT2RM4000511
 F-NT2RM4000514
 F-NT2RM4000515//CIT-HSP-2285L3. TR CIT-HSP Homo sap iens genomic clone 2285L3, genomic survey sequenc

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e.//0.0012:200:66//AQ000113
 F-NT2RM4000520
 F-NT2RM4000531//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//2.9e-31:732:64//M58297
 F-NT2RM4000532//HS_3231_B1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093
 F-NT2RM4000534
 F-NT2RM4000585//CITBI-E1-2508I18.TR CITBI-E1 Homo sapiens genomic clone2508I18, genomic survey sequence.//1.1e-34:208:93//AQ260706
 F-NT2RM4000590//CIT-HSP-2291M14.TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125
 F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence.//1.2e-09:203:66//AC005288
 F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390
 F-NT2RM4000611//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870
 F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786
 F-NT2RM4000674
 F-NT2RM4000689//CIT-HSP-2381013.TF CIT-HSP Homo sapiens genomic clone 2381013, genomic survey sequence.//2.6e-31:174:97//AQ110303
 F-NT2RM4000698
 F-NT2RM4000700
 F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789
 F-NT2RM4000717
 F-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379
 F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303
 F-NT2RM4000741
 F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593
 F-NT2RM4000764
 F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790
 F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//5.5e-172:810:98//AB007920
 F-NT2RM4000787//Human DNA sequence from PAC 370M22

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on chromosome 22q12-qter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRO N-SULFUR SUBUNIT PRECURSOR (UQCRFS1) exon, ESTs, S TS, CA repeat and CpG island.//0.0057:163:69//Z82206
 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//6.9e-39:237:94//AC005306
 F-NT2RM4000795//Rattus norvegicus neuroligin 3 mRNA A, complete cds.//5.9e-97:857:74//U41663
 F-NT2RM4000796//HS_3214_B1_F11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence.//1.1e-14:254:68//AQ175988
 F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//6.2e-78:816:72//AF023451
 F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds.//0.33:276:63//M63109
 F-NT2RM4000820//, complete sequence.//2.6e-142:450:97//AC005406
 F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//1.9e-52:501:71//AC004373
 F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence.//1.0:477:56//AC005940
 F-NT2RM4000852
 F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//3.4e-29:229:83//AC003957
 F-NT2RM4000887
 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds.//2.1e-20:407:64//AB011004
 F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35unordered pieces.//0.41:311:64//AC004929
 F-NT2RM4000971//RPCI11-53H3.TJ RPCI11 Homo sapiens genomic clone R-53H3, genomic survey sequence.//1.0:208:64//AQ053735
 F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//1.3e-19:207:78//AC005245
 F-NT2RM4000996//CITBI-E1-2506B10.TF CITBI-E1 Homo sapiens genomic clone2506B10, genomic survey sequence.//1.4e-73:361:98//AQ263651
 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//5.1e-170:803:98//AB018272

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F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//3.3e-125:584:99//AB014539
 F-NT2RM4001032//Gallus gallus chicken brain factor -2 (CBF-2) mRNA, complete cds.//0.00034:777:58//U47276
 F-NT2RM4001047//M025 gene [mice, embryos, mRNA, 2322 nt].//2.5e-92:776:74//S51858
 F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds.//3.1e-102:859:76//M96629
 F-NT2RM4001084//CIT-HSP-2330F9. TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence.//4.6e-78:379:99//AQ044479
 F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-71b1, genomic survey sequence.//1.1e-12:152:75//B05776
 F-NT2RM4001116
 F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence.//1.9e-136:717:93//AC004593
 F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-ORF5) genes, complete cds; 3427 base-pairs.//0.0083:368:60//L06249
 F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds.//3.9e-120:764:85//U04706
 F-NT2RM4001160
 F-NT2RM4001187
 F-NT2RM4001191//CIT-HSP-2010E7. TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence.//6.2e-12:181:72//B53378
 F-NT2RM4001200//H. sapiens HZF10 mRNA for zinc finger protein.//1.3e-66:799:69//X78933
 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//4.2e-152:707:99//AF004828
 F-NT2RM4001204
 F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (ENC-1) mRNA, complete cds.//1.6e-62:715:70//AF005381
 F-NT2RM4001256//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884
 F-NT2RM4001258//BS_3171_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=N, genomic survey sequence.//2.5e-18:215:77//AQ149676
 F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163
 F-NT2RM4001313//H. sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973
 F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002
 F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016
 F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127
 F-NT2RM4001344//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388
 F-NT2RM4001347
 F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786
 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799
 F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393
 F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023
 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526
 F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183
 F-NT2RM4001414//Homo sapiens full length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563
 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226
 F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901
 F-NT2RM4001454
 F-NT2RM4001455

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dogene, EST, GSS, complete sequence.//4.9e-28:526:66//AL022163
 F-NT2RM4001313//H. sapiens mRNA for phosphatidylinositol 3-kinase.//2.5e-77:474:89//Z46973
 F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11.//1.2e-16:230:73//U97002
 F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.1e-41:642:66//D89016
 F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.//0.0040:141:68//AQ025127
 F-NT2RM4001344//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//5.5e-06:469:60//AL021388
 F-NT2RM4001347
 F-NT2RM4001371//Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence.//0.10:400:61//AC004786
 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.2e-167:790:98//AF098799
 F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//0.99:255:59//AL021393
 F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//0.027:336:58//AP000023
 F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//5.9e-124:783:85//AF020526
 F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP-c mRNA, complete cds.//2.2e-34:418:71//AF050183
 F-NT2RM4001414//Homo sapiens full length insert cDNA clone ZE16C11.//9.1e-76:363:100//AF086563
 F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBNL H146), complete sequence.//2.0e-47:623:69//AC004226
 F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds; and unknown gene.//3.6e-09:566:58//AF068901
 F-NT2RM4001454
 F-NT2RM4001455

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F-NT2RM4001483//Human zinc finger protein ZNF136. /
/3.2e-36:329:78//U09367
F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 pro
tein, complete cds.//1.2e-155:724:99//AB014585
F-NT2RM4001519//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC69 genomicsequence, WORKING DRAFT SEQUE
NCE, 4 unordered pieces.//0.00019:418:59//AC004688
F-NT2RM4001522//Human HepG2 3' region MboI cDNA, c
lone hmd6a08m3.//1.4e-16:130:88//D17274
F-NT2RM4001557
F-NT2RM4001565
F-NT2RM4001566
F-NT2RM4001569//HS_2050_B1_C08_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2050 Col=15 Row=F, genomic surveysequenc
e.//2.7e-09:109:84//AQ234720
F-NT2RM4001582//Mus musculus COP9 complex subunit
7b (COPS7b) mRNA, complete cds.//1.2e-127:740:89//
AF071317
F-NT2RM4001592//M.musculus mRNA of enhancer-trap-1 20
ocus 1.//7.3e-117:710:88//X69942
F-NT2RM4001594//Homo sapiens chromosome 9q34, clon
e 107G20, WORKING DRAFT SEQUENCE, 2 ordered piece
s.//0.34:388:59//AC002355
F-NT2RM4001597//M.musculus red-1 gene.//6.2e-139:7
88:90//X92750
F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 pro
tein, complete cds.//3.3e-162:750:99//AB018334
F-NT2RM4001611//Synechocystis sp. PCC6803 complete
genome, 12/27, 1430419-1576592.//2.5e-05:490:58// 30
D90910
F-NT2RM4001629//Mus musculus palmytoylated protein
p55 mRNA, complete cds.//0.65:186:64//U38196
F-NT2RM4001650//*** SEQUENCING IN PROGRESS *** Hom
o sapiens chromosome 4, BAC clone C0435P12; HTGS p
hase 1, WORKING DRAFT SEQUENCE, 10 unorderedpiece
s.//0.99:422:59//AC004689
F-NT2RM4001662//Human mRNA for KIAA0322 gene, part
ial cds.//2.6e-81:449:93//AB002320
F-NT2RM4001666
F-NT2RM4001682//Mus musculus clone OST9187, genomi
c survey sequence.//3.2e-35:240:87//AF046699
F-NT2RM4001710//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 126A5, WORKING DRAFT SE
QUENCE.//1.9e-151:564:97//AL031447
F-NT2RM4001714//Human mRNA for KIAA0202 gene, part
ial cds.//7.0e-85:748:74//D86957
F-NT2RM4001715//Human DNA sequence from clone 931K
24 on chromosome 20p12Contains ESTs and GSSs, comp
lete sequence.//1.2e-91:488:94//AL034430

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F-NT2RM4001731//Orang-utan involucrin gene, comple
te cds.//0.40:530:59//M25312
F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:73
7:90//X56123
F-NT2RM4001746//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 316G12, WORKING DRAFT S
EQUENCE.//2.3e-49:320:89//AL031709
F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPC15-118
OD12 (Roswell Park Cancer Institute Human PAC Libr
ary) complete sequence.//6.3e-64:379:76//AC005831
F-NT2RM4001758//R.norvegicus mRNA for serine/threo
nine kinase MARK1.//3.7e-146:871:87//Z83868
F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 pro
tein, partial cds.//2.3e-173:803:99//AB018270
F-NT2RM4001783//Homo sapiens clone DJ0981007, comp
lete sequence.//2.0e-165:593:99//AC006017
F-NT2RM4001810
F-NT2RM4001813//Homo sapiens BAC clone NH0364H22 f
rom 2, complete sequence.//7.1e-31:176:84//AC00503
6
F-NT2RM4001819//Human p58/GTA (galactosyltransfera
se associated proteinkinase) mRNA, complete cds.//
4.4e-34:195:95//M37712
F-NT2RM4001823//Mus musculus zinc finger protein
(Zfp64) mRNA, completecds.//3.3e-51:490:75//U49046
F-NT2RM4001828//Human zinc finger containing prote
in ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:68
8:72//U28687
F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Co
smid Clone 2h In DCCRRegion, complete sequence.//
1.0:406:60//AC000076
F-NT2RM4001841//Mus musculus A kinase anchor prote
in (AKAP-KL) mRNA, alternatively spliced isoform
2, complete cds.//1.6e-131:831:86//AF033275
F-NT2RM4001842//HS_3163_A2_G10_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3163 Col=20 Row=M, genomic surveysequenc
e.//1.5e-05:355:60//AQ168513
F-NT2RM4001856//Caenorhabditis elegans cosmid K08F
40 11.//4.0e-23:823:60//U70855
F-NT2RM4001858//Notophthalmus viridescens NvTbox1
mRNA, partial cds.//6.4e-11:266:66//U64433
F-NT2RM4001865//Homo sapiens mRNA for atopy relate
d autoantigen CALC.//6.9e-149:704:98//Y17711
F-NT2RM4001876//F.rubripes GSS sequence, clone 060
E22bA4, genomic surveysequence.//5.7e-48:600:68//Z
88651
F-NT2RM4001880//CIT-HSP-2348J1.TF CIT-HSP Homo sap
iens genomic clone 2348J1, genomic survey sequenc
e.//0.0025:61:88//AQ060809

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F-NT2RM4001905//R.norvegicus CYP3A1 gene, 5' flanking region. //2.5e-29:535:67//X98335
 F-NT2RM4001922//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence. //2.2e-73:364:98//AQ033732
 F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence. //4.9e-10:269:63//AB005248
 F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence. //7.6e-152:311:100//AC005207
 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds. //1.1e-170:808:98//AF098162
 F-NT2RM4001953//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces. //2.7e-45:310:86//AC004046
 F-NT2RM4001965//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11. //1.6e-107:622:90//AB020868
 F-NT2RM4001969//R.norvegicus mRNA for IP63 protein. //3.9e-24:221:76//X99330
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds. //1.0e-61:527:76//AB018341
 F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X. //5.8e-07:502:60//Z82253
 F-NT2RM4001987//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence. //2.6e-33:177:99//AQ051701
 F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence. //0.019:65:90//AC005921
 F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence. //1.0:527:57//L15344
 F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat. //0.11:322:60//AL008712
 F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds. //0.015:513:61//U01882
 F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces. //2.0e-44:473:76//AC005283
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds. //1.0e-171:803:98//AB014540
 F-NT2RM4002062//Drosophila melanogaster; Chromosome 50

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e 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.0031:298:59//AC005122
 F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds. //1.1e-147:705:98//U82267
 F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds. //3.4e-73:889:69//D83783
 F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence. //1.1e-53:295:76//AC005216
 F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds. //7.8e-25:277:75//AF072758
 F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds. //9.0e-23:588:61//AF059569
 F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1. //3.1e-68:544:69//X60789
 F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds. //2.0e-121:762:86//D12646
 F-NT2RM4002128//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=C, genomic survey sequence. //7.7e-18:117:95//AQ186312
 F-NT2RM4002140
 F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence. //1.8e-49:736:65//AC004152
 F-NT2RM4002146//Homo sapiens MACOH mRNA, complete cds. //6.5e-70:454:85//AF035940
 F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial. //4.2e-151:763:96//AJ130763
 F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome. //2.1e-16:580:60//AE000540
 F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs. //1.0e-07:792:61//AL008636
 F-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds. //3.2e-132:782:87//AF030430
 F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds. //1.5e-40:292:84//L14684
 F-NT2RM4002213
 F-NT2RM4002226//Mus musculus p190-B gene, complete cds. //0.099:350:59//U67160
 F-NT2RM4002251//Homo sapiens chromosome 17, clone HClT187M2, complete sequence. //1.0:428:58//AC00444

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 F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959
 F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006I18aG12, genomic survey sequence.//3.3e-12:217:67//AL024779
 F-NT2RM4002278//HS_3089_A1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653
 F-NT2RM4002281
 F-NT2RM4002287//CIT-HSP-2327E14.TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457
 F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881
 F-NT2RM4002323//Human DNA sequence from clone 59B1 6 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPIISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a corepeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822
 F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865
 F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849
 F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549
 F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978
 F-NT2RM4002383//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284
 F-NT2RM4002390
 F-NT2RM4002398//CIT-HSP-2288N22.TR CIT-HSP Homo sapiens genomic clone 2288N22, genomic survey sequence.//3.4e-35:184:100//AQ001110
 F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE01092
 F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336

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F-NT2RM4002446//Human DNA sequence from cosmid 443 D9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845
 F-NT2RM4002452
 F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 22, complete sequence.//2.2e-24:201:86//Z85988
 F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690
 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591
 F-NT2RM4002493
 F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484
 F-NT2RM4002504//Human DNA sequence from clone 3910 22 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence.//3.8e-31:233:87//AL031577
 F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162
 F-NT2RM4002532
 F-NT2RM4002534
 F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759
 F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:902:89//AF022962
 F-NT2RM4002567//CITBI-E1-2503J7.TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402
 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344
 F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875
 F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454
 F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122

- F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds. //3.9e-111:582:95//AB013385
- F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP). //1.1e-153:747:96//AJ012449
- F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE. //1.6e-125:243:88//AP000047
- F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence. //9.6e-09:414:59//Z92784
- F-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsal2. //2.8e-183:548:91//X98834
- F-NT2RP1000101//H. sapiens CpG island DNA genomic Msel fragment, clone 28b4, forward read cpg28b4.ft1a. //6.0e-27:163:95//Z60555
- F-NT2RP1000111//CIT-HSP-2307014. TR CIT-HSP Homo sapiens genomic clone 2307014, genomic survey sequence. //1.2e-11:128:81//AQ016069
- F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds. //1.0e-38:324:81//M86699
- F-NT2RP1000124//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL4P1, WORKING DRAFT SEQUENCE. //0.59:476:59//AL034557
- F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor. //2.7e-35:535:68//E08546
- F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds. //6.7e-05:77:90//AF011792
- F-NT2RP1000170//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, unordered pieces. //1.9e-20:431:64//AC006030
- F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence. //2.5e-138:679:97//AF070535
- F-NT2RP1000191
- F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds. //5.3e-05:220:61//D89496
- F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence. //4.7e-51:508:69//AC004373
- F-NT2RP1000259
- F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeats mRNA, complete cds. //7.8e-142:866:88//AF042383
- F-NT2RP1000324//RPC111-81021. TJ RPC111 Homo sapiens genomic clone R-81021, genomic survey sequence. //2.8e-29:182:92//AQ285136
- F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds. //4.2e-147:693:98//AF053551
- F-NT2RP1000333//Caenorhabditis elegans cosmid C03D 50
- 6, complete sequence. //1.4e-08:281:61//Z75525
- F-NT2RP1000348//H. sapiens CpG island DNA genomic Msel fragment, clone 12f1, reverse read cpg12f1.rt1c. //1.7e-09:71:100//Z56610
- F-NT2RP1000357
- F-NT2RP1000358
- 5.7e-16:403:61//AC005456
- F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds. //9.8e-125:497:86//AB014538
- F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds. //1.8e-176:877:96//AF064594
- F-NT2RP1000409//Homo sapiens repetitive sequences, aliphoid DNA, 2482bp. //4.6e-106:700:84//AJ001558
- F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds. //9.4e-178:710:98//AB011159
- F-NT2RP1000416
- F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds. //1.0:198:60//L40178
- F-NT2RP1000439//HS_2182_A1_D06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence. //2.1e-68:441:87//AQ024305
- F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE. //3.8e-57:185:88//AP000047
- F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence. //2.7e-132:204:99//AC004453
- F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence. //4.9e-80:196:95//AC002985
- F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds. //1.9e-55:440:80//U47634
- F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs. //2.6e-92:562:88//Z99297
- F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds. //2.0e-130:622:98//D87686
- F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds' s. //0.11:360:58//M81648
- F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, unordered pieces. //4.9e-34:20

3301

9:93//AC004895

F-NT2RP1000547//Cricetus griseus COP-coated vesicle membrane protein CHOP24 mRNA, partial cds.//1.2e-08:331:63//U26264

F-NT2RP1000574//Homo sapiens homeobox protein MEIS 2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418

F-NT2RP1000577//HS_2228_B2_C05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128

F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620

F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770

F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M62419

F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 22 Contains EST, complete sequence.//1.0:203:63//Z85989

F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943

F-NT2RP1000688//H. sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907

F-NT2RP1000695

F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//I30536

F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3unordered pieces.//1.1e-19:188:81//AC004932

F-NT2RP1000730

F-NT2RP1000733//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//1.3e-30:315:75//U95742

F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//8.0e-122:604:96//AF101434

F-NT2RP1000746//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//1.5e-83:466:92//AQ186344

F-NT2RP1000767//Homo sapiens full length insert cDNA clone ZD81B04.//2.8e-21:144:91//AF086442

F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

3302

F-NT2RP1000796//T. thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213

F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244

F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837

F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020

F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398

F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629

F-NT2RP1000851//Homo sapiens PAC clone 267D11 from 12, complete sequence.//1.6e-144:724:96//AC004812

F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

F-NT2RP1000860//Homo sapiens KLO4P mRNA, complete cds.//6.7e-106:551:95//AF064094

F-NT2RP1000902//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199

F-NT2RP1000915//H. sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761

F-NT2RP1000916

F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362

F-NT2RP1000944//HS_2179_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269

F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483

F-NT2RP1000954//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//0.030:89:78//B01950

50 F-NT2RP1000958//Caenorhabditis elegans cosmid K01C

3303

8, complete sequence.//3.9e-11:445:61//Z49068
 F-NT2RP1000959//Homo sapiens PAC clone 278C19 from
 12q, complete sequence.//3.3e-57:326:92//AC004263
 F-NT2RP1000966//Human nucleolin gene, complete cd
 s.//3.4e-64:197:98//M60858
 F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sa
 piens genomic clone 2314B10, genomic survey sequen
 ce.//0.32:137:68//AQ017126
 F-NT2RP1000988//Human chromosome 3p21.1 gene seque
 nce.//8.0e-72:665:80//L13435
 F-NT2RP1001011//Drosophila melanogaster DNA repair
 protein (mei-41) gene, complete cds, and TH1 gen
 e, partial cds.//1.3e-31:497:65//U34925
 F-NT2RP1001013//HS_3068_B1_B09_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3068 Col=17 Row=D, genomic surveysequenc
 e.//1.0e-24:414:66//AQ127667
 F-NT2RP1001014//HS_3252_B1_B05_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3252 Col=9 Row=D, genomic survey sequenc
 e.//0.00052:83:81//AQ304711
 F-NT2RP1001033//Homo sapiens chromosome 17, clone
 hRPC.1073_F_15, complete sequence.//1.3e-134:241:9
 9//AC004686
 F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 f
 rom 7p21, complete sequence.//2.5e-59:451:83//AC00
 4993
 F-NT2RP1001079//Oryctolagus cuniculus sarcosine ox
 idase (SOX) mRNA, complete cds.//4.5e-93:476:96//U
 82267
 F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORK
 ING DRAFT SEQUENCE, 18unordered pieces.//6.6e-54:2
 17:89//AC004938
 F-NT2RP1001113
 F-NT2RP1001173
 F-NT2RP1001177//Rattus norvegicus histone macroH2A
 1.2 mRNA, complete cds.//8.1e-26:373:68//U79139
 F-NT2RP1001185//Homo sapiens clone NH0319F03, WORK
 ING DRAFT SEQUENCE, 3unordered pieces.//3.5e-32:38
 8:73//AC006039
 F-NT2RP1001199
 F-NT2RP1001247//Homo sapiens signaling molecule LE
 FTY-A gene, exon 1.//2.0e-29:166:96//AF081508
 F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC
 clone pDJ356d6, complete sequence.//7.3e-50:128:99
 //AC002036
 F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA,
 complete cds.//4.3e-91:344:93//AF029914
 F-NT2RP1001286//Homo sapiens chromosome X region f
 rom filamin (FLN) geneto glucose-6-phosphate dehyd

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rogenase (G6PD) gene, complete cds's.//0.54:292:63
 //L44140
 F-NT2RP1001294
 F-NT2RP1001302
 F-NT2RP1001310//Rabbit skeletal muscle mRNA for ry
 anodine receptor.//1.5e-07:335:64//X15750
 F-NT2RP1001311//RPCI11-67014.TK RPCI11 Homo sapien
 s genomic clone R-67014, genomic survey sequence./
 /0.26:80:75//AQ239291
 10 F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PA
 C clone pDJ519o13 containing human gene for ferrit
 in heavy chain (FTH), complete sequence.//8.8e-75:
 304:98//AC004228
 F-NT2RP1001361//B.taurus CI-B14.5b mRNA for NADH d
 ehydrogenase (ubiquinone).//2.7e-57:412:84//X68647
 F-NT2RP1001385
 F-NT2RP1001395//Mus musculus COP9 complex subunit
 7a (COPS7a) mRNA, complete cds.//1.4e-72:535:83//A
 F071316
 20 F-NT2RP1001410//Homo sapiens DNA sequence from PAC
 257I20 on chromosome22q13.1-13.2. Contains cytoch
 rome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D),
 TCF20, NADH ubiquinone oxidoreductase B14 subunit,
 ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL02
 1878
 F-NT2RP1001424
 F-NT2RP1001432
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequ
 ence.//1.7e-84:422:97//AF052149
 30 F-NT2RP1001457//Xenopus laevis notchless (nle) mRN
 A, complete cds.//1.3e-47:471:73//AF069737
 F-NT2RP1001466//HS_3006_A2_D08_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3006 Col=16 Row=G, genomic surveysequenc
 e.//0.56:289:60//AQ154336
 F-NT2RP1001475//H.sapiens genomic DNA fragment (cl
 one NLMA194R).//0.00011:91:79//Z95375
 F-NT2RP1001482//Mouse oncogene (ect2) mRNA, comple
 te cds.//4.0e-87:563:85//L11316
 40 F-NT2RP1001494
 F-NT2RP1001543//Drosophila melanogaster DNA sequen
 ce (P1 DS01142 (D148)), complete sequence.//1.9e-2
 7:387:67//AC004280
 F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPA
 N-3) mRNA, complete cds.//8.0e-63:314:98//AF054840
 F-NT2RP1001569//Mus musculus signal recognition pa
 rticle receptor beta subunit mRNA, complete cds.//
 1.2e-68:514:81//U17343
 F-NT2RP1001616//Human clone 23665 mRNA sequence.//
 7.6e-40:496:74//U90913

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F-NT2RP1001665//CIT-HSP-2059N5.TF CIT-HSP Homo sapiens genomic clone 2059N5, genomic survey sequence. //2.4e-45:305:88//B69912

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence. //1.5e-135:685:96//AF091081

F-NT2RP2000006//HS_3061_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence. //1.9e-17:394:67//AQ178856

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds. //3.5e-14:241:68//AB002390

F-NT2RP2000008//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE. //1.7e-34:147:99//AL034424

F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence. //1.4e-32:345:75//AC005066

F-NT2RP2000032//F.rubripes GSS sequence, clone 060 E22aG10, genomic survey sequence. //5.0e-41:445:72//Z88655

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds. //1.9e-76:383:97//AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds. //2.4e-95:467:97//AF061749

F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence. //3.3e-39:236:91//AQ043092

F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds. //3.2e-50:311:90//D78610

F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds. //3.0e-55:766:66//AF059485

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence. //2.0e-118:597:95//AC005754

F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence. //0.0017:423:60//AC006037

F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds. //2.1e-77:278:97//AF050079

F-NT2RP2000079//H.sapiens CpG island DNA genomic Msel fragment, clone 40c2, forward read cpg40c2.ft1 k. //3.2e-33:197:95//Z55440

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds. //2.2e-158:752:98//AB018338

F-NT2RP2000091//HS_2228_A2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence. //0.26:55:90//AQ146363

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F-NT2RP2000097

F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2unordered pieces. //2.5e-05:482:60//AC004961

F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence. //1.0e-22:274:69//AC003973

F-NT2RP2000114//Homo sapiens mRNA for CM3 synthase, complete cds. //4.9e-114:551:97//AB018356

F-NT2RP2000120//HS_3000_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence. //1.8e-21:129:97//AQ090365

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds. //4.2e-119:607:96//AF054177

F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence. //1.3e-07:339:63//AC004827

20 F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds. //9.0e-101:638:85//M62419

F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Norrie Disease (Pseudoglioma)) gene and a CC1.3 Splicing Factor pseudogene. Contains ESTs, STSs and GS Ss, complete sequence. //0.45:377:58//AL034370

F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //4.0e-73:317:87//AC005924

30 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence. //3.0e-14:123:90//AQ263431

F-NT2RP2000173

F-NT2RP2000175

F-NT2RP2000183//F.rubripes GSS sequence, clone 168 M02aC2, genomic survey sequence. //3.7e-06:152:66//AL007295

F-NT2RP2000195//Human DNA sequence from clone 45I4 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence. //7.6e-62:170:99//AL023581

F-NT2RP2000205

F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmids R29828 and F25496, complete sequence. //7.2e-80:170:90//AC003030

F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence. //5.5e-64:400:85//AC004382

F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1

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(HIV-1 transcriptional elongation factor TATcofactor or TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CpG island, ESTs and STSs. //2.2e-07:280:66//Z97632
 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAC) mRNA, complete cds. //8.8e-30:508:67//U88401
 F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence. //4.0e-79:504:87 //AC004066
 F-NT2RP2000248
 F-NT2RP2000257//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE. //0.0078:286:60//AL021388
 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence. //5.7e-82:416:97//AQ059184
 F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence. //4.5e-29: 20 310:73//AC006116
 F-NT2RP2000274
 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor. //6.3e-20:260:73//X74904
 F-NT2RP2000288
 F-NT2RP2000289
 F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPPF1, -2, and -9. //4.6e-69:744:70//M27877
 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E 30 9. //4.4e-05:502:59//AL021530
 F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces. //2.1e-13:173:76//AC006082
 F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence. //8.3e-144:731:95//AL022398
 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence. //1.9e-102:555:90//AL034430
 F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds. //6.4e-105:639:87 //M25757
 F-NT2RP2000337//HS_2060_B1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence. //0.78:218:60//AQ243333

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F-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds. //3.6e-129:627:97//U83981
 F-NT2RP2000369//HS_2182_B1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence. //2.5e-87:421:99//AQ024835
 F-NT2RP2000412//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs. //0.72:170:65//AL021327
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds. //5.0e-66:375:93//L28010
 F-NT2RP2000420//Homo sapiens full length insert cDNA YQ86E07. //9.2e-77:423:93//AF075093
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-6-phosphate mutase mRNA, complete cds. //2.1e-126:609:96//AF102265
 F-NT2RP2000438//CITBI-E1-2519019.TR CITBI-E1 Homo sapiens genomic clone 2519019, genomic survey sequence. //0.96:61:78//AQ276878
 F-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. //7.1e-17:341:67//AC004691
 F-NT2RP2000459//H.sapiens mRNA for imogen 38. //5.7e-21:158:87//Z68747
 F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs. //3.2e-11:160:73//Z92844
 F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence. //0.0031:187:66//AC005229
 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066G04aC1, genomic survey sequence. //8.8e-07:179:64//AL026277
 F-NT2RP2000516//Mus musculus testis-specific protein (Tctex2) gene, wild type, promoter sequence. //0.19:72:81//U21671
 F-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE. //5.0e-115:570:96//AL022318
 F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds. //8.4e-37:196:98//AB005543
 F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence. //0.81:354:60//AC005321
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds. //1.3e-149:732:97//AB014514
 F-NT2RP2000644//HS_3211_A1_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence. 50

- e.//3.6e-42:282:86//AQ175486
 F-NT2RP2000656
 F-NT2RP2000658//CITBI-E1-2518N15.TF CITBI-E1 Homo sapiens genomic clone2518N15, genomic survey sequence.//0.57:141:66//AQ278386
 F-NT2RP2000668
 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12unordered pieces.//4.3e-22:433:62//AC004916
 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB -484017 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913
 F-NT2RP2000710//Drosophila melanogaster; Chromosome 2L; Region 36B1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122
 F-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42unordered pieces.//0.97:115:70//AC004965
 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1(LIMK1) gene, complete cds.//9.7e-16:162:77//U62293
 F-NT2RP2000764//HS_2254_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic surveysequence.//0.071:45:95//AQ068887
 F-NT2RP2000809
 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698
 F-NT2RP2000814
 F-NT2RP2000816
 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292
 F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479
 F-NT2RP2000845
 F-NT2RP2000863//Human partial cDNA sequence, clone x874;.//5.9e-29:173:94//Z47045
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284
 F-NT2RP2000892
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//3.4e-129:610:98//AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-37:212:84//AC005014
 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.//1.6e-126:682:93//Z69890
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//5.8e-112:533:98//AB018298
 F-NT2RP2000965
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//9.2e-101:505:96//AL021393
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//1.6e-72:498:82//AC005277
 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//7.4e-12:171:77//AC002394
 F-NT2RP2001036//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//1.2e-37:390:76//AC004167
 F-NT2RP2001044//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence.//0.21:276:61//AQ069224
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//3.2e-144:696:97//AB007957
 F-NT2RP2001065
 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//4.3e-104:775:81//U91561
 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds.//3.7e-69:488:82//AF000423
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS.//7.4e-11:490:61//Z86063
 F-NT2RP2001119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//5.1e-30:316:76//AL031596
 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds.//1.1e-31:519:63//D87072
 F-NT2RP2001137//HS_2193_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic surveysequence.//1.8e-11:136:78//AQ032187
 F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h In DGCRRegion, complete sequence.//6.2e-29:247:78//AC000076
 F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding ex

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on of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (*Drosophila*) homolog); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, 5' Tss, GSSs, and a putative CpG island, complete sequence. //0.23:207:66//AL009178

F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds. //2.3e-112:567:96//AB007949

F-NT2RP2001174//RPC111-58L2.TK RPC111 Homo sapiens genomic clone R-58L2, genomic survey sequence. //7.6e-07:196:64//AQ237306

F-NT2RP2001196

F-NT2RP2001218

F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1. //1.1e-09:320:65//U92893

F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein. //6.1e-71:681:72//X51760

F-NT2RP2001245//HS_3062_B1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence. //1.5e-05:268:63//AQ143177

F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds. //2.5e-106:514:97//AB018353

F-NT2RP2001277//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence. //0.32:183:64//AE001430

F-NT2RP2001290//M. musculus mRNA for I47 clone. //8.6e-102:641:86//X61455

F-NT2RP2001295//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE. //0.20:171:63//AL022594

F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds. //0.98:253:58//M22967

F-NT2RP2001327//Human B12 protein mRNA, complete cds. //5.8e-29:359:71//M80783

F-NT2RP2001328//CIT-HSP-2335A5.TF CIT-HSP Homo sapiens genomic clone 2335A5, genomic survey sequence. //1.3e-65:366:94//AQ038539

F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease. //3.8e-31:325:77//AJ003147

F-NT2RP2001366//H. sapiens CpG island DNA genomic Msel fragment, clone 4e11, forward read cpg4e11.f1a. //1.7e-12:98:92//Z61305

F-NT2RP2001378//HS_3054_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence. //9.8e-17:131:89//AQ100721

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e. //9.8e-17:131:89//AQ100721

F-NT2RP2001381//Arabidopsis thaliana BAC T2L5. //0.080:434:59//AF096371 F-NT2RP2001392//S. pristinaespiralis snbC gene & snbDE gene. //0.019:267:59//Y11548

F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat. //1.9e-16:133:78//Z93242

F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds. //1.3e-63:419:84//AF080219

F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds. //3.1e-98:747:79//U76759

F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds. //3.7e-34:269:85//AF015454

F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence. //3.2e-13:164:78//AC003065

F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence. //3.0e-06:136:71//AF046702

F-NT2RP2001440//cDNA sequence coding for gamma protein. //7.9e-83:553:86//E02350

F-NT2RP2001445//P. falciparum complete gene map of plastid-like DNA (IR-A). //1.5e-09:829:57//X95275

F-NT2RP2001449//B. taurus mRNA for cleavage and polyadenylation specificity factor. //1.3e-136:766:90//X75931

F-NT2RP2001450

F-NT2RP2001467

F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence. //7.9e-14:151:80//AQ109561

F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds. //2.6e-22:462:64//AF005355

F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1. //2.0e-136:657:97//Y14494

F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence. //1.2e-37:357:64//AC004596

F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds. //1.6e-103:384:94//AF035586

F-NT2RP2001560

F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488. //4.4e-123:590:98//AB007957

F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds. //0.038:580:58//U32943

- F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds.//6.5e-09:222:66//AF030430
- F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.//0.0057:361:60//U72648
- F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//7.2e-137:647:98//AB018340
- F-NT2RP2001613
- F-NT2RP2001628//H.sapiens (xsl28) mRNA, 380bp.//1.7e-15:279:68//Z36784
- F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds.//5.4e-123:606:96//AF030233
- F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//4.2e-144:687:97//AF058718
- F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alpha-enolase.//1.0e-36:372:74//X84907
- F-NT2RP2001675//S.pombe chromosome I cosmid c2G11.//0.070:507:59//Z54354
- F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence.//2.0e-60:232:96//AC005259
- F-NT2RP2001678//HS_2007_A2_A04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence.//7.3e-62:370:91//AQ269699
- F-NT2RP2001699//RPC111-57B17.TK RPC111 Homo sapiens genomic clone R-57B17, genomic survey sequence.//0.99:141:63//AQ115592
- F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//9.4e-117:604:95//AC004079
- F-NT2RP2001721//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//1.0:273:61//AL030998
- F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCRRRegion, complete sequence.//1.0:356:62//AC000090
- F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds.//3.7e-18:151:86//D14697
- F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.0e-145:715:97//AC004783
- F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378
- F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347
- F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y16610
- F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219
- F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309
- F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.8e-87:496:92//AL031864
- F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//9.2e-112:633:90//M74161
- F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281
- F-NT2RP2001907//H.sapiens CpG island DNA genomic Msel fragment, clone 97f11, forward read cp97f11.f11a.//4.2e-26:206:84//Z64125
- F-NT2RP2001926//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688
- F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856
- F-NT2RP2001943//Drosophila melanogaster cosmid 25E8.//0.00036:248:60//AL009196
- F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033
- F-NT2RP2001947//Homo sapiens full length insert cDNA clone ZD81B04.//2.0e-28:172:94//AF086442
- F-NT2RP2001969//H.sapiens CpG island DNA genomic Msel fragment, clone 152a8, reverse read cp9152a8.r11a.//1.0e-20:123:99//Z59378
- F-NT2RP2001976
- F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117
- F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022
- F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299

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F-NT2RP2002032//Homo sapiens chromosome 5, Bac clone 5m9 (LBNL H220), complete sequence.//0.76:189:65//AC005895

F-NT2RP2002033//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2unordered pieces.//2.9e-12:160:79//AC004825

F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029

F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems HumanBAC library) complete sequence.//2.2e-86:722:77//AC004552

F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375

F-NT2RP2002058//S.cerevisiae chromosome XII reading frame ORF YLR129w.//9.7e-11:480:60//Z73301

F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306

F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin beta subunit 63 kda isoform/membraneskeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083

F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127:643:96//AF052183

F-NT2RP2002078//F12016-T7.1 IGF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//0.14:191:64//AQ249805

F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917

F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//9.8e-111:533:97//AJ007509

F-NT2RP2002105//H.sapiens CpG island DNA genomic Msel fragment, clone 10h8, forward read cpg10h8.ft1a.//2.4e-29:178:94//Z58857

F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468

F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874

F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:258:63//D85923

F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169

3316

F-NT2RP2002185//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//2.8e-18:109:100//AQ201833

F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl) mRNA, complete cds.//2.7e-36:363:78//U09215

F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-82:477:89//AF032872

F-NT2RP2002208

10 F-NT2RP2002219//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557

F-NT2RP2002231//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomicsequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.60:560:56//AC005308

F-NT2RP2002235//P.falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998

F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394

20 F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418

F-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL033527

F-NT2RP2002270//RPCI11-77C23.TV RPCI11 Homo sapiens genomic clone R-77C23, genomic survey sequence.//2.9e-18:79:93//AQ268098

F-NT2RP2002292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033

30 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.5e-93:467:96//AF069532

F-NT2RP2002316//HS_2171_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=22 Row=H, genomic surveysequence.//7.3e-94:463:97//AQ119673

F-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//3.9e-123:640:95//AB015594

40 F-NT2RP2002333

F-NT2RP2002373//F.rubripes GSS sequence, clone 026 F10aB8, genomic surveysequence.//0.46:234:61//Z87330

F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958

F-NT2RP2002394//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275

50 F-NT2RP2002408//F.rubripes GSS sequence, clone 080 G11aA8, genomic surveysequence.//5.7e-15:220:71//A

3317

L015615
 F-NT2RP2002426//Sus scrofa SCAMP1 gene, exon 9.//
 7.1e-71:582:80//AJ223742
 F-NT2RP2002439//Caenorhabditis elegans cosmid T07D
 3.//0.0018:210:67//AF016682
 F-NT2RP2002442//Caenorhabditis elegans cosmid T03F
 1.//2.8e-18:295:67//U88169
 F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clo
 ne CIT987SK-44W2, complete sequence.//1.9e-06:281:
 66//AC004381
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, comp
 lete cds.//0.039:207:63//D42045
 F-NT2RP2002475
 F-NT2RP2002479//Homo sapiens mRNA for ABC transpor
 ter 7 protein, complete cds.//2.4e-123:607:96//ABO
 05289
 F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//
 0.73:395:57//AF069300
 F-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, c
 omplete sequence.//7.2e-18:134:90//AC006213
 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 pro
 tein, complete cds.//1.2e-157:761:97//AB018334
 F-NT2RP2002520
 F-NT2RP2002537
 F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac
 pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pie
 ces.//0.83:252:60//AC004127
 F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone
 pDJ457j11 containing DNA polymerase gamma (polg) g
 ene, complete sequence.//5.9e-93:186:99//AC005317
 F-NT2RP2002591//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 54B20, WORKING DRAFT SE
 QUENCE.//4.0e-38:175:78//Z98304
 F-NT2RP2002595//Sequence 2 from patent US 5763220.
 //1.5e-84:430:95//AR012155
 F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, com
 plete cds.//1.9e-43:282:87//U19181
 F-NT2RP2002609//Mus musculus defender against deat
 h 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF05
 1310
 F-NT2RP2002618//H.sapiens mRNA for arginine methyl
 transferase, splice variant, 1316 bp.//5.6e-27:46
 0:63//Y10806
 F-NT2RP2002621
 F-NT2RP2002643//Rat calmodulin III gene for calmod
 ulin, promoter region and exon 1.//0.023:322:60//D9
 0397
 F-NT2RP2002672//Homo sapiens chromosome 10 clone C
 IT-HSP-1326H7 map 10q24.3-10q25.1, complete sequen
 ce.//3.9e-149:794:94//AC005384

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F-NT2RP2002701//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 50024, WORKING DRAFT SE
 QUENCE.//9.2e-10:129:75//AL034380
 F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:
 63//Y10980
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 pro
 tein, complete cds.//2.5e-40:631:65//AB014572
 F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, co
 mplete cds.//4.8e-65:600:73//AF041107
 10 F-NT2RP2002736//S.pombe chromosome II cosmid c887.
 //0.17:352:58//AL033388
 F-NT2RP2002740//Absidia glauca ORF, 3' end; (+) ma
 ting type surface protein (PSSP15) gene, complete
 cds; ORF, 5' end.//0.0073:274:66//M94861
 F-NT2RP2002741//Homo sapiens mRNA for Neuroblastom
 a, complete cds.//7.5e-29:628:62//D89016
 F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC G
 SHB-214D18 (Genome Systems Human BAC Library) comp
 lete sequence.//3.6e-31:568:67//AC005296
 20 F-NT2RP2002752//Human BAC clone RG317M02 from 7p15
 -p21, complete sequence.//1.7e-08:206:63//AC002433
 F-NT2RP2002753//Human DNA sequence from cosmid B11
 B7 on chromosome 22 contains ESTs.//2.8e-71:195:89
 //Z82171
 F-NT2RP2002769//Streptomyces fradiae ty lactone syn
 thase, starter module and modules 1-7, (tylG) gene,
 complete cds.//0.0016:412:60//U78289
 F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sap
 iens genomic clone 2059C5, genomic survey sequenc
 e.//6.8e-18:186:79//B69837
 30 F-NT2RP2002800
 F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PA
 C clone pDJ688p12 containing uteroglobin gene, WOR
 KING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-4
 1:134:94//AC006078
 F-NT2RP2002857//Rat T-cell receptor active beta-ch
 ain V-region (V-beta6-J-beta2.5) mRNA, partial cd
 s, clone TRB-4.//0.85:93:68//M18845
 F-NT2RP2002862//HS_3084_A1_H03_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3084 Col=5 Row=0, genomic survey sequenc
 e.//5.0e-67:390:91//AQ186344
 40 F-NT2RP2002880
 F-NT2RP2002891//CIT-HSP-2310014.TF CIT-HSP Homo sa
 piens genomic clone 2310014, genomic survey sequen
 ce.//0.11:53:90//AQ019792
 F-NT2RP2002925//Pig mRNA for carbonyl reductase, c
 omplete cds.//0.66:194:65//D16511
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing fac
 tor (PRP17) mRNA, complete cds.//2.3e-135:628:99//
 50

- AF038392
F-NT2RP2002929//F.rubripes GSS sequence, clone 123 I23aA1, genomic surveysequence.//3.9e-06:66:83//AL017246
F-NT2RP2002939
F-NT2RP2002954
F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483
F-NT2RP2002979//CIT-HSP-2340D12. TF CIT-HSP Homo sapiens genomic clone 2340D12, genomic survey sequence.//4.6e-96:476:97//AQ057233
F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230
F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, completecds.//2.4e-09:272:61//AF059569
F-NT2RP2002987//Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958
F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424
F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765
F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//4.2e-23:202:82//AC005703
F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822
F-NT2RP2003099//HS_3008_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic surveysequence.//1.4e-71:362:96//AQ089786
F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362
F-NT2RP2003117//HS_2034_B2_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic surveysequence.//1.5e-88:461:96//AQ230797
F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, completecds.//4.3e-46:470:72//AF079765
F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329
F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915
F-NT2RP2003137//CIT-HSP-2300J6. TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976
F-NT2RP2003157//Human DNA sequence from cDNA 16pHQ G;16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716
F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025
F-NT2RP2003161//CITBI-E1-2506E20. TR CITBI-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657
F-NT2RP2003164
F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328
F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040
F-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597
F-NT2RP2003206
F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794
F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:86//AF023657
F-NT2RP2003237//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447
F-NT2RP2003243//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107
F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cellline NCD5) mRNA, complete cds.//6.0e-114:696:87//L38481
F-NT2RP2003272//RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833
F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525
F-NT2RP2003280//RPCI11-14I2. TVB RPCI-11 Homo sapiens genomic clone RPCI-11-14I2, genomic survey sequence.//6.4e-77:400:95//B85286
F-NT2RP2003286//CIT-HSP-2336D3. TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024
F-NT2RP2003293//Homo sapiens DNA from chromosome 1

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9, BAC 33152, complete sequence. //1.5e-54:508:74//A
C003973
F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 me-
lating protein, complete cds. //6.1e-85:416:97//ABO
06572
F-NT2RP2003297//S.pombe pho2 gene for specific p-n
itrophenylphosphatase. //0.60:309:64//X62722
F-NT2RP2003307//Mus musculus kinesin light chain 2
(Klc2) mRNA, complete cds. //1.0e-45:442:75//AF0556
66
F-NT2RP2003308//D.melanogaster crn mRNA. //1.1e-63:
697:70//X58374
F-NT2RP2003329//Homo sapiens chromosome 17, clone
hCIT.131_K_11, complete sequence. //0.040:145:64//A
C005288
F-NT2RP2003339
F-NT2RP2003347//Plasmodium falciparum MAL3P7, comp
lete sequence. //0.12:275:60//AL034559
F-NT2RP2003367//Homo sapiens chromosome 4 clone B3
68A9 map 4q25, complete sequence. //0.83:225:63//AC
005510
F-NT2RP2003391
F-NT2RP2003393//HS_3218_A2_B09_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3218 Col=18 Row=C, genomic survey sequenc
e. //0.021:93:79//AQ204356
F-NT2RP2003394
F-NT2RP2003401
F-NT2RP2003433//Rattus rattus sec61 homologue mRN
A, complete cds. //4.2e-61:533:75//M96630
F-NT2RP2003445//Homo sapiens genomic DNA, chromoso
me 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE. //
2.1e-49:301:72//AP000023
F-NT2RP2003446
F-NT2RP2003456//Rickettsia prowazekii strain Madri
d E, complete genome; segment 3/4. //0.0018:366:60//
AJ235272
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CI
T-HSP-311e8 (BC269730) containing the hFEN1 gene, c
omplete sequence. //7.5e-16:189:68//AC004770
F-NT2RP2003480//Mouse interleukin 2 receptor (p55
IL-2R) mRNA, 5' end. //1.9e-25:197:85//M21977
F-NT2RP2003499
2.1e-08:408:61//AB000826
F-NT2RP2003506//Homo sapiens clone NH0479C13, WORK
ING DRAFT SEQUENCE, 12unordered pieces. //1.9e-33:1
92:96//AC005236
F-NT2RP2003511//Ceratopteris richardii mRNA for CR
HB11, partial cds. //1.0:328:60//AB013801
F-NT2RP2003513//Human mRNA for KIAA0270 gene, part

3322

1al cds. //7.3e-76:403:93//D87460
F-NT2RP2003517//Human osteosarcoma cell line U-2 O
S mRNA fragment for PDGF-B chain (PDGF= platelet-d
erived growth factor). //1.5e-24:151:95//X03702
F-NT2RP2003522//Mouse interleukin 2 receptor (p55
IL-2R) mRNA, 5' end. //1.3e-101:564:91//M21977
F-NT2RP2003533//Human DNA sequence from cosmid F11
21 on chromosome 6. //2.0e-40:315:75//Z80899
F-NT2RP2003543
10 F-NT2RP2003559//H.sapiens CpG island DNA genomic M
sel fragment, clone 90a5, reverse read cpg90a5.rtl
a. //1.1e-20:122:99//Z56144
F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/S
SA mRNA, complete cds. //8.8e-27:664:63//M34551
F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 pro
tein, partial cds. //4.1e-113:541:98//AB007931
F-NT2RP2003581
F-NT2RP2003596//F.rubripes GSS sequence, clone 036
L10aF12, genomic survey sequence. //1.9e-11:210:65/
20 /AL012756
F-NT2RP2003604//Homo sapiens alpha-catenin-like pr
oteins (CTNNA1) mRNA, complete cds. //1.9e-123:587:9
8//AF030233
F-NT2RP2003629
F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetyl
neuraminic acid synthetase. //7.8e-88:582:84//AJ006
215
F-NT2RP2003668//Homo sapiens clone RC270D13, WORKI
NG DRAFT SEQUENCE, 18unordered pieces. //5.6e-47:33
30 5:83//AC005081
F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5
(Genome Systems Human BAC library) complete sequen
ce. //1.2e-06:133:74//AC003684
F-NT2RP2003691//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 525L6, WORKING DRAFT SE
QUENCE. //1.7e-47:337:81//AL023807
F-NT2RP2003702//Rattus norvegicus ovarian-specific
protein mRNA, complete cds. //1.3e-65:458:82//U448
03
40 F-NT2RP2003704//H.sapiens CpG island DNA genomic M
sel fragment, clone 2a9, reverse read cpg2a9.rtl.e.
//3.8e-17:170:84//Z60615
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 pro
tein, partial cds. //2.6e-108:518:98//AB011097
F-NT2RP2003713//HS_2016_B1_B05_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2016 Col=9 Row=D, genomic survey sequenc
e. //1.3e-11:102:90//AQ226895
F-NT2RP2003714//Homo sapiens DNA from chromosome 1
9, BAC 33152, complete sequence. //1.4e-27:249:78//A

C003973

F-NT2RP2003727//RPC111-77119.TV RPC111 Homo sapiens genomic clone R-77119, genomic survey sequence.//3.4e-26:294:74//AQ268303

F-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951

F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964

F-NT2RP2003760//B. primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987

F-NT2RP2003764//Homo sapiens gene for MTC16, exon 1b, partial sequence.//1.0:109:69//AB013275

F-NT2RP2003769

F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//3.0e-96:467:98//AC004771

F-NT2RP2003777

F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986nt].//7.2e-107:731:82//S70011

F-NT2RP2003793//CIT-BSP-2326L12.TF CIT-BSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761

F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491

F-NT2RP2003840//Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167

F-NT2RP2003857//HS_3227_A2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=M, genomic survey sequence.//0.96:257:61//AQ303467

F-NT2RP2003859

F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375

F-NT2RP2003885//CITBI-E1-2514D6.TF CITBI-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722

F-NT2RP2003912//nekl=serine/threonine- and tyrosine-specific protein kinase [mice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828

F-NT2RP2003952

F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458

F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the altern

atively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282

F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347

F-NT2RP2003984

F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382

F-NT2RP2003988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681

F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//3.0e-123:693:91//AL023580

F-NT2RP2004014

F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780

F-NT2RP2004042

F-NT2RP2004066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555

F-NT2RP2004081

F-NT2RP2004098//HS_2216_A1_B12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694

F-NT2RP2004124//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993

F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8K14, complete sequence.//1.0:220:62//AB007645

F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence.//0.93:480:56//AC002493

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F-NT2RP2004165//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140

F-NT2RP2004170//*Homo sapiens* distal-less homeobox protein (DLX7) gene, complete cds.//1.0:162:66//AF028235

F-NT2RP2004172//*S. pombe* chromosome II cosmid c24E9.//1.7e-06:466:59//AL021816

F-NT2RP2004187//*Homo sapiens* full length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093

F-NT2RP2004194//*Rattus norvegicus* Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998

F-NT2RP2004196

F-NT2RP2004207//Human von Willebrand factor pseudo gene corresponding to exons 23 through 34.//0.0023:386:61//M60676

F-NT2RP2004226//HS_2186_A1_D03_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2186 Col=5 Row=G, genomic survey sequence.//7.8e-58:370:87//AQ063813

F-NT2RP2004232//*H. sapiens* mRNA for protein kinase C mu.//1.2e-34:448:67//X75756

F-NT2RP2004239//*Homo sapiens* lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718

F-NT2RP2004240//*Pyrococcus horikoshii* OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006

F-NT2RP2004242

F-NT2RP2004245

F-NT2RP2004270//*Streptomyces coelicolor* cosmid 1A9.//7.5e-07:462:62//AL034446

F-NT2RP2004300//*Homo sapiens* chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781

F-NT2RP2004316//*Homo sapiens* EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416

F-NT2RP2004321//*Drosophila melanogaster* DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423

F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519

F-NT2RP2004347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650

F-NT2RP2004364

F-NT2RP2004365

F-NT2RP2004366//Human DNA sequence from clone 612B 50

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18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//0.92:427:57//AL031864

F-NT2RP2004373//*Homo sapiens* cosmid Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397

F-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969

F-NT2RP2004392

F-NT2RP2004396//*Homo sapiens* BAC clone RG135C18 from 7q21, complete sequence.//1.1e-171:875:95//AC005164

F-NT2RP2004399//*Homo sapiens* SYBL1 gene.//1.4e-24:467:64//AJ004799

F-NT2RP2004400//*Arabidopsis thaliana* BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441

F-NT2RP2004412//*H. sapiens* CpG island DNA genomic Msel fragment, clone 34g4, reverse read cp34g4.rtl a.//5.0e-27:154:98//Z65369

F-NT2RP2004425

F-NT2RP2004463//*Streptomyces coelicolor* cosmid 2E9.//0.0053:196:65//AL021530

F-NT2RP2004476//*Drosophila melanogaster* cosmid 67A9.//5.2e-15:377:63//AL034388

F-NT2RP2004490//*Homo sapiens* chromosome 16, P1 clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591

F-NT2RP2004512//*Plasmodium falciparum* MAL3P5, complete sequence.//2.3e-07:815:57//AL034556

F-NT2RP2004523//*Homo sapiens* clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890

F-NT2RP2004538//*Homo sapiens* mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163

F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP *Homo sapiens* genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555

F-NT2RP2004568//*H. vulgare* GAA-satellite DNA.//2.0e-07:292:62//Z50100

F-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755

F-NT2RP2004587//*Candida albicans* cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908

F-NT2RP2004594//nbxb0019H13r CUGI Rice BAC Library *Oryza sativa* genomic clone nbxb0019H13r, genomic s

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urvey sequence.//0.053:324:60//AQ258020
 F-NT2RP2004600
 F-NT2RP2004602//Homo sapiens chromosome 19, cosmid
 F21431, complete sequence.//0.12:109:73//AC005176
 F-NT2RP2004614
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich
 protein.//2.6e-102:496:98//AJ006291
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 pro
 tein, partial cds.//1.6e-153:728:98//AB007929
 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, W 10
 ORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:
 239:61//AC005805
 F-NT2RP2004681//Human DNA sequence from clone 51J2
 3 on chromosome Xq26.3-27.3. Contains an EST and C
 SSSs, complete sequence.//1.0:236:61//AL031312
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 pro
 tein, partial cds.//1.3e-59:327:94//AB014525
 F-NT2RP2004709//HS_2033_B2_E04_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2033 Col=8 Row=J, genomic survey sequenc 20
 e.//1.9e-15:187:74//AQ230714
 F-NT2RP2004710//HS_3185_B2_D07_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3185 Col=14 Row=H, genomic surveysequenc
 e.//9.9e-10:110:84//AQ172885
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 pro
 tein, complete cds.//6.4e-117:582:96//AB007947
 F-NT2RP2004743//Human DNA sequence from PAC 37M17
 chromosome X.//0.14:138:71//Z78022
 F-NT2RP2004767//H. sapiens CpG island DNA genomic M 30
 sel fragment, clone 65c11, reverse read cpg65c11.r
 tla.//1.3e-24:217:81//Z62210
 F-NT2RP2004768//Homo sapiens STE20-like kinase 3
 (mst-3) mRNA, completecds.//1.6e-45:541:71//AF0246
 36
 F-NT2RP2004775//Plasmodium falciparum chromosome
 2, section 35 of 73 ofthe complete sequence.//5.8e
 -13:697:59//AE001398
 F-NT2RP2004791//Human HeLa mRNA isolated as a fals
 e positive in a two-hybrid-screen.//5.0e-53:353:84 40
 //U56252
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl
 -CoA synthetase beta subunit (SCS) mRNA, partial c
 ds.//1.5e-116:594:95//AF058953
 F-NT2RP2004802
 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRN
 A, complete cds.//2.1e-101:495:97//AF054179
 F-NT2RP2004841//Human DNA sequence from cosmid J13
 8017, between markersDXS6791 and DXS8038 on chromo
 some X contains EST CA repeat and an endogenous re 50

3328

troviral like element.//7.6e-82:531:84//Z72519
 F-NT2RP2004861//Fugu rubripes GSS sequence, clone
 040017bA3, genomic survey sequence.//0.96:183:64//
 AL025645
 F-NT2RP2004897//Human Chromosome X clone bWXd187,
 complete sequence.//4.8e-142:710:96//AC004383
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase,
 complete cds.//2.0e-82:418:95//AB007144
 F-NT2RP2004936
 F-NT2RP2004959//HS_3197_A2_G11_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3197 Col=22 Row=M, genomic surveysequenc
 e.//3.5e-25:218:83//AQ150183
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger
 suppressor protein 1(KS1) mRNA, complete cds.//2.
 5e-59:339:79//U56732
 F-NT2RP2004962//Human hereditary haemochromatosis
 region, histone 2A-like protein gene, hereditary h
 aemochromatosis (HLA-H) gene, RoRet gene, and sodi
 um phosphate transporter (NPT3) gene, complete cd 20
 s.//3.6e-19:187:72//U91328
 F-NT2RP2004967//Plasmodium falciparum MAL3P6, comp
 lete sequence.//0.0020:297:61//Z98551
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mR
 NA, complete cds.//0.22:162:69//L29029
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana
 genomic clone F26D4, genomic survey sequence.//0.1
 3:273:61//B12642
 F-NT2RP2004985//Human mRNA for KIAA0144 gene, comp
 lete cds.//1.5e-20:431:65//D63478
 F-NT2RP2004999
 F-NT2RP2005000//R. rattus gene for beta-1 subunit o
 f Na,K-ATPase.//0.019:240:63//X63375
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 pro
 tein, complete cds.//6.0e-159:782:97//AB014515
 F-NT2RP2005003//H. sapiens Staf50 mRNA.//3.1e-42:43
 0:75//X82200
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, c
 omplete cds.//1.4e-98:501:96//AF100141
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 f
 rom 7q33-q35, complete sequence.//1.0:209:63//AC004
 849
 F-NT2RP2005020
 F-NT2RP2005022//Human Chromosome 3 pac pDJ70i11, W
 ORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-4
 3:98:93//AC000380
 F-NT2RP2005031//HS_2052_B2_G10_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2052 Col=20 Row=N, genomic surveysequenc
 e.//0.019:363:61//AQ231464

3329

F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454

F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//0.20:519:57//AC005696

F-NT2RP2005108

F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564

F-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myo-regulated dead box protein).//2.9e-27:157:98//X9 10 8743

F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012

F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527

F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF0455 83

F-NT2RP2005147//HS_3184_A1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226

F-NT2RP2005159//H. sapiens CpG island DNA genomic Msel fragment, clone 132g6, forward read cpg132g6.f tla.//1.1e-13:93:97//Z59162

F-NT2RP2005162//Caenorhabditis elegans cosmid F01F 1.//2.6e-20:394:64//U13070

F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.4e-125:633:96//AJ007509

F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808

F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005 189

F-NT2RP2005239//S. pombe chromosome II cosmid c21D1 0.//1.3e-22:356:67//AL031536

F-NT2RP2005254

F-NT2RP2005270//H. sapiens genomic DNA (chromosome 3; clone NL197R).//0.58:132:65//X87513

F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666

F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//3.4e-37:302:84//L26 335

F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLC mRNA, complete cds.//7.1e-122:604:96//AF060219

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F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590

F-NT2RP2005293//HS_3245_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576

F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, complete cds.//8.2e-22:166:90//U11701

F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138

F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92 844

20 F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247

F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358

F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184

F-NT2RP2005407

F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LANL), complete sequence.//0.014:235:62//AC005346

30 F-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//4.0e-107:532:97//AQ055548

F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865

F-NT2RP2005457//B. taurus CI-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647

40 F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679

F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//6.5e-18:152:75//AC006116

F-NT2RP2005472//Human DNA sequence from clone 1118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kD) (TNF Bindi

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ng Protein 2, TBP11, TNF-R2, CD120B, TNFBR). Contains ESTs, STSs, GSSs, genomic marker DIS434 and a c a repeat polymorphism, complete sequence. //4.4e-12:89:97//AL031276

F-NT2RP2005476//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence. //4.3e-40:463:73//AC004130

F-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1unordered pieces. //3.2e-115:228:99//AC006030

F-NT2RP2005491//HS_2253_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence. //4.6e-23:234:80//AQ116847

F-NT2RP2005495

F-NT2RP2005496//HS_3064_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence. //5.3e-90:436:98//AQ143097

F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds. //1.4e-63:503:78//M64931

F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence. //0.86:183:63//AC005880

F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28. //1.0:160:65//U82695

F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds. //3.9e-81:444:92//AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds. //6.9e-18:112:99//AB018307

F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds. //1.1e-06:282:60//M14993

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP). //2.9e-153:747:97//AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds. //5.9e-130:618:98//AB007963

F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence. //3.1e-43:277:89//AF046734

F-NT2RP2005555//HS_2188_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=C, genomic survey sequence. //8.0e-05:195:65//AQ086723

F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds. //2.5e-44:473:71//AF062529

F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence. //0.99:213:65//AC005016

F-NT2RP2005600//H.sapiens CpG island DNA genomic M 50

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sel fragment, clone 172d12, reverse read cp9172d12.rt1a. //0.32:134:63//Z57359

F-NT2RP2005605

F-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds. //9.8e-91:447:97//AF062085

F-NT2RP2005622

F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205. //8.6e-17:411:61//U10556

10 F-NT2RP2005637//NATI (NATI*10)=acetyltransferase 1 {3' region, polyadenylation polymorphism} [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt]. //0.22:156:65//S78829

F-NT2RP2005640//Mouse U6 RNA gene. //5.5e-19:249:76//X06980

F-NT2RP2005645//HS_2201_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence. //0.30:159:65//AQ066763

F-NT2RP2005651//H.sapiens DNA sequence. //0.00037:150:66//Z22493

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds. //4.7e-07:351:62//AB006626

F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds. //8.2e-98:472:98//AF064605

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds. //2.4e-94:462:98//AF089814

30 F-NT2RP2005683//HS-1024-B1-H05-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence. //0.99:156:64//B34405

F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds. //7.7e-10:328:61//M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC111-28 8K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //0.72:160:65//AC005183

F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds. //1.6e-124:599:97//AB018342

40 F-NT2RP2005719//R.norvegicus mRNA for metallothionein-III. //0.86:117:64//X89603

F-NT2RP2005722//Human zinc finger protein ZNF136. //2.6e-44:415:77//U09367

F-NT2RP2005723//Human BAC clone GS542D18 from 7q31-q32, complete sequence. //6.9e-15:153:81//AC002528

F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28unordered pieces. //5.1e-41:138:95//AC005627

F-NT2RP2005732//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT S

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EQUENCE. //0.61:303:60//Z93017
 F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS. //0.52:116:67//Y16270
 F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial. //0.11:136:66//X52342
 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds. //7.8e-22:134:96//AF068868
 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds. //1.2e-100:486:98//AF 10 082516
 F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds. //0.00073:425:56//D21853
 F-NT2RP2005767//G.gallus PBI gene. //2.1e-73:544:80//X90849
 F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds. //6.2e-15:153:82//M77836
 F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds. //1.2e-121:649:88//D11336
 F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds. //0.96:184:60//AB015853
 F-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE. //1.9e-63:222:96//AL034423
 F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds. //2.6e-07:232:64//AF010579
 F-NT2RP2005812
 F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease I. //0.031:358:59//X74103
 F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds. //2.5e-107:449:91//AB002086
 F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X. //5.1e-05:144:73//Z68873
 F-NT2RP2005853//RPC11-24D4.TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-24D4, genomic survey sequence. //6.4e-13:130:85//AQ013490
 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds. //1.7e-174:8 40 29:98//AF092564
 F-NT2RP2005859//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 914P20, WORKING DRAFT SEQUENCE. //0.25:174:62//AL034553
 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103I24aF4, genomic survey sequence. //7.8e-06:92:79//AL027276
 F-NT2RP2005886//HS_3187_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=C, genomic survey sequence

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e. //7.1e-95:494:95//AQ155885
 F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds. //2.7e-32:660:66//L11316
 F-NT2RP2005901//H.sapiens CpG island DNA genomic Msel fragment, clone 15b5, reverse read cpg15b5.rt1a. //0.0026:66:84//Z54729
 F-NT2RP2005908//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence. //6.4e-49:481:75//AC004241
 F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds. //6.6e-61:657:73//U63840
 F-NT2RP2005942//H.sapiens PAP mRNA. //1.6e-46:618:67//X76770
 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence. //1.0e-48:533:71//AC005207
 F-NT2RP2006023//HS_3048_A1_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence. //2.1e-25:167:91//AQ126553
 F-NT2RP2006038//CIT-HSP-384K4.TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence. //3.9e-06:102:74//B51912
 F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds. //1.9e-05:418:59//U19495
 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55. //0.0035:226:65//AF016861
 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5. //3.9e-11:121:85//D17047
 F-NT2RP2006071
 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence. //0.46:264:59//AF027207
 F-NT2RP2006100//Human Chromosome X, complete sequence. //3.2e-94:488:95//AC004073
 F-NT2RP2006103//HS_2254_A2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence. //5.7e-27:156:96//AQ129602
 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence. //1.2e-62:655:71//AC000378
 F-NT2RP2006141//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE. //1.2e-69:316:98//AL034405
 F-NT2RP2006166//Homo sapiens chromosome 4 clone B3218, complete sequence. //3.1e-45:387:81//AC004063
 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds. //0.99:111:73//U62587

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F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554
 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232
 F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-83:239:94//AC006057
 F-NT2RP2006219//H.sapiens mRNA for DCCR6 protein.//1.4e-116:618:93//X96484
 F-NT2RP2006237//CIT-HSP-2300P9.TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480
 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//7.6e-102:635:86//U49055
 F-NT2RP2006258//RPC11-9N9.TP RPC1-11 Homo sapiens genomic clone RPC1-11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//0.44:111:71//X97630
 F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262
 F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973
 F-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532
 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893
 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514
 F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590
 F-NT2RP2006393//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL022727
 F-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808
 F-NT2RP2006441

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F-NT2RP2006454//Sequence 8 from Patent W09517522.//2.9e-06:180:66//A45338
 F-NT2RP2006456
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266
 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding ch1-ch4 and secretion domains, partial cds.//0.061:201:66//U50149
 F-NT2RP2006472
 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//8.8e-10:273:66//Z93929
 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966
 F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503:63//M20855
 F-NT2RP2006573//Mollusca contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315
 F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537
 F-NT2RP3000002//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972
 F-NT2RP3000046//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320
 F-NT2RP3000047
 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HFP1, -2, and -9.//1.0e-67:626:74//M27877
 F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227
 F-NT2RP3000068
 F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746
 F-NT2RP3000080//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391
 F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536
 F-NT2RP3000092//RPC11-22M5.TV RPC1-11 Homo sapien

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s genomic clone RPCI-11-22M5, genomic survey sequence. //3.3e-27:157:97//B84237
 F-NT2RP3000109//Arabidopsis thaliana l-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds. //0.92:185:64//L29260
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence. //1.2e-112:286:89//AC005189
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds. //9.0e-181:849:98//AB011164
 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.264_B_14, complete sequence. //4.2e-24:155:94//AC005884
 F-NT2RP3000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE. //7.2e-43:269:81//AL023583
 F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9. //0.098:405:57//L39063
 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 DS00164 (D269)), complete sequence. //0.96:608:55//AC004716
 F-NT2RP3000220
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds. //2.0e-18:509:58//AF059569
 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-D2, complete sequence. //3.5e-05:224:65//AC004101
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds. //2.1e-109:691:86//D86972
 F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence. //0.20:119:68//Z70213
 F-NT2RP3000252//Homo sapiens cosmid 1F1, complete sequence. //9.8e-78:174:88//AF065393
 F-NT2RP3000255
 F-NT2RP3000267
 F-NT2RP3000299//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds. //5.9e-48:374:82//U48853
 F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds. //4.9e-22:583:63//J02932
 F-NT2RP3000320//RPCI11-36J1.TP RPCI-11 Homo sapiens genomic clone RPCI-11-36J1, genomic survey sequence. //4.4e-06:87:88//AQ047107
 F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds. //5.5e-26:283:79//U78090
 F-NT2RP3000333//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 973M2, WORKING DRAFT SEQUENCE. //1.0:309:60//AL033533

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F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence. //6.7e-42:465:74//Z97181
 F-NT2RP3000348
 F-NT2RP3000350//Homo sapiens cosmid 1F1, complete sequence. //3.4e-79:174:88//AF065393
 F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds. //2.2e-127:816:85//M25757
 F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds. //0.0075:288:58//D83743
 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds. //7.1e-134:693:94//L04966
 F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor. //0.049:308:60//AJ011318
 F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c. //0.00012:441:58//Z72642
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds. //5.0e-174:841:97//AF071185
 F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053_B_8, complete sequence. //7.9e-53:817:68//AC006083
 F-NT2RP3000433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE. //6.1e-31:590:63//AL031681
 F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence. //4.0e-19:169:81//AL026471
 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1Hs-gamma pseudogene, STS and CpG island. //2.4e-41:459:65//Z84488
 F-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE. //1.1e-100:365:87//AL031650
 F-NT2RP3000451//HS_2024_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=I, genomic survey sequence. //0.011:367:57//AQ229420
 F-NT2RP3000456//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence. //1.5e-89:458:96//AQ055548
 F-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE. //0.043:147:70//Z97353
 F-NT2RP3000487//H.sapiens CpG island DNA genomic M

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sel fragment, clone 11b11, forward read cpg11b11.f tla.//1.7e-11:96:92//Z64440
 F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667
 F-NT2RP3000526//Homo sapiens full length insert cDNA clone YZ38E04.//4.1e-30:283:76//AF086071
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966
 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260
 F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//0.00019:361:60//AC002554
 F-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//9.0e-171:827:98//AC006012
 F-NT2RP3000562
 F-NT2RP3000578//F.rubripes GSS sequence, clone 013 G07cE7, genomic surveysequence.//1.7e-25:284:74//AL011271
 F-NT2RP3000582//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597
 F-NT2RP3000584
 F-NT2RP3000590//H.sapiens CpG island DNA genomic M sel fragment, clone 170d7, forward read cpg170d7.f tla.//3.0e-22:128:100//Z59723
 F-NT2RP3000592//CIT-HSP-2288J7.TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868
 F-NT2RP3000596//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305
 F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043
 F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320
 F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128
 F-NT2RP3000622//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104
 F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890
 F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome Xq21.Contains Eukaryotic Translat

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ion Initiation Factor EIF3 P35 Subunit and60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313
 F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363
 F-NT2RP3000644//Homo sapiens clone RC315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089
 F-NT2RP3000661
 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237
 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961
 F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872
 F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930
 F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65(GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264
 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, completecds.//4.7e-37:429:70//U16655
 F-NT2RP3000753
 F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281
 F-NT2RP3000815//HS_2237_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic surveysequence.//0.79:151:61//AQ067252
 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
 F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.025:291:62//U02513
 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, completecds, clone 9C4.//0.69:563:57//M29009
 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:66

6: 68//Z86062

F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581

F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938

F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082

F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome1q24. Contains the LNHR (SEL L) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-ME L, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectinprecursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940

F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831

F-NT2RP3000865

F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367

F-NT2RP3000875//HS_2236_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic surveysequence.//0.98:153:68//AQ154007

F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL27) gene, complete cds.//0.44:213:65//AF021340

F-NT2RP3000904//Rat Na⁺ channel mRNA, 3' end.//3.6e-106:505:99//M27223

F-NT2RP3000917//Mouse mRNA for Dhml protein, complete cds.//3.1e-132:691:93//D38517

F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264

F-NT2RP3000968//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326

F-NT2RP3000980//R.norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335

F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Ge 50

omic Sperm Library CHomo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529

F-NT2RP3001004//H.sapiens CpG island DNA genomic Msel fragment, clone 39c1, reverse read cpg39c1.rtl a.//5.9e-27:150:99//Z60925

F-NT2RP3001007//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3unordered pieces.//0.11:610:57//AC006039

F-NT2RP3001055//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653

F-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927

F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219

F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325

F-NT2RP3001096//CIT-HSP-2305P8.TF CIT-HSP Homo sapiens genomic clone 2305P8, genomic survey sequence.//3.4e-37:222:93//AQ021278

F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969

F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ457j11 containingDNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317

F-NT2RP3001111

30 F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871

F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.9e-170:821:98//AC005189

F-NT2RP3001116//HS_3075_A1_F01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581

40 F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-121:598:97//AL031864

F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367

F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078

F-NT2RP3001133//Nephila clavipes minor ampullate s

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ilk protein MlSpl mRNA, partial cds.//0.00021:529:60//AF027735

F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305

F-NT2RP3001147//RPCI11-3M16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859

F-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379

F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:891:98//AJ006266

F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-69:207:97//AL034351

F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507

F-NT2RP3001216//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845

F-NT2RP3001221

F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619

F-NT2RP3001236

F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X51396

F-NT2RP3001245//CITBI-E1-2505C1.TF.1 CITBI-E1 Homo sapiens genomic clone 2505C1, genomic survey sequence.//8.5e-70:337:100//AQ242007

F-NT2RP3001253//CITBI-E1-2505N14.TR CITBI-E1 Homo sapiens genomic clone 2505N14, genomic survey sequence.//0.83:235:60//AQ260430

F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete cds.//3.8e-47:761:64//AB018269

F-NT2RP3001268//Homo sapiens zinc finger protein (HZF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513

F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101

F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561

F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318_A.15, complete sequence.//5.9e-39:304:70//AC005837

F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457

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F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465

F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00022:624:60//AC004709

F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790

F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966

F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935

F-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105

F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052

F-NT2RP3001356

F-NT2RP3001374

F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.00082:365:61//AL008628

F-NT2RP3001384//Homo sapiens HRIHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332

F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198

F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296

F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046

F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//5.4e-20:245:73//AC005521

F-NT2RP3001407//RPCI11-41A20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031

F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327

F-NT2RP3001426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447

F-NT2RP3001427//CIT-HSP-2302H24.TF CIT-HSP Homo sapiens genomic clone 2302H24, genomic survey sequence.//8.1e-36:212:94//AQ020997

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F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr)mRNA, complete cds.//8.5e-73:431:91//U69668

F-NT2RP3001432//HS_3032_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619

F-NT2RP3001447

F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282

F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065

F-NT2RP3001457

F-NT2RP3001459

F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836

F-NT2RP3001490

F-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//1.0e-26:191:90//U13395

F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//8.5e-171:804:98//AF064801

F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds.//8.9e-140:743:91//U36499

F-NT2RP3001529//Streptomyces griseus DNA for ribosome protein L21, ribosomal protein L27, Obg, complete cds.//2.1e-14:517:59//D87916

F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence.//4.7e-05:217:63//AF078176

F-NT2RP3001554//Rattus norvegicus microtubule-associated

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protein 1A MAP1A (Mtap-1) mRNA, complete cds.//4.3e-17:332:67//M83196

F-NT2RP3001580//RPCI11-91E19.TV RPCI11 Homo sapiens genomic clone R-91E19, genomic survey sequence.//4.2e-15:110:91//AQ281332

F-NT2RP3001587//S.pombe chromosome II cosmid c16H5.//6.6e-28:491:64//AL022104

F-NT2RP3001589//RPCI11-68M15.TK RPCI11 Homo sapiens genomic clone R-68M15, genomic survey sequence.//8.7e-108:517:98//AQ237629

F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//1.0e-09:257:65//AC004674

F-NT2RP3001608//Methylococcus capsulatus methanomonooxygenase component A alpha chain, methanomonooxygenase A beta chain and methanomonooxygenase component C genes, complete cds.//0.59:450:57//M90050

F-NT2RP3001621//Human DNA sequence from clone 24ol8 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VN0-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.8e-42:278:79//AL021808

F-NT2RP3001629

F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein.//1.5e-63:276:97//AJ130978

F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence.//0.018:127:66//Z68117

30 F-NT2RP3001646

F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.4e-171:816:98//AJ012449

F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds.//1.6e-38:542:66//U49793

F-NT2RP3001676//HS_3090_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence.//3.1e-07:333:64//AQ123250

40 F-NT2RP3001678//Drosophila melanogaster; Chromosome 3L; Region 63C5-63D3; P1 clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0:539:57//AC004358

F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.8e-130:355:96//AB020860

F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds.//2.1e-37:512:70//AF059273

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F-NT2RP3001690//CIT-HSP-2300P9. TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence. //2.8e-19:123:95//AQ012480
 F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds. //9.4e-11:167:74//D31962
 F-NT2RP3001708//H.sapiens CpG island DNA genomic Msel fragment, clone 4g7, reverse read cpg4g7.rt1d. //1.3e-17:113:97//Z61312
 F-NT2RP3001712//M.musculus mRNA for HP1-BP74 protein. //2.2e-95:601:88//X99642
 F-NT2RP3001716
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds. //1.4e-159:565:97//AF054177
 F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2)mRNA, partial cds. //1.7e-132:786:88//AF008554
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds. //3.9e-104:811:78//D50918
 F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PA C Clone p201m18 In DCCR Region, complete sequence. //6.5e-07:178:69//AC000097
 F-NT2RP3001752//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence. //5.2e-31:311:77//AL031311
 F-NT2RP3001753//Sequence 29 from patent US 5658882. //0.11:513:58//I62381
 F-NT2RP3001764//Sequence 6 from Patent W09706245. //6.4e-47:673:66//A59888
 F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10. //0.078:290:63//U39644
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds. //2.8e-151:710:98//AB007928
 F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds. //1.2e-26:213:85//U13262
 F-NT2RP3001799//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE. //8.4e-51:168:95//AL031284
 F-NT2RP3001819//S. glaucus genes strU, strX, st

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rV and strW for 5'-hydroxystreptomycin production and transport polypeptide s. //0.084:526:58//X89010
 F-NT2RP3001844//HS_3110_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row =J, genomic survey sequence. //1.5e-40:232:82//AQ140433
 F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.14:452:58//AC005505
 F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknox1) mRNA, complete cds. //2.7e-39:575:67//AF061270
 F-NT2RP3001857//M. musculus tex292 mRNA (5' region). //8.7e-07:106:81//X80434
 F-NT2RP3001896
 F-NT2RP3001898//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE. //0.094:456:60//AL008733
 F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence. //0.58:482:56//Z73969
 F-NT2RP3001926//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE. //0.42:401:58//AL034557
 F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence. //3.1e-28:263:77//AC004651
 F-NT2RP3001931
 F-NT2RP3001938//CIT-HSP-2165E8. TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence. //3.6e-24:182:91//B95475

- F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds.//1.8e-165:815:96//AB014575
- F-NT2RP3001944
- F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//4.8e-62:304:89//AC005844
- F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9(cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//8.2e-10:564:60//AF030694
- F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//2.5e-57:361:80//Z83822
- F-NT2RP3002004//Sequence 3 from patent US 5798245.//1.6e-26:104:100//AR025386
- F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.0053:633:58//AC004137
- F-NT2RP3002014//Drosophila melanogaster DNA sequence (P1s DS07528 (D169)and DS06665 (D220)), complete sequence.//1.3e-32:334:68//AC004640
- F-NT2RP3002033//H. sapiens DNA sequence.//0.012:214:63//Z22493
- F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin.//8.7e-116:713:86//X53773
- F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162.//1.6e-12:613:60//AL021841
- F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X.//0.17:566:59//Z77249
- F-NT2RP3002057//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//3.3e-24:167:82//AC005682
- F-NT2RP3002062
- F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//0.24:508:58//AJ235272
- F-NT2RP3002081//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence.//9.7e-22:155:90//AQ218494
- F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence.//9.6e-66:562:77//AC006210
- F-NT2RP3002102//CIT-HSP-2307B10. TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence.//5.9e-16:214:74//AQ018040
- F-NT2RP3002108
- F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.6e-29:414:68//AC004020
- F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds.//0.96:434:60//AF003370
- 10 F-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE.//1.3e-63:380:91//AL031710
- F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence.//9.9e-60:315:80//U95742
- F-NT2RP3002163
- F-NT2RP3002165//M. musculus HCNGP mRNA.//1.4e-142:867:87//X68061
- F-NT2RP3002166//Homo sapiens chromosome X, clone h CIT.200_L_4, complete sequence.//0.090:394:59//AC006121
- 20 F-NT2RP3002173//HS_3062_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence.//3.3e-101:509:96//AQ193219
- F-NT2RP3002181//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VN0-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//4.5e-106:432:84//AL021808
- F-NT2RP3002244//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.63:353:60//AC005321
- F-NT2RP3002248//HS_3029_A1_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence.//3.5e-10:125:79//AQ094880
- F-NT2RP3002255//Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.//5.6e-09:629:59//L14321
- F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//4.9e-35:366:74//B03004
- F-NT2RP3002276//B. taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex.//0.023:326:60//X64898
- F-NT2RP3002303//Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.//3.8e-12:643:57//AE000810
- 50

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F-NT2RP3002304//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.6e-09:490:60//AC005504

F-NT2RP3002330//Human DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches.//1.9e-93:572:88//Z49862
F-NT2RP3002343//HS_3010_A2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence.//9.0e-75:373:97//AQ119068

F-NT2RP3002351//Human mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15).//4.9e-64:588:75//X16396

F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form.//1.3e-164:770:98//Y16355

F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds.//1.4e-190:911:98//AB018331

F-NT2RP3002399

F-NT2RP3002402//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//7.2e-25:249:79//D89340

F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds.//1.2e-138:649:99//AB014578

F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP Homo sapiens genomic clone 367N3, genomic survey sequence.//5.0e-18:115:96//B78927

F-NT2RP3002501//Caenorhabditis elegans cosmid K01C8, complete sequence.//0.00020:170:65//Z49068

F-NT2RP3002512//Homo sapiens clone 664 unknown mRNA A, partial sequence.//1.6e-59:308:97//AF091088

F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds.//1.4e-144:763:93//U35246

F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.8e-178:833:98//AB018272

F-NT2RP3002549//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-26:123:72//AC004821

F-NT2RP3002566//Streptomyces viridifaciens sigma factor (hrdD) gene, complete cds.//0.76:459:59//U60418

F-NT2RP3002587//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//4.6e-13:199:76//AC004617

F-NT2RP3002590//Porphyra purpurea chloroplast, complete genome.//0.88:284:60//U38804

F-NT2RP3002602//CIT978SK-A-441H11-2.TPB CIT978SK Homo sapiens genomic clone A-441H11, genomic survey

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sequence.//2.0e-22:140:95//B68331

F-NT2RP3002603

F-NT2RP3002628//C. acetobutylicum dnaJ and orfB genes.//2.0e-05:333:60//X69050

F-NT2RP3002631

F-NT2RP3002650//Mus musculus mRNA for cartilage-associated protein (CASP).//1.5e-20:641:62//AJ006469

F-NT2RP3002659//Bovine herpesvirus type 1 UL22-35 genes.//5.2e-05:621:59//Z78205

10 F-NT2RP3002660//Homo sapiens PAC clone DJ1006K12 from 7q31.2-q31, complete sequence.//0.98:453:57//AC004946

F-NT2RP3002663//Homo sapiens chromosome 19, cosmid F6697, complete sequence.//3.3e-22:407:67//AC006129

F-NT2RP3002671//S.pombe chromosome III cosmid c553.//1.0e-12:336:66//AL023704

F-NT2RP3002682//Caenorhabditis elegans cosmid F17C11, complete sequence.//1.3e-21:448:64//Z72507

20 F-NT2RP3002687//CIT978SK-A-789B1.TP CIT978SK Homo sapiens genomic clone A-789B1, genomic survey sequence.//2.5e-25:173:91//B51656

F-NT2RP3002688//Mouse mRNA for kinesin-like protein (Kif1b), complete cds.//1.2e-73:728:74//D17577

F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 Homo sapiens genomic clone 2507L14, genomic survey sequence.//0.0012:55:92//AQ263530

F-NT2RP3002713

F-NT2RP3002763//Caenorhabditis elegans cosmid T20F10, complete sequence.//0.98:209:63//Z81594

F-NT2RP3002770

F-NT2RP3002785//Homo sapiens laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds.//0.78:515:57//AF029325

F-NT2RP3002799//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//1.9e-21:167:79//AL022718F-NT2RP3002810//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//0.32:187:66//AC005549

40 F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds.//6.9e-54:615:70//AF004715

F-NT2RP3002861//Caenorhabditis elegans cosmid M03F4.//4.2e-05:226:65//U64601

F-NT2RP3002869//Mus musculus semaphorin VIa mRNA, complete cds.//2.0e-93:638:83//AF030430

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F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds.//8.5e-89:557:88//AB001895
 F-NT2RP3002877//Homo sapiens chromosome 12p13.3 clone RPC11-433J6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//7.9e-12:160:78//AC006087
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//5.7e-180:853:98//AB018314
 F-NT2RP3002911//RPC11-24N15.TPC RPC1-11 Homo sapiens genomic clone RPC1-11-24N15, genomic survey sequence.//2.3e-13:442:61//B88815
 F-NT2RP3002948//, complete sequence.//2.2e-110:637:91//AC005500
 F-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.7e-166:793:98//AC005754
 F-NT2RP3002955//Human HepG2 partial cDNA, clone hmd3c02m5.//0.00011:61:95//D17024
 F-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.2e-128:808:85//D30666
 F-NT2RP3002972//H.sapiens (xs168) mRNA, 381bp.//1.5e-43:312:85//Z36820
 F-NT2RP3002978//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00044:527:57//AC005505
 F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence.//0.92:341:60//AC001644
 F-NT2RP3002988//HS_3015_A1_B07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence.//4.4e-05:379:58//AQ091708
 F-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes.//1.4e-72:197:79//AF109905
 F-NT2RP3003032//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-80, complete sequence.//1.6e-08:809:58//AL010153
 F-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//4.1e-111:804:81//U78090
 F-NT2RP3003061//Human mRNA for ankyrin (variant 2.1).//1.4e-12:633:59//X16609
 F-NT2RP3003068//Human BAC clone RG264L19 from 7p15-p21, complete sequence.//0.034:282:60//AC002410
 F-NT2RP3003071//H.sapiens CpG island DNA genomic Msel fragment, clone 13d12, reverse read cpg13d12.rtlc.//6.8e-15:95:100//Z64565
 F-NT2RP3003078

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F-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//8.1e-72:732:71//D88315
 F-NT2RP3003121
 F-NT2RP3003133//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.5e-12:168:76//AC004510
 F-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//4.0e-148:908:87//D12646
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639
 F-NT2RP3003150
 F-NT2RP3003157//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds.//8.6e-06:228:65//AF064868
 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933
 F-NT2RP3003197
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//4.1e-48:640:67//AF015264
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059
 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//6.3e-75:776:74//U20286
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064
 F-NT2RP3003242//Homo sapiens stannocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460
 F-NT2RP3003251//H.sapiens Staf50 mRNA.//3.5e-67:651:76//X82200
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153
 F-NT2RP3003278//H.sapiens CpG island DNA genomic Msel fragment, clone 28b4, forward read cpg28b4.ft1a.//4.0e-27:174:93//Z60555
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983

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F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:71//AF004162
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//D85610
 F-NT2RP3003302//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.6e-95:680:82//AC006213
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527
 F-NT2RP3003313//Streptomyces coelicolor cosmid 5A7.//0.0084:403:61//AL031107
 F-NT2RP3003327//H. sapiens Staf50 mRNA.//2.5e-29:253:67//X82200
 F-NT2RP3003330
 F-NT2RP3003344
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//9.0e-41:296:84//AC005284
 F-NT2RP3003353//Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069
 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360
 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874
 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:63//U90653
 F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317
 F-NT2RP3003427//HS-1051-A1-D03-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173
 F-NT2RP3003433//HS_2219_B2_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828

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F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268
 F-NT2RP3003491//CIT-HSP-234401.TR CIT-HSP Homo sapiens genomic clone 234401, genomic survey sequence.//1.2e-39:213:97//AQ057124
 F-NT2RP3003500//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347
 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (LANL), complete sequence.//0.95:279:60//AC004234
 F-NT2RP3003552//Homo sapiens clone UWGC:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049
 F-NT2RP3003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985
 F-NT2RP3003564//HS_3141_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798
 F-NT2RP3003572
 F-NT2RP3003576//Homo sapiens clone RC031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632
 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387
 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.//6.0e-88:463:84//AC004235
 F-NT2RP3003625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600
 F-NT2RP3003656
 F-NT2RP3003659//F. rubripes GSS sequence, clone 013 G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096
 F-NT2RP3003672
 F-NT2RP3003680//Drosophila melanogaster; Chromosome 2R; Region 39B1-39B3; P1 clone DS05527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811
 F-NT2RP3003686//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993

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F-NT2RP3003701

F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.6e-10 7:788:82//U42975

F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300

F-NT2RP3003746//CIT-HSP-2306A10.TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785

F-NT2RP3003795//Human DNA sequence from clone 333H 23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGRIA, SYBGRIB, SYNGRIC), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D22S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326

F-NT2RP3003799//Homo sapiens DNA from chromosome 1 9-cosmids R31158, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458

F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031

F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321

F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801

F-NT2RP3003819

F-NT2RP3003825

F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626

F-NT2RP3003831//RPCI11-50N15.TJ RPCI11 Homo sapiens genomic clone R-50N15, genomic survey sequence.//1.1e-21:174:85//AQ082633

F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611

F-NT2RP3003842//RPCI11-44E5.TJ RPCI11 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884

F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268

F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343

F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181

F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554

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F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)mRNA, complete cds.//2.6e-47:404:77//AF057358

F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504
F-NT2RP3003989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661

F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNGC2) mRNA, complete cds.//0.021:433:58//U58837

F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4e-164:838:94//X84692

F-NT2RP3004016//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726

F-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400

F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317

F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939

30 F-NT2RP3004078//M.musculus (BALB/c) MRFX2 mRNA.//1.9e-102:684:83//X76089

F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433

F-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038

F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973

F-NT2RP3004125//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560

F-NT2RP3004145

F-NT2RP3004148

F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900

F-NT2RP3004189//M.musculus tex292 mRNA (5' region).//1.1e-06:102:82//X80434

50 F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:

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715:71//X58374
 F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009
 F-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//8.4e-55:184:84//D42052
 F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//0.22:458:60//AC006084
 F-NT2RP3004242//Caenorhabditis elegans cosmid ZK63 2, complete sequence.//1.6e-29:409:69//Z22181
 F-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385
 F-NT2RP3004253//H. sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353
 F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-88:489:91//AF013967
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871
 F-NT2RP3004332
 F-NT2RP3004334//L. esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908
 F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020
 F-NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
 F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
 F-NT2RP3004378//Drosophila melanogaster; Chromosome 2R; Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
 F-NT2RP3004399//H. sapiens mRNA for leucine-rich primary response protein1.//7.2e-140:804:90//X97249
 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
 F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
 F-NT2RP3004451//RPCI11-51J15.TK RPCI11 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917

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F-NT2RP3004466//HS_3038_B2_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
 F-NT2RP3004470//H. sapiens CpG island DNA genomic Msel fragment, clone 81a11, reverse read cpg81a11.rta.//7.0e-25:148:96//Z56029
 F-NT2RP3004472//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023
 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673
 F-NT2RP3004504//M. musculus mRNA for CPEB protein.//2.0e-110:618:91//Y08260
 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.3e-46:433:76//AC005328
 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Emzf1) mRNA, complete cds.//6.9e-18:433:64//AF031955
 F-NT2RP3004569//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds.//1.0e-179:860:97//AF026445
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered pieces.//9.3e-14:36

O:65//AC004977

F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355

F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350

F-NT2RP3004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882

F-NT2RP4000008//Homo sapiens chromosome X, clone h CIT.200_L_4, complete sequence.//1.5e-155:844:92//AC006121

F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.//0.012:417:59//AB012242

F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//AC005035

F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA A, complete cds.//2.1e-81:556:85//AF029761

F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469

F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449

F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558

F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//4.4e-166:774:99//AB011538

F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931

F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952

F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776

F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681

F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA A, partial sequence.//2.2e-62:360:92//AF091088

F-NT2RP4000159//RPCI11-75N16.TJ RPCI11 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551

F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210

F-NT2RP4000185//Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989

F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 pro

tein, partial cds.//4.9e-174:825:98//AB014600

F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300

F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HS P-444n24, complete sequence.//1.8e-161:751:99//AC005261

F-NT2RP4000218//RPCI11-69B7.TJ RPCI11 Homo sapiens genomic clone R-69B7, genomic survey sequence.//1.7e-84:413:98//AQ268504

10 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470

F-NT2RP4000246//Mus musculus neural variant mena++ + protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523

F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA A, complete sequence.//2.8e-128:604:99//AF091092

F-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.27:124:69//AQ043515

F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408

F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481

F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322

F-NT2RP4000323

F-NT2RP4000355

30 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195

F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4.//2.0e-23:524:62//AJ235272

F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//I30536

40 F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//4.3e-05:450:58//D63850

F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//9.2e-37:336:69//AC006116

F-NT2RP4000415//Caenorhabditis elegans cosmid C42D8.//0.30:222:60//U56966

F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086

50 F-NT2RP4000424//Homo sapiens chromosome 17, clone

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HRPC41C23, complete sequence.//1.6e-42:265:81//ACO03101
 F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194
 F-NT2RP4000449//CIT-HSP-2366N18.TR CIT-HSP Homo sapiens genomic clone 2366N18, genomic survey sequence.//2.4e-42:236:95//AQ076183
 F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982
 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.0034:532:57//Z72499
 F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//U10483
 F-NT2RP4000481
 F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125
 F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904
 F-NT2RP4000515
 F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//1.6e-179:851:98//AC006238
 F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840
 F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720
 F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498
 F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386
 F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 DS02109 (D53)), complete sequence.//1.3e-05:498:58//AC002443
 F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465
 F-NT2RP4000560//Murine genomic DNA; partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580
 F-NT2RP4000588//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 414D7, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730
 F-NT2RP4000638//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl

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one Plate=3042 Col=10 Row=H, genomic survey sequence.//3.0e-06:78:89//AQ099333
 F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335
 F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904
 10 F-NT2RP4000704//Homo sapiens mRNA expressed in 19 week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852
 F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149
 F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178
 F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//1.0:504:58//L19301
 20 F-NT2RP4000739//CIT-HSP-2010022.TR CIT-HSP Homo sapiens genomic clone 2010022, genomic survey sequence.//1.1e-24:161:93//B57903
 F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917
 F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818
 30 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189
 F-NT2RP4000837//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420
 F-NT2RP4000839//RPCI11-6D8.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6D8, genomic survey sequence.//1.5e-44:281:91//B48216
 F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515
 F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367
 F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616
 F-NT2RP4000879//N.tabaccum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804
 50 F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich

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-repeat protein, complete cds.//6.8e-153:934:86//D45913
 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901
 F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 DS04106 (D172)), complete sequence.//2.0e-08:609:58//AC004290
 F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975
 F-NT2RP4000927//H. sapiens genomic DNA (chromosome 3; clone NRL062R).//0.75:175:62//X87547
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532
 F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004688
 F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519
 F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657
 F-NT2RP4000975//CIT-HSP-230716.TF CIT-HSP Homo sapiens genomic clone 230716, genomic survey sequence.//6.5e-31:317:79//AQ015742
 F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//M22942
 F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823
 F-NT2RP4000989//F. rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911
 F-NT2RP4000996//Panaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358
 F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424
 F-NT2RP4001004
 F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176
 F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140
 F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086
 F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170

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F-NT2RP4001057
 F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469
 F-NT2RP4001078//Streptomyces coelicolor cosmid 1C2.//0.0025:474:59//AL031124
 F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018
 F-NT2RP4001080//H. sapiens PTB-4 gene for polypyrimidine tract binding protein.//9.0e-64:628:70//X65372
 F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164
 F-NT2RP4001095
 F-NT2RP4001100//CITBI-E1-2503J7. TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402
 F-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//1.0e-143:760:87//M96629
 F-NT2RP4001122
 F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668
 F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969
 F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//AR008079
 F-NT2RP4001148//Homo sapiens clone RC332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095
 F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067
 F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952
 F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476
 F-NT2RP4001174//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494
 F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds.//0.032:453:58//U82511
 F-NT2RP4001207//HS_2248_A1_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358
 F-NT2RP4001210//Homo sapiens chromosome 10 clone CIT987SK-1019018 map 10p11.2-10p12.1, complete sequ

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ence. //0.93:515:58//AC005877
 F-NT2RP4001213//Human KRAB zinc finger protein (ZN F177) mRNA, splicing variant, complete cds. //3.6e-44:187:74//U37251
 F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H 9C, complete sequence. //1.3e-15:288:67//AL032657
 F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds. //2.2e-26:855:60//AF059569
 F-NT2RP4001235//RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence. //2.7e-15:101:98//B88081
 F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds. //1.0:459:59//U33061
 F-NT2RP4001260//Sequence 2 from Patent W09601901. //0.0018:246:63//A48324
 F-NT2RP4001274//Homo sapiens, complete sequence. //2.5e-05:201:67//AC005854
 F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence. //3.5e-18:138:92//AQ040728
 F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds. //7.4e-30:535:65//AF043250
 F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5. //3.5e-145:795:91//AJ001119
 F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence. //8.4e-16:109:94//B89870
 F-NT2RP4001339//HS_3205_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence. //7.1e-24:305:73//AQ183725
 F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence. //1.9e-17:106:91//AC004918
 F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase. //7.6e-40:631:66//X91011
 F-NT2RP4001351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE. //2.7e-30:608:64//AL031428
 F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7. //0.23:540:57//AL031107
 F-NT2RP4001372//RPCI11-49L11.TJ RPCI11-Homo sapiens genomic clone R-49L11, genomic survey sequence. //8.5e-23:129:100//AQ051701
 F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1. //0.15:213:61//X78609

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F-NT2RP4001375
 F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311_F_12, complete sequence. //7.3e-28:153:88//AC005722
 F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. //7.2e-47:518:73//AC004691
 F-NT2RP4001407//P.falciparum glutamic acid-rich protein gnen, complete cds. //0.00079:686:57//J03998
 F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds. //2.0e-76:818:71//D86957
 F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein. //3.5e-87:839:73//X78933
 F-NT2RP4001442
 F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds. //0.21:218:63//AB018326
 F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence. //7.6e-14:109:90//U49884
 F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds. //2.5e-59:480:75//D10523
 F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds. //9.7e-39:392:72//AF049612
 F-NT2RP4001502//H.sapiens (D8S135) DNA segment containing GT repeat. //2.7e-24:147:96//X61693
 F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds. //0.87:583:58//M32513
 F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.93:394:58//AC005308
 F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds. //3.1e-143:820:89//U20086
 F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR048w. //2.2e-05:319:61//Z71663
 F-NT2RP4001551//S.pombe chromosome II pl p8B7. //0.64:335:60//AL032684
 F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPCI11-36 OE11 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //1.0:309:58//AC004806
 F-NT2RP4001567//HS_2166_B1_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence. //0.99:188:59//AQ086290
 F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds. //7.0e-53:566:72//D79989
 F-NT2RP4001571//RPCI11-21F20.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F20, genomic survey sequence. //2.8e-19:119:97//B85885

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F-NT2RP4001574//*B. primigenius* mRNA for coat protein gamma-cop. //5.8e-129:813:85//X92987
 F-NT2RP4001575//*Rattus norvegicus* mRNA for ARE1 protein. //3.4e-131:795:86//AJ223830
 F-NT2RP4001592//*S. aureus* gene for isoleucyl-tRNA synthetase. //1.3e-14:663:59//X74219
 F-NT2RP4001610//*Homo sapiens* Xp22 Cosmids U15E4, U115H5, U132E12, U115B9(Lawrence Livermore human cosmid library) complete sequence. //6.4e-10:135:73//AC002364
 F-NT2RP4001614//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence. //3.4e-06:78:89//AQ099333
 F-NT2RP4001634
 F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid *Homo sapiens* genomic clone cSRL-161F1, genomic survey sequence. //4.9e-12:144:76//B02870
 F-NT2RP4001644//*M. musculus* mRNA for map kinase interacting kinase, Mnk2. //3.8e-69:437:86//Y11092
 F-NT2RP4001656//HS_2013_A1_D01_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence. //2.0e-30:207:89//AQ224793
 F-NT2RP4001677//*Hylobates lar* huntingtin gene, partial exon. //0.23:105:71//L49362
 F-NT2RP4001679//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462023, WORKING DRAFT SEQUENCE. //2.7e-45:351:84//AL031431
 F-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence. //1.8e-30:163:88//U96629
 F-NT2RP4001725//*Drosophila melanogaster* DNA sequence (P1 DS08860 (D181)), complete sequence. //1.1e-13:402:63//AC004296
 F-NT2RP4001730//RPC111-37M21.TK RPC1-11 *Homo sapiens* genomic clone RPC1-11-37M21, genomic survey sequence. //0.88:177:67//AQ029840
 F-NT2RP4001739
 F-NT2RP4001753//*H. sapiens* telomeric DNA sequence, clone 12QTEL023, read12QTEL00023.seq. //4.9e-36:192:98//Z96232
 F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds. //2.3e-140:866:86//L11316
 F-NT2RP4001790//*Homo sapiens* clone NH0569124, complete sequence. //1.4e-29:327:74//AC005678
 F-NT2RP4001803
 F-NT2RP4001822//*Homo sapiens* tetraspan TM4SF (TSPAN-4) mRNA, complete cds. //1.0e-16:576:60//AF054841
 F-NT2RP4001823//Human DNA sequence from clone 181C

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9 on chromosome 22q13.2-13.33. Contains a PHAPI2 Leucine Rich Acidic Nuclear Protein pseudogene, part of a putative novel gene, ESTs, STSs and GSSs, complete sequence. //2.1e-08:601:59//Z98743
 F-NT2RP4001828
 F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds. //2.2e-53:555:73//D31888
 F-NT2RP4001841
 F-NT2RP4001849//*Homo sapiens* mRNA for KIAA0672 protein, complete cds. //1.7e-55:813:65//AB014572
 F-NT2RP4001861//Human simple repeat polymorphism. //0.0014:145:66//M87691
 F-NT2RP4001889//HS_2052_B1_H06_T7 CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence. //1.0e-23:187:86//AQ270425
 F-NT2RP4001893//*Homo sapiens* BAC clone GS166A23 from 7p21, complete sequence. //7.3e-76:178:95//AC005014
 F-NT2RP4001896//T3B4TFC TAMU *Arabidopsis thaliana* genomic clone T3B4, genomic survey sequence. //0.99:354:61//B26193
 F-NT2RP4001901//*Streptomyces griseus* genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds. //0.031:409:60//AB011413
 F-NT2RP4001927//HS_2216_B1_D03_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=2216 Col=5 Row=H, genomic survey sequence. //4.9e-32:216:89//AQ184677
 F-NT2RP4001938//*Mus musculus* zinc finger protein (Zfp64) mRNA, complete cds. //1.2e-83:709:79//U49046
 F-NT2RP4001946//HS_3021_B2_H10_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence. //7.6e-09:120:76//AQ133185
 F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //2.1e-18:421:65//AL022577
 F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP *Homo sapiens* genomic clone 2294D14, genomic survey sequence. //0.030:358:61//AQ005028
 F-NT2RP4001966//*Mus musculus* DOC4 (Doc4) mRNA, complete cds. //2.5e-68:812:68//AF059485
 F-NT2RP4001975//*Homo sapiens* chromosome 17, clone hCIT.91_J_4, complete sequence. //1.9e-57:555:75//AC

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F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950

F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 8003.//1.6e-29:520:64//U17243

F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-T7 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

F-NT2RP4002078//RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//F.rubripes GSS sequence, clone 190022bB9, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//M.musculus tex27 mRNA.//8.2e-77:456:89//X80437

F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LET-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901

F-NT2RP5003477//Human Chromosome 3 pac pDJ70111, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365

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F-NT2RP5003506//H.sapiens CpG island DNA genomic Msel fragment, clone 71h2, reverse read cpg71h2.rtl a.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236

F-NT2RP5003524//Homo sapiens beta-spectrin (BSP1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H.sapiens CpG island DNA genomic Msel fragment, clone 14c10, forward read cpg14c10.ft1b.//0.00013:70:91//Z54631

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934

F-OVARC1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510

F-OVARC1000006//Gallus gallus histone H2A (H2A-VII1) gene, complete cds.//9.1e-56:392:84//U38933

F-OVARC1000013

F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922

F-OVARC1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674

F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

F-OVARC1000058

F-OVARC1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

F-OVARC1000068//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARC1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

F-OVARC1000087//HS_2004_B2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARC1000091//nxb0020P17r CUCI Rice BAC Library Oryza sativa genomic clone nxb0020P17r, genomic s

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- urvey sequence. //5.2e-05:238:64//AQ258489
 F-OVARC1000092//Homo sapiens chromosome Y, clone 2
 64,M,20, complete sequence. //1.1e-10:720:58//AC004
 617
 F-OVARC1000106//HS_3212_B2_G12_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3212 Col=24 Row=N, genomic surveysequenc
 e. //9.9e-05:141:73//AQ175369
 F-OVARC1000109
 F-OVARC1000113//Homo sapiens okadaic acid-inducibl
 e phosphoprotein (OA48-18) mRNA, complete cds. //1.
 6e-133:663:96//AF069250
 F-OVARC1000114//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 1111N9, WORKING DRAFT S
 EQUENCE. //2.3e-51:547:70//AL022574
 F-OVARC1000133//Homo sapiens clone GS512I21, WORKI
 NG DRAFT SEQUENCE, 9 unordered pieces. //0.62:349:6
 1//AC005027
 F-OVARC1000139//Caenorhabditis elegans cosmid F09D
 1. //2.5e-18:314:64//AF040640
 F-OVARC1000145//HS_2257_B2_D11_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2257 Col=22 Row=H, genomic surveysequenc
 e. //5.8e-30:203:90//AQ304854
 F-OVARC1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sa
 piens genomic clone 2345A22, genomic survey sequen
 ce. //1.1e-26:146:100//AQ056703
 F-OVARC1000151//Sequence 1 from patent US 5665588.
 //2.6e-61:677:70//I64695
 F-OVARC1000168//Homo sapiens chromosome 19, cosmid
 R31343, complete sequence. //4.9e-19:381:63//AC005
 764
 F-OVARC1000191//Plasmodium falciparum DNA *** SEQU
 ENCING IN PROGRESS ***from MAL4P1, WORKING DRAFT S
 EQUENCE. //1.3e-06:745:57//AL034557
 F-OVARC1000198//*** SEQUENCING IN PROGRESS *** Hom
 o sapiens chromosome 4, BAC clone C0366H07; HTGS p
 hase 1, WORKING DRAFT SEQUENCE, 28 unorderedpiece
 s. //6.4e-161:781:97//AC004604
 F-OVARC1000209//Oryza sativa submergence induced p
 rotein 2A mRNA, complete cds. //9.2e-33:511:65//AF0
 68332
 F-OVARC1000212//F.rubripes GSS sequence, clone 185
 L11aC1, genomic surveysequence. //1.1e-13:139:79//A
 L019910
 F-OVARC1000240//Sequence 1 from patent US 5710024.
 //1.4e-129:623:98//181226
 F-OVARC1000241//Mus musculus hypoxia inducible fac
 tor three alpha mRNA, complete cds. //1.1e-112:697:8
 7//AF060194
 F-OVARC1000288
 2.2e-22:181:83//J00345
 F-OVARC1000302//A-192A9.TP CIT978SK Homo sapiens g
 enomic clone A-192A9, genomic survey sequence. //4.8
 e-18:110:99//B18003
 F-OVARC1000304//Mouse mRNA from Mov10 locus. //5.5e
 -100:631:85//X52574
 F-OVARC1000309
 F-OVARC1000321//Homo sapiens clone NH0479C13, WORK
 ING DRAFT SEQUENCE, 12unordered pieces. //3.1e-122:
 325:95//AC005236
 F-OVARC1000326//Rattus norvegicus lamina-associate
 d polypeptide 1C (LAP1C) mRNA, complete cds. //4.0e
 -46:339:84//U19614
 F-OVARC1000335//Caenorhabditis elegans cosmid F15B
 10. //0.020:545:57//AF036696
 F-OVARC1000347//Homo sapiens clone GS051M12, compl
 ete sequence. //0.71:252:59//AC005007
 F-OVARC1000384//Homo sapiens expanded SCA7 CAG rep
 eat. //2.2e-09:276:64//AF020275
 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone
 pDJ915f1 containing KvLQT1 gene, complete sequenc
 e. //0.61:343:59//AC003693
 F-OVARC1000411//S.cerevisiae chromosome XI reading
 frame ORF YKL202w. //0.075:242:60//Z28201
 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 f
 rom 7q31, complete sequence. //0.00088:285:62//AC00
 5166
 F-OVARC1000420//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 371H6, WORKING DRAFT SE
 QUENCE. //0.14:487:60//AL031718
 F-OVARC1000427//Homo sapiens clone UWCC:rg041a03 f
 rom 7p14-15, complete sequence. //4.9e-30:195:84//AC
 005826
 F-OVARC1000431//Plasmodium falciparum MAL3P2, comp
 lete sequence. //1.3e-05:651:59//AL034558
 F-OVARC1000437//Chicken tensin mRNA, complete cds.
 //9.6e-54:296:78//M74165
 F-OVARC1000440//Human PINCH protein mRNA, complete
 cds. //2.7e-19:116:99//U09284
 F-OVARC1000442//Human DNA sequence from clone 816K
 17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN
 -GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR(EC 2.
 3.2.13) (TGASE E3) (TRANSGLUTAMINASE 3), and anoth
 er member of theTransglutaminase family, complete
 sequence. //1.0e-21:202:79//AL031678
 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 pro
 tein, complete cds. //1.0e-138:566:99//AB014583
 F-OVARC1000461
 F-OVARC1000465//Bos taurus guanine nucleotide-exch

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ange protein (ARF-GEPI) mRNA, complete cds.//4.7e-124:650:93//AF023451

F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221

F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomicsurvey sequence.//2.5e-06:272:62//AJ227191

F-OVARC1000479//cDNA encoding novel rat protein TlP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829

F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs.//1.7e-13:709:60//Z99297

F-OVARC1000496//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031733

F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850

F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17unordered pieces.//8.0e-149:716:98//AC005024

F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510

F-OVARC1000543//HS_3055_A2_F10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic surveysequence.//0.19:104:71//AQ102820

F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS.CpG island, complete sequence.//4.4e-136:670:97//AL022069

F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence, complete sequence.//1.3e-15:262:69//AC002985

F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733

F-OVARC1000573//HS_3241_B1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942

F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unorderedpieces.//9.7e-97:445:90//AC002414

F-OVARC1000578//Homo sapiens DNA from chromosome 1

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9, BAC 33152, completesequence.//9.1e-27:354:72//AC003973

F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775

F-OVARC1000605

F-OVARC1000622//Homo sapiens (subclone 2_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648

F-OVARC1000640//Human BAC clone RC326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069

F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772

F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162

F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244

F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713

F-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424

F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.5e-151:549:99//AF027156

F-OVARC1000689//nxb0003aG01f CUGI Rice BAC Library Oryza sativa genomicclone nxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003

F-OVARC1000700

F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925

F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661

F-OVARC1000730

F-OVARC1000746

F-OVARC1000769//HS_2056_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic surveysequence.//8.8e-19:147:86//AQ245905

F-OVARC1000771//M.musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403

F-OVARC1000781//Sequence 5 from Patent W09722695.//1.9e-89:705:78//A63552

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F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542

F-OVARC1000800//Human Chromosome 11q23 PAC clone p DJ254e13, complete sequence.//1.7e-32:295:80//AC003691

F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469

F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711

F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543

F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584

F-OVARC1000862//M.musculus mRNA for FT1.//2.6e-109:769:83//Z67963

F-OVARC1000876//S.cerevisiae.chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125

F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086

F-OVARC1000885//B.subtilis 25 kb genomic DNA segment (from sspE to katA).//0.25:231:61//Z82044

F-OVARC1000886//CIT-HSP-2171H6.TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721

F-OVARC1000890

F-OVARC1000891

F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494

F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320

F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172

F-OVARC1000924//HS_2022_A1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493

F-OVARC1000936//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.2e-113:476:91//AC003983

F-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL031848

F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549

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F-OVARC1000948//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276

F-OVARC1000959//CIT-HSP-2348016.TR CIT-HSP Homo sapiens genomic clone 2348016, genomic survey sequence.//0.99:270:59//AQ062850

F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181

F-OVARC1000964//P.falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270

F-OVARC1000971//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841

F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274

F-OVARC1000996//M025 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858

F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785

F-OVARC1001000//HS_2247_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=0, genomic survey sequence.//3.1e-60:315:96//AQ153910

F-OVARC1001004//Homo sapiens from UWGC:y18c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190

F-OVARC1001010//CIT-HSP-2034M3.TF CIT-HSP Homo sapiens genomic clone 2034M3, genomic survey sequence.//1.0:151:60//B74290

F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021

F-OVARC1001032//Yeast (S.cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451

F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:737:86//AF001533

F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149

F-OVARC1001040//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18unordered pieces.//9.8e-29:277:76//AC005081

F-OVARC1001044//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:61//AL031319

F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds.//0.012:112:74//AF053768

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F-OVARC1001055//Sequence 1 from patent US 5580754.
//3.3e-45:381:81//I30292
F-OVARC1001062//nbxb0026H08r CUGI Rice BAC Library
Oryza sativa genomic clone nbxb0026H08r, genomic survey
sequence.//0.018:344:59//AQ271878
F-OVARC1001065//S.pombe chromosome I cosmid c29E6.
//0.86:338:59//Z66525
F-OVARC1001068//Homo sapiens Era GTPase A protein
(HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082
657
F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gen
e, partial cds and flanking repeat regions.//9.3e-
24:285:65//AF003529
F-OVARC1001074//Human DNA sequence from clone 23K2
0 on chromosome Xq25-26.2 Contains EST, STS, GSS,
complete sequence.//2.0e-07:652:59//AL022153
F-OVARC1001085//Homo sapiens c-syn protooncogene m
RNA, complete cds.//5.0e-35:187:99//M14333
F-OVARC1001092//Homo sapiens mRNA for JM5 protein,
complete CDS (clone IMAGE 53337, LLNLc110F1857Q7
(RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//
/4.0e-74:289:95//AJ005897
F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete
cds.//3.6e-72:351:86//AF015913
F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1)
mRNA, complete cds.//6.4e-150:710:98//AF051782
F-OVARC1001117//Homo sapiens chromosome 5, P1 clon
e 328E3 (LBNL H53), complete sequence.//0.99:148:6
7//AC005178
F-OVARC1001118//Human Chromosome 11 pac pDJ197h17,
WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.6
e-35:302:74//AC000382
F-OVARC1001129//CIT-HSP-647P20.TP CIT-HSP Homo sap
iens genomic clone 647P20, genomic survey sequenc
e.//0.94:106:66//B79052
F-OVARC1001154//R.norvegicus mRNA for epithelin 1
and 2.//1.8e-95:462:79//X62322
F-OVARC1001161//Homo sapiens chromosome 4 clone B7
1M12 map 4q25, complete sequence.//2.9e-90:496:84/
/AC004069
F-OVARC1001162
F-OVARC1001167//Homo sapiens clone DJ1098J04, WORK
ING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:21
9:64//AC004961
F-OVARC1001169//Borrelia burgdorferi (section 27 o
f 70) of the complete genome.//1.0:265:59//AE001141
F-OVARC1001170//H.sapiens (xsl70) mRNA, 350bp.//4.
6e-58:355:90//Z36823
F-OVARC1001171//CIT-HSP-2285E22.TF CIT-HSP Homo sa
piens genomic clone 2285E22, genomic survey sequen

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ce.//1.5e-25:152:83//AQ002315
F-OVARC1001173//Human DNA sequence from clone 243E
7 on chromosome 22q12.1. Contains ESTs, STSs and G
SSs, complete sequence.//0.0024:94:80//AL022323
F-OVARC1001176//Streptomyces plicatus B-N-acetylhe
xosaminidase (hex) gene, complete cds.//1.0:356:60
//AF063001
F-OVARC1001180//G.gallus DNA for polyubiquitin gen
e Ub II.//0.0062:275:60//X58195
10 F-OVARC1001188//Homo sapiens full length insert cD
NA clone ZD93F03.//1.8e-32:180:97//AF086486
F-OVARC1001200
F-OVARC1001232//Caenorhabditis elegans cosmid F10B
5, complete sequence.//0.013:128:67//Z48334
F-OVARC1001240//Human Chromosome 11 pac pDJ360p17,
WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7
e-131:811:87//AC001235
F-OVARC1001243//Human BAC clone GS117010 from 7q21
-q22, complete sequence.//0.044:457:59//AC003078
20 F-OVARC1001244//Human homolog of Drosophila female
sterile homeotic mRNA, complete cds.//8.4e-18:11
8:95//M80613
F-OVARC1001261//Mus musculus putative membrane-ass
ociated guanylate kinase 1 (Magi-1) mRNA, alternat
ively spliced c form, partial cds.//1.4e-95:649:84
//AF027505
F-OVARC1001268//Rattus norvegicus ADP-ribosylation
factor-directed GTPase activating protein mRNA, c
omplete cds.//0.00051:72:83//U35776
30 F-OVARC1001270
F-OVARC1001271//Homo sapiens mRNA for KIAA0643 pro
tein, partial cds.//2.1e-142:644:96//AB014543
F-OVARC1001282//RPC111-60K8.TK RPC111 Homo sapiens
genomic clone R-60K8, genomic survey sequence.//0.
0089:285:58//AQ195857
F-OVARC1001296//Homo sapiens echinoderm microtubul
e-associated protein homolog HuEMAP mRNA, complete
cds.//3.0e-20:263:73//U97018
F-OVARC1001306//nbxb0002M13r CUGI Rice BAC Library
40 Oryza sativa genomic clone nbxb0002M13r, genomic s
urvey sequence.//0.98:170:66//AQ156061
F-OVARC1001329//Homo sapiens BAC clone RG370M10 fr
om 7p15, complete sequence.//1.3e-05:432:61//AC003
986
F-OVARC1001330//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC1383 genomic sequence, WORKING DRAFT SE
QUENCE, 3 unordered pieces.//0.027:444:59//AC00550
4
F-OVARC1001339//Homo sapiens chromosome 17, clone
hCIT.124_H_2, complete sequence.//0.76:89:74//AC006

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F-OVARC1001341//CITBI-E1-2503J7. TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence. //0.99:45:86//AQ263402

F-OVARC1001342

F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 781 Col=4 Row=0, genomic survey sequence. //1.5e-07:254:67//B44456

F-OVARC1001357//Homo sapiens Xp22-149 BAC RPC111-4 6604 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //0.83:376:61//AC005297

F-OVARC1001360

F-OVARC1001369//Homo sapiens clone 162B15, complete sequence. //0.0066:99:76//AC004811

F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds. //2.7e-142:683:98//AF034801

F-OVARC1001376//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE. //1.9e-52:382:73//AL031680

F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL. //1.2e-147:683:99//AJ224819

F-OVARC1001391//S.coelicolor whiB gene. //0.018:45:4:59//X62287

F-OVARC1001399//CIT-HSP-229118. TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence. //1.7e-11:104:87//AQ007611

F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds. //3.9e-149:707:98//AB006651

F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds. //4.9e-48:586:69//U52426

F-OVARC1001425//Human DNA sequence from clone 1048 E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence. //0.0019:96:78//Z99714

F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds. //0.77:519:59//U96387

F-OVARC1001442//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE. //1.0:167:64//AL031687

F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS. //4.4e-64:376:79//Z84482

F-OVARC1001476//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y24F12, WORKING DRAFT SEQUENCE. //0.20:107:71//AL022277

F-OVARC1001480

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F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.20:281:63//AC005140

F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds. //8.1e-85:479:92//AF016507

F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 -complete genomic sequence, complete sequence. //1.2e-98:503:83//AC002039

F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon1. //1.7e-13:87:100//M16411

F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5. //0.43:190:68//X69219

F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.017:533:56//AC005140

20 F-OVARC1001555//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7unordered pieces. //7.4e-159:416:99//AC005037

F-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene. //2.4e-115:540:99//AF031165

F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence. //5.5e-13:529:62//AF043945

F-OVARC1001610//, complete sequence. //1.4e-12:152:77//AC005409

F-OVARC1001611

F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12Contains STS, GSS, complete sequence. //0.022:146:70//AL031682

F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds. //6.5e-109:358:96//AB005543

F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds. //1.8e-47:393:81//AB006867

40 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence. //0.94:85:69//B92840

F-OVARC1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE. //1.9e-06:489:61//Z97651

F-OVARC1001713//Rattus norvegicus neuroligin 2 mRNA, complete cds. //1.0:262:59//U41662

F-OVARC1001726//Human telomere associated repeat sequence, complete sequence. //7.5e-08:283:65//M57752

50 F-OVARC1001731//Mus musculus gene for beta-tropomy

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osin. //2.6e-83:606:81//X12650
 F-OVARC1001745//HS_3007_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic surveysequence. //0.00020:269:60//AQ164522
 F-OVARC1001762//S.pombe chromosome III cosmid c338. //3.0e-17:624:61//AL023781
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds. //4.2e-149:706:98//U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds. //3.0e-115:580:96//AB014575
 F-OVARC1001768
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence. //5.7e-64:477:78//AC005066
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4q25, complete sequence. //6.5e-11:171:76//AC004704
 F-OVARC1001802//CITBI-E1-2502A17.TR CITBI-E1 Homo sapiens genomic clone2502A17, genomic survey sequence. //0.98:214:61//AQ264481
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence. //9.5e-151:712:99//AL023694
 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds. //2.7e-56:522:75//AF068748
 F-OVARC1001812//Homo sapiens chromosome 17, clone HCIT104N19, complete sequence. //1.7e-63:526:81//AC003662
 F-OVARC1001813//Human DNA sequence from cosmid U14A10, between markers DXS366 and DXS87 on chromosome X contains STS. //0.17:214:65//Z70224
 F-OVARC1001820//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 445N2, WORKING DRAFT SEQUENCE. //3.2e-55:379:82//AL031779
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence. //2.8e-17:509:62//AC005609
 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X. //0.35:403:58//Z73361
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence. //2.4e-25:148:96//B94622

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F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence. //1.2e-18:122:95//AF070611
 F-OVARC1001879//HS_3026_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic surveysequence. //4.9e-29:204:87//AQ207748
 F-OVARC1001880//Human interferon regulatory factor 5 (Hmif5) mRNA, complete cds. //3.5e-05:489:60//U51127
 10 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces. //1.9e-29:350:74//AC005020
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds. //8.6e-56:300:96//AF061749
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and CSSs, complete sequence. //2.3e-10:253:66//AL031904
 F-OVARC1001911//HS_2196_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic surveysequence. //3.4e-09:123:78//AQ294069
 F-OVARC1001916//HS_3054_B1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic surveysequence. //1.2e-31:126:97//AQ099979
 F-OVARC1001928
 F-OVARC1001942//H.sapiens CpG island DNA genomic Msel fragment, clone 21d7, forward read cpg21d7.ft1a. //7.2e-12:83:98//Z60390
 30 F-OVARC1001943//Aplysia californica potassium channel modulatory factormRNA, complete cds. //3.5e-50:535:69//AF059179
 F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds. //1.7e-16:294:67//U37263
 F-OVARC1001950//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE. //1.5e-20:261:68//AJ011929
 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4. //0.99:447:57//Z19021
 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces. //2.9e-19:178:83//AC005995
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence. //0.17:232:62//AL034559
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds. //2.1e-158:739:98//AB007934
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE. //3.0e-17:781:59//AP000011
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F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6unordered pieces.//5.4e-136:683:96//AC006015

F-OVARC1002107//Homo sapiens BAC clone RC276003 from 7q22-q31.1, complete sequence.//1.0:220:61//AC004668

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//6.1e-115:557:98//AF041483

F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//0.013:461:57//AC006241

F-OVARC1002138//Caenorhabditis elegans cosmid F32D1.//1.0e-29:545:64//AF016427

F-OVARC1002143//CIT-HSP-2343H20. TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence.//2.3e-11:258:67//AQ055576

F-OVARC1002156

F-OVARC1002158//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//1.8e-16:383:66//B11616

F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase.//0.0041:300:64//X79568

F-OVARC1002182//F.rubripes GSS sequence, clone 123I23aA7, genomic survey sequence.//1.4e-10:240:66//AL017241

F-PLACE1000004//CIT-HSP-2294H13. TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence.//8.2e-10:158:75//AQ003859

F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1.//4.8e-15:89:93//M12585

F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//3.8e-51:550:72//AF022789

F-PLACE1000014

F-PLACE1000031//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5unordered pieces.//0.91:333:61//AC004821

F-PLACE1000040//Homo sapiens DNA sequence from PAC958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.6e-20:279:67//Z93023

F-PLACE1000048//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//3.6e-63:488:82//AC005177

F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence.//2.3e-10:141:75//U31508

F-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//1.9e-30:190:94//L22154

F-PLACE1000066//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74

3386

//AC005521

F-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848

F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R28461, genomic sequence, complete sequence.//0.52:390:60//AC002389

F-PLACE1000094

F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580

F-PLACE1000142//H.sapiens AUH mRNA.//6.4e-09:328:62//X79888

F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291

F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//176211

20 F-PLACE1000213

F-PLACE1000214//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504

F-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818

30 F-PLACE1000246//HS_2008_A2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=C, genomic survey sequence.//0.96:153:61//AQ269813

F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584

F-PLACE1000308//D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.//0.00013:369:59//X54011

40 F-PLACE1000332//HS_2016_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106

F-PLACE1000347//CIT-HSP-2326A16. TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350

F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891

F-PLACE1000380//F.rubripes GSS sequence, clone 047P21aA10, genomic survey sequence.//0.43:198:62//Z88163

50 F-PLACE1000383//Homo sapiens myotubularin related

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protein 1 (MTMR1) mRNA, partial cds.//8.7e-149:74
0:96//U58032
F-PLACE1000401//Pinctada fucata mRNA for insoluble
protein, complete cds.//0.22:484:56//D86074
F-PLACE1000406//Human nuclear matrix protein 55 (n
mt55) mRNA, complete cds.//3.3e-19:372:65//U89867
F-PLACE1000420//Homo sapiens chromosome 17, clone
hRPK.227_C_15, complete sequence.//1.6e-85:421:87
//AC005899
F-PLACE1000421//Human GT334 protein (GT334) gene, 10
exons 16 and 17.//0.88:145:68//U61515
F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 f
rom 7p12-p14, complete sequence.//0.076:196:66//AC0
05189
F-PLACE1000435//HS_3217_A2_A12_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3217 Col=24 Row=A, genomic surveysequenc
e.//2.2e-47:438:76//AQ181698
F-PLACE1000444//Homo sapiens Chromosome 16 BAC clo
ne CIT987SK-A-152E5, complete sequence.//6.9e-61:6 20
16:71//AC004382
F-PLACE1000453//Murine genomic DNA; partially dige
sted Sau3A fragment, cloned into cosmid vector pEM
BLcos2, complete sequence.//5.8e-18:314:69//AF0595
80
F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Co
smid Clone 94a In DGCRRegion, complete sequence.//
1.1e-33:349:76//AC002491
F-PLACE1000492//Rat vacuolar protein sorting homol
og r-vps33b mRNA, complete cds.//1.1e-34:256:83//U 30
35245
F-PLACE1000540//P.falciparum complete gene map of
plastid-like DNA (IR-B).//0.099:336:58//X95276
F-PLACE1000547//Arabidopsis thaliana GDP-mannose p
yrophosphorylase (GMP1) mRNA, complete cds.//5.4e-
11:279:63//AF076484
F-PLACE1000562//, complete sequence.//1.7e-97:559:
88//AC005409
F-PLACE1000564
F-PLACE1000583//Figure 2. Nucleotide and translate 40
d protein sequences ofHPPF1, -2, and -9.//3.3e-46:6
31:68//M27877.
F-PLACE1000588//Human guanylate binding protein is
oform I (GBP-2) mRNA, complete cds.//7.3e-84:503:88
//M55542
F-PLACE1000596//Homo sapiens mRNA for NS1-binding
protein (NS1-BP).//3.8e-164:798:97//AJ012449
F-PLACE1000599//P.falciparum complete gene map of
plastid-like DNA (IR-B).//0.018:295:61//X95276
F-PLACE1000610//HS_2056_A1_D10_T7 CIT Approved Hum 50

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an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2056 Col=19 Row=G, genomic surveysequenc
e.//5.3e-24:188:87//AQ235967
F-PLACE1000611//Rattus norvegicus neural membrane
protein 35 mRNA, complete cds.//2.4e-47:687:66//AF
044201
F-PLACE1000636
F-PLACE1000653//Homo sapiens N-acetylglucosamine-p
hosphate mutase mRNA, complete cds.//1.5e-152:747:9
6//AF102265
F-PLACE1000656//Homo sapiens mRNA for JM4 protein,
complete CDS (clone IMAGE 546750 and LLNLc110F185
7Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896
F-PLACE1000706//nuclear protein TIF1 [mice, mRNA,
3951 nt].//8.0e-60:675:70//S78219
F-PLACE1000712
F-PLACE1000716//HS-1057-A1-A03-MR.abi CIT Human Ge
nomic Sperm Library CHomo sapiens genomic clone Pl
ate=CT 779 Col=5 Row=A, genomic survey sequence.//
2.7e-42:266:82//B43026
F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sap
iens genomic clone 2372J8, genomic survey sequenc
e.//0.023:157:68//AQ113109
F-PLACE1000749//Plasmodium falciparum MAL3P7, comp
lete sequence.//0.099:664:57//AL034559
F-PLACE1000755//H.sapiens DNA 3' flanking simple s
equence region clone wg2c3.//0.00068:206:62//X7658
9
F-PLACE1000769//RPCI11-3J18.TPB RPCI-11 Homo sapie
ns genomic clone RPCI-11-3J18, genomic survey sequ
ence.//6.5e-08:93:89//B63806
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 pro
tein, partial cds.//3.5e-138:663:98//AB014548
F-PLACE1000786//Drosophila melanogaster cosmid 80H
7.//1.4e-43:589:68//AL031027
F-PLACE1000793//H.sapiens CpG island DNA genomic M
sel fragment, clone 13d12, reverse read cpg13d12.r
t1c.//4.6e-09:71:100//Z64565
F-PLACE1000798//Human Chromosome 16 BAC clone CIT9
87SK-A-635H12, complete sequence.//5.0e-14:235:72/
/AC002310
F-PLACE1000841//Homo sapiens clone NH0441G08, WORK
ING DRAFT SEQUENCE, 12unordered pieces.//0.013:40
4:60//AC006158
F-PLACE1000849//H.sapiens CpG island DNA genomic M
sel fragment, clone 72a10, reverse read cpg72a10.r
t1a.//3.3e-09:82:92//Z62712
F-PLACE1000856//Hydra vulgaris HT4 mRNA for collag
en-like protein, partial cds.//1.0:317:59//AB00893
5

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F-PLACE1000863//H.sapiens CpG island DNA genomic M
sel fragment, clone 53d2, forward read cpg53d2.ft1
b.//7.3e-37:199:98//Z55621
F-PLACE1000909//H.sapiens CpG island DNA genomic M
sel fragment, clone 173f8, reverse read cpg173f8.r
tla.//1.5e-17:128:92//Z57391
F-PLACE1000931//Human DNA sequence from PAC 212P9
on chromosome 1p34.1-1p35. Contains delta opiate r
eceptor, CpG island, CA repeat.//8.1e-55:647:72//
AL009181
F-PLACE1000948
F-PLACE1000972//RPC111-61B1.TJ RPC111 Homo sapiens
genomic clone R-61B1, genomic survey sequence.//1.
0e-26:148:99//AQ194348
F-PLACE1000977//Homo sapiens mRNA for KIAA0672 pro
tein, complete cds.//6.1e-08:413:61//AB014572
F-PLACE1000979//H.sapiens CpG island DNA genomic M
sel fragment, clone 76e8, reverse read cpg76e8.rtl
a.//2.7e-10:84:94//Z55963
F-PLACE1000987//Homo sapiens mRNA for KIAA0724 pro
tein, complete cds.//8.0e-140:694:96//AB018267
F-PLACE1001000//Herpetomonas muscarum muscarum kin
etoplast 12S rRNA gene.//0.0056:443:58//U01011
F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sa
piens genomic clone 2013L15, genomic survey sequen
ce.//0.99:277:58//B58681
F-PLACE1001010//Human cosmid g1572c101, complete s
equence.//3.6e-55:294:88//AC000357
F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 f
rom 7p21, complete sequence.//7.2e-33:333:73//AC00
4741
F-PLACE1001024
F-PLACE1001036//CIT-HSP-2373I10.TF CIT-HSP Homo sa
piens genomic clone 2373I10, genomic survey sequen
ce.//1.1e-80:393:98//AQ108662
F-PLACE1001054//Arabidopsis thaliana genomic DNA,
chromosome 5, TAC clone: K9I9, complete sequence./
/8.8e-40:483:66//AB013390
F-PLACE1001062//Mus musculus mRNA encoding lysine-
ketoglutarate reductase/saccharopine dehydrogenas
e.//1.2e-23:224:80//AJ224761
F-PLACE1001076//HS_2195_B1_D05_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2195 Col=9 Row=H, genomic survey sequenc
e.//0.0014:168:66//AQ066659
F-PLACE1001088
F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA,
complete cds.//3.1e-95:489:96//AF065485
F-PLACE1001104//Caprine arthritis-encephalitis vir
us envelope glycoprotein (env) gene, partial cds./

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/0.0073:253:62//U81400
F-PLACE1001118//Homo sapiens KRAB domain zinc fing
er protein (ZFP37) mRNA, complete cds.//2.5e-64:67
6:71//AF022158
F-PLACE1001136//Human amphiregulin (AR) gene, exon
5, clones lambda-ARH(6,12).//3.8e-26:174:93//M307
02
F-PLACE1001168
F-PLACE1001171//Homo sapiens subtelomeric cosmid 1
1b-1, complete sequence.//7.6e-23:245:68//AC005603
F-PLACE1001185//Human DNA sequence from clone 889N
15 on chromosome Xq22.1-22.3. Contains part of the
gene for a novel protein similar to X. laevis Cor
tical Thymocyte Marker CTX, the possibly alternati
vely spliced gene for 26S Proteasome subunit p28.
(Ankyrin repeat protein), a novel gene and exons 36
through 45 of the COL4A6 for Collagen Alpha 6(I
V). Contains ESTs, STSs, GSSs and a putative CpG is
land, complete sequence.//0.010:102:70//AL031177
F-PLACE1001238//Mouse mRNA for RNA polymerase I as
sociated factor (PAF53), complete cds.//9.3e-82:68
4:77//D14336
F-PLACE1001241
F-PLACE1001257//Caenorhabditis elegans cosmid R12E
2.//1.1e-16:480:60//AF067219
F-PLACE1001272//H.sapiens subunit of coatomer comp
lex.//0.31:50:96//X70476
F-PLACE1001279//Plasmodium falciparum 3D7 chromoso
me 12 PFYACB8-628 genomic sequence, WORKING DRAFT
SEQUENCE, 9 unordered pieces.//0.054:352:60//AC005
507
F-PLACE1001280//Bovine herpesvirus type 1 early-in
termediate transcription control protein (BICP4) g
ene, complete cds.//1.0e-10:620:61//L14320
F-PLACE1001294//M.musculus GEG-154 mRNA.//5.0e-10
7:826:80//X71642
F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger
protein ZFP-35.//1.2e-67:510:77//X17617
F-PLACE1001311//Homo sapiens clone DJ0826E18, WORK
ING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-47:49
1:73//AC005282
F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Ge
nomic Sperm Library CHomo sapiens genomic clone Pl
ate=CT 328 Col=20 Row=C, genomic survey sequence./
/9.6e-26:142:100//B31181
F-PLACE1001351
F-PLACE1001366//Homo sapiens mRNA for KIAA0799 pro
tein, partial cds.//8.6e-25:155:95//AB018342
F-PLACE1001377//H.sapiens MADM gene (exon 1).//1.6
e-43:393:79//Z48614

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F-PLACE1001383//Human DNA sequence from clone 246H 3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, C A repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324

F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319

F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//157340

F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177

F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.0e-145:700:98//AC005412

F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087

F-PLACE1001414//Homo sapiens chromosome 9, clone h RPK.202_H_3, complete sequence.//8.2e-121:608:97//AC006241

F-PLACE1001440//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.3e-06:437:61//AC000384

F-PLACE1001456//Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106

F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148

F-PLACE1001484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660

F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon 1.//0.00015:333:59//L78720

F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (D80)), complete sequence.//0.00016:161:66//AC004373

F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786

F-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667

F-PLACE1001545//Homo sapiens chromosome 3, clone h RPK.165_I_16, complete sequence.//2.7e-139:482:96//AC005669

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F-PLACE1001551//Homo sapiens chromosome 19, CIT-HS P-444n24, complete sequence.//6.9e-116:681:89//AC005261

F-PLACE1001570//HS_3105_A1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817

F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.8e-102:217:99//AB020860

F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984

F-PLACE1001608//HS_2189_A1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959

F-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.4e-114:552:98//AC005037

F-PLACE1001611//Human DNA sequence from clone 1039 K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, genes similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587

F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341

F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032

F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//7.7e-159:788:97//AC005971

F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165

F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.1e-149:760:96//AC005921

F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thio esterhydrolase (MCH), complete cds.//2.9e-57:643:71//M16200

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F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958_E.11, WORKINGDRAFT SEQUENCE, 2 ordered pieces.//3.9e-18:284:71//AC005883
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776
 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 In IGLC Region, complete sequence.//1.0:274:59//AC000051
 F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124
 F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607
 F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221
 F-PLACE1001745
 F-PLACE1001746//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P1, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744
 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243
 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPC111-303E5, WORKING DRAFT SEQUENCE, 65 unordered pieces.//1.9e-54:274:81//AC005842
 F-PLACE1001761//HS_3027_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972
 F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394
 F-PLACE1001781
 1.3e-08:238:65//AC005637
 F-PLACE1001799//HS_3075_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474
 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence.//0.00035:196:66//AB020749
 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953
 F-PLACE1001821//RPC111-35D17.TK RPC1-11 Homo sapiens genomic clone RPC1-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286
 F-PLACE1001844//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//2.8e-67:443:86//AC005177
 F-PLACE1001845//Arabidopsis thaliana chromosome I

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BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850
 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244
 F-PLACE1001897//RPC111-46D15.TJ RPC111 Homo sapiens genomic clone R-46D15, genomic survey sequence.//9.3e-08:383:63//AQ194408
 F-PLACE1001912
 10 F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935
 F-PLACE1001928//HS_2220_B2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361
 F-PLACE1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596
 F-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755
 F-PLACE1002004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996
 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//U58337
 F-PLACE1002052//HS_2178_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=H, genomic survey sequence.//4.8e-22:140:95//AQ307908
 F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284
 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195
 F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178
 40 F-PLACE1002090//Homo sapiens full length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131
 F-PLACE1002115//nbxb0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0038A20r, genomic survey sequence.//0.039:210:69//AQ291086
 F-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527
 F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete seq

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uence. //2.1e-125:491:98//AL022162
 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence. //0.12:408:61//AL034556
 F-PLACE1002157//Homo sapiens BAC clone NH0335J18 from 2, complete sequence. //1.1e-44:515:71//AC005539
 F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence. //0.98:210:65//AE000662
 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence. //1.2e-06:283:60//AC004805
 F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds. //1.0e-24:313:71//U06244
 F-PLACE1002205//Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces. //1.6e-05:428:60//AC005720
 F-PLACE1002213//HS_3238_B1_G03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence. //2.2e-74:371:98//AQ206965
 F-PLACE1002227//HS-1056-B1-C01-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence. //2.1e-07:174:71//B42800
 F-PLACE1002256//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-72, complete sequence. //0.022:458:59//AL010142
 F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, C A repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence. //3.5e-91:637:84//AL022324
 F-PLACE1002319
 F-PLACE1002342//Caenorhabditis elegans cosmid M03A1. //0.47:403:58//U49956
 F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence. //1.9e-127:487:93//AC004623
 F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence. //5.6e-05:474:59//AC005922
 F-PLACE1002433//Drosophila melanogaster fidiptidine gene, exons 1-7. //1.7e-11:613:58//AJ011928
 F-PLACE1002437//M.musculus abc1 mRNA. //5.5e-62:452:85//X75926

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F-PLACE1002438//Dictyostelium discoideum developmental protein DG1098 (DG1098) gene, partial cds. //0.013:372:59//AF081801
 F-PLACE1002450//HS_3233_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence. //3.1e-07:449:59//AQ204769
 F-PLACE1002465
 F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds. //1.5e-110:720:85//U69262
 F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence. //3.9e-05:195:71//AC005926
 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPCI4-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //0.020:301:60//AC006060
 F-PLACE1002499
 F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds. //2.1e-58:465:80//U50927
 F-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE. //3.7e-08:139:76//Z93930
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds. //9.0e-143:583:95//AB018256
 F-PLACE1002532//Homo sapiens BAC clone RC300E22 from 7q21-q31.1, complete sequence. //0.00019:193:65//AC004774
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence. //4.7e-25:198:84//AL031575
 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA, complete cds. //2.0e-13:400:60//L25314
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GS HB-555C13, complete sequence. //3.5e-11:167:72//AC002523
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds. //4.2e-09:370:61//U31443
 F-PLACE1002591//H. sapiens mRNA for coronin. //7.2e-26:279:74//X89109
 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces. //0.0013:375:64//AC005537
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence. //4.7e-05:556:59//D31785

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F-PLACE1002625
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180
 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//173723
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273
 F-PLACE1002772//HS_3058_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=C, genomic survey sequence.//0.0046:192:64//AQ134567
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927
 F-PLACE1002794//CIT-HSP-2368A17.TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691
 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//9.3e-41:240:93//M27877
 F-PLACE1002839//Human BAC clone RC205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140
 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126

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F-PLACE1002881//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CKII) mRNA, complete cds.//0.00012:200:64//U19889
 F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120
 F-PLACE1002962
 10 F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558
 F-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755
 F-PLACE1002993//CIT-HSP-2338I16.TF CIT-HSP Homo sapiens genomic clone 2338I16, genomic survey sequence.//1.9e-13:100:95//AQ054760
 F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980
 20 F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551
 F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088
 F-PLACE1003044//cDNA encoding novel rat protein TIPI20 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829
 F-PLACE1003045//H.sapiens CpG island DNA genomic Msel fragment, clone 47g6, forward read cpg47g6.ft1a.//0.0064:52:96//Z61200
 30 F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158
 F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875
 F-PLACE1003108
 F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.//6.3e-46:606:68//AC004219
 F-PLACE1003145
 40 F-PLACE1003153//RPCI11-13P16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206
 F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495
 F-PLACE1003176//HS_2255_A2_B01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934
 50 F-PLACE1003190//Homo sapiens clone RG332P12, WORKI

3399

NG DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:90//AC005095

F-PLACE1003200//P.falciparum complete gene map of plastid-like DNA (IR-B).//8.7e-06:728:57//X95276

F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466

F-PLACE1003238//HS_3239_A2_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954

F-PLACE1003249

F-PLACE1003256

F-PLACE1003258//HS_3223_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317

F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429

F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPP1, -2, and -9.//2.3e-92:485:95//M27877

F-PLACE1003334

F-PLACE1003342

F-PLACE1003343//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951

F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715

F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095

F-PLACE1003366

F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558

F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247

F-PLACE1003375

F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//2.3e-157:779:96//AB020878

F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//M83680

F-PLACE1003401//RPC11-71J5.TJ RPC11 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588

F-PLACE1003420//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone YIE3, WORKING DRAFT SEQUENCE.//0.0015:286:60//AL021388

3400

F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470

F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401

F-PLACE1003493

F-PLACE1003516//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//8.2e-41:379:78//AC002994

10 F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.2e-21:247:76//AF064859

F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:79//AL008729

F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336

F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831

F-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297

F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547

30 F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688

F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, C A repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324

F-PLACE1003584//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-56, complete sequence.//0.0038:465:57//AL010230

F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557

F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476

F-PLACE1003596//Mus musculus integral membrane protein 1 (Itm1) mRNA, complete cds.//1.4e-54:685:68//L34260

50 F-PLACE1003602//Homo sapiens mRNA expressed in pla

3401

centa.//1.1e-138:679:97//D83200

F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.//0.0074:265:63//AC005356

F-PLACE1003611//HS_2198_B1_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475

F-PLACE1003618//Homo sapiens chromosome 4 clone C011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226

F-PLACE1003625//HS_2238_B2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662

F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478

F-PLACE1003669

F-PLACE1003704//RPCI11-23H21.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830

F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305

F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:166:99//AL021920

F-PLACE1003723//HS_2231_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672

F-PLACE1003738//Human zinc finger protein 42 (MZF-1) mRNA, complete cds.//5.9e-33:592:67//M58297

F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840

F-PLACE1003762

F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014

F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160

F-PLACE1003783//HS_2190_A2_C02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757

F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309 50

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P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210

F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p15 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//0.015:296:60//U52112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

F-PLACE1003850//P.falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332011 on chromosome 1q24-1q25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

F-PLACE1003870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//D42108

F-PLACE1003892//RPCI11-24P17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPSH) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo

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sapiens genomic clone2387C11, genomic survey sequence.//1.0:223:62//AQ239494
 F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413
 F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954
 F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666
 F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 In CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052
 F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651
 F-PLACE1004128//M.musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658
 F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355
 F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p12.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099
 F-PLACE1004161
 F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071
 F-PLACE1004197
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493
 F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326
 F-PLACE1004256//HS_2010_B2_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434
 F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034
 F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806
 F-PLACE1004270//Human IgA C alpha 1 switch region (Sal).//1.7e-08:622:61//L19121
 F-PLACE1004274//H.sapiens CpG island DNA genomic map fragment, clone 18g6, forward read cpg18g6.ft1

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b.//8.6e-37:196:98//Z57691
 F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:97//AF084830
 F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence.//0.0060:635:57//AB011480
 F-PLACE1004289//HS_3023_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451
 F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411
 F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588
 F-PLACE1004336//Drosophila melanogaster DNA sequence (P1 DS07968 (D117)), complete sequence.//0.87:206:59//AC004267
 F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1mRNA, complete cds.//5.9e-139:688:97//AF100153
 F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631
 F-PLACE1004384//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653
 F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:615:62//U70855
 F-PLACE1004405//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027
 F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532
 F-PLACE1004428//R.norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188
 F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283
 F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon Induced 56Kd pseudogene and ESTs.//4.8e-23:231:71//Z74739
 F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954
 F-PLACE1004467//HS_2058_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence

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e. //2.4e-87:433:98//AQ242700
 F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9. //1.4e-74:65:70//M27877
 F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence. //3.3e-20:140:92//B80243
 F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //9.9e-05:794:57//AC004709
 F-PLACE1004506//Human Gx-alpha gene. //1.0e-05:231:63//D90150
 F-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds. //3.2e-146:699:98//AF040701
 F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST. //1.4e-33:367:71//Z86001
 F-PLACE1004518
 F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds. //2.6e-05:318:62//U86962
 F-PLACE1004550//Human FMR1 gene, 5' end. //0.0018:142:66//L19476
 F-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor. //1.7e-114:513:85//X75931
 F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds. //0.00013:188:67//AB001868
 F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome; segment 138/162. //0.66:337:60//Z95120
 F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds. //1.1e-19:326:63//AF035673
 F-PLACE1004658//H.sapiens CpG island DNA genomic Msel fragment, clone 55h1, forward read cpg55h1.ft1a. //2.4e-34:188:98//Z61632
 F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence. //1.0:148:65//Z81140
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds. //1.9e-101:182:95//U07561
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds. //4.3e-109:625:91//AF035606
 F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //1.9e-152:759:96//AB020860

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F-PLACE1004686//Homo sapiens DNA sequence from PAC179N16 on chromosome6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence. //1.2e-34:320:71//Z95152
 F-PLACE1004691//HS_3044_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence. //0.018:191:63//AQ098323
 F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //0.28:573:57//AL022577
 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence. //0.00081:428:59//Z98551
 F-PLACE1004722//HS_3052_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence. //2.3e-05:104:75//AQ134959
 F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence. //1.3e-24:180:88//AQ080498
 F-PLACE1004740//RPCI11-58A7.TJ RPCI11 Homo sapiens genomic clone R-58A7, genomic survey sequence. //8.6e-26:522:65//AQ195766
 F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds. //1.1e-112:711:86//AF061555
 F-PLACE1004751
 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds. //5.4e-171:828:97//AF084367
 F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7. //4.2e-134:763:90//AJ001713
 F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spinclin homolog (PROTEIN DXF34), hypothetical protein EST, STS, GSS, complete sequence. //9.3e-132:759:90//AL022157
 F-PLACE1004804
 F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces. //6.5e-06:403:58//AC004710
 F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence. //9.8e-39:207:99/

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/AC005921
 F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence. //8.1e-15:203:73//AC004613
 F-PLACE1004824//G.gallus PB1 gene. //1.1e-103:759:80//X90849
 F-PLACE1004827//HS_2230_A2_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence. //4.1e-38:330:81//AQ299313
 F-PLACE1004836//H.sapiens nidogen gene (exon 8). //0.97:116:68//X84825
 F-PLACE1004838//HS_3241_A2_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence. //1.8e-87:425:98//AQ206740
 F-PLACE1004840//Sequence 2 from patent US 5728819. //6.7e-47:285:91//I92819
 F-PLACE1004868
 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9. //0.14:465:59//Z97344
 F-PLACE1004900
 F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence. //3.6e-06:56:100//AQ261184
 F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence. //2.6e-151:770:91//AC005058
 F-PLACE1004918//Mus musculus signaling molecule (A TTP) mRNA, complete cds. //2.6e-68:459:84//U97571
 F-PLACE1004930//Homo sapiens TNF-induced protein G G2-1 mRNA, complete cds. //4.4e-106:545:95//AF070671
 F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence. //3.5e-45:226:84//AL020989
 F-PLACE1004937
 F-PLACE1004969
 F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence. //0.012:316:61//AC004843
 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat; complete sequence. //4.7e-39:394:77//AL031073
 F-PLACE1004982//Caenorhabditis elegans cosmid B0507. //0.16:167:65//U64833

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F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence. //8.8e-14:590:61//AE001373
 F-PLACE1005026
 F-PLACE1005027
 F-PLACE1005046
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces. //2.1e-135:675:97//AC005867
 10 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds. //1.9e-159:761:98//AB011148
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds. //9.2e-10:757:56//AF059569
 F-PLACE1005077
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence. //6.9e-29:253:77//AC004673
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence. //6.5e-52:446:78//AC002316
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces. //2.0e-146:734:96//AC005225
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence. //9.8e-83:254:95//AC004476
 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence. //0.46:179:64//AC003081
 30 F-PLACE1005111
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds. //0.00051:287:63//L14320
 F-PLACE1005146//HS_3071_A1_E03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=I, genomic survey sequence. //7.4e-38:299:82//AQ103361
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence. //2.6e-44:346:82//AC002451
 40 F-PLACE1005176
 F-PLACE1005181//CIT-HSP-234005.TR CIT-HSP Homo sapiens genomic clone 234005, genomic survey sequence. //0.99:211:63//AQ054651
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence. //2.7e-07:80:90//AQ074445
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence. //0.98:216:61//AC000061
 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces. //0.70:245:

- 63//AC004965
F-PLACE1005243
F-PLACE1005261//*Caenorhabditis elegans* cosmid T05H10, complete sequence.//0.00041:254:61//Z47812
F-PLACE1005266//*H. sapiens* mRNA (fetal brain cDNA a 4_2g).//9.6e-33:177:98//Z70695
F-PLACE1005277//*Homo sapiens* mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182
F-PLACE1005287//*Plasmodium falciparum* (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183
F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757
F-PLACE1005308//*Clethrionomys glareolus* endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621
F-PLACE1005313//*Caenorhabditis elegans* cosmid D2092.//8.8e-11:342:62//U88167
F-PLACE1005327//HS_3080_B2_A12_MR CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116
F-PLACE1005331//*Homo sapiens* chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794
F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380
F-PLACE1005373
F-PLACE1005374//*Homo sapiens* chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104
F-PLACE1005409//Human BAC clone RC167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991
F-PLACE1005453//*Caenorhabditis elegans* DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854
F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859
F-PLACE1005471//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581
F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191
F-PLACE1005480//*Homo sapiens* DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021050
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F-PLACE1005481//RPC111-74L17.TJ RPC111 *Homo sapiens* genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885
F-PLACE1005494//*Homo sapiens* transient receptor potential protein 6 mRNA, complete cds.//2.1e-67:325:99//AF080394
F-PLACE1005502//*Homo sapiens* BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589
F-PLACE1005526//*H. sapiens* CpG island DNA genomic Msel fragment, clone 9f1, reverse read cpg9f1.rta.//3.6e-27:159:96//Z66485
F-PLACE1005528//*Homo sapiens* genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038
F-PLACE1005530//*Homo sapiens* clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860
F-PLACE1005550//*Fugu rubripes* GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925
F-PLACE1005554//*Leishmania tarentolae* mitochondria l 12S ribosomal RNA gene.//0.43:209:66//X02354
F-PLACE1005557//*Homo sapiens* chromosome 17, clone hRPC.117_B_12, complete sequence.//9.3e-113:536:97//AC004707
F-PLACE1005574//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:514:59//AC005504
F-PLACE1005584//*Homo sapiens* mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517
F-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//1.2e-111:262:89//AC004126
F-PLACE1005603
F-PLACE1005611//F1605TFC IGF Arabidopsis thaliana genomic clone F1605, genomic survey sequence.//2.0e-10:209:66//B98589
F-PLACE1005623
F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840
F-PLACE1005639//HS_3095_B1_A03_MF CIT Approved Human Genomic Sperm Library D *Homo sapiens* genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022
F-PLACE1005646//*Homo sapiens* RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255

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F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase. //1.3e-51:480:74//X59618

F-PLACE1005666//RPCI11-78015.TV RPCI11 Homo sapiens genomic clone R-78015, genomic survey sequence. //8.7e-05:243:62//AQ284667

F-PLACE1005698//Human membrane-associated lectin type-C mRNA. //1.9e-63:374:85//M98457

F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence. //0.69:633:57//AE001422

F-PLACE1005730//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence. //2.0e-24:286:74//AQ231147

F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds. //2.8e-55:621:71//U15635

F-PLACE1005755//HS_2213_A2_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=0, genomic survey sequence. //1.4e-25:290:75//AQ136844

F-PLACE1005763//Rat medium-chain S-acyl fatty acid synthetase thio esterhydrolase (MCH), complete cds. //4.5e-40:297:70//M16200

F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5. //0.91:287:63//Y12517

F-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence. //5.0e-109:530:98//AC004827

F-PLACE1005803//HS_3092_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence. //2.4e-08:76:96//AQ103695

F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds. //1.4e-126:636:96//AF027156

F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //2.6e-154:739:98//AF065482

F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces. //2.2e-37:355:77//AC004150

F-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-105, complete sequence. //0.00080:663:58//AL010283

F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.00015:340:58//AC004153

F-PLACE1005850//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence

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e. //1.8e-46:278:85//AL031432

F-PLACE1005851

F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor. //5.0e-120:701:89//X75931

F-PLACE1005884//CIT-HSP-2333012.TR CIT-HSP Homo sapiens genomic clone 2333012, genomic survey sequence. //4.6e-78:385:98//AQ039226

F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Bem46+) mRNA, partial cds. //9.3e-16:638:57//U29892

F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds. //1.0:178:65//U67136

F-PLACE1005921//M.musculus mRNA for immunity associated protein 38. //6.6e-17:614:59//Y08026

F-PLACE1005923//RPCI11-33G19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-33G19, genomic survey sequence. //4.0e-10:535:57//AQ046151

F-PLACE1005925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE. //0.17:159:65//AL034405

F-PLACE1005932

F-PLACE1005934//H.sapiens CpG island DNA genomic Msel fragment, clone 165g2, forward read cpg165g2.f1a. //8.3e-43:247:93//Z57153

F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence. //0.91:116:68//AL014719

F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dorS), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds. //0.0022:495:59//AF016236

F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence. //2.9e-05:442:61//AC004081

F-PLACE1005955//Caenorhabditis elegans cosmid F01F1. //4.3e-20:409:64//U13070

F-PLACE1005966//P.falciparum aarp3 gene, exon. //0.0083:270:64//Y08925

F-PLACE1005968

F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces. //1.0e-100:513:96//AC005866

F-PLACE1006002//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE. //2.5e-54:444:77//Z86090

F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Ge

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omic Sperm Library Chomo sapiens genomic clone Plate=CT 781 Col=2 Row=M, genomic survey sequence.//3.4e-05:214:64//B44442

F-PLACE1006011//Mus musculus poly-(ADPribosyl)-transferase homolog PARPmRNA, complete cds.//4.3e-71:580:79//AF072521

F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 ~complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299

F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-147:719:97//X99906

F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023

F-PLACE1006129

F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597

F-PLACE1006143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015

F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone: B2.//0.048:290:60//D85750

F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-105402 map 10q25, complete sequence.//3.2e-129:466:96//AC005661

F-PLACE1006164//HS_3003_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239

F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433

F-PLACE1006195//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658

F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125

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F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931

F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803

F-PLACE1006225//CIT-HSP-2335I23. TF CIT-HSP Homo sapiens genomic clone 2335I23, genomic survey sequence.//2.1e-19:149:90//AQ039880

F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.//0.51:290:58//U91327

F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142

F-PLACE1006246//RPCI11-36I23. TK RPCI-11 Homo sapiens genomic clone RPCI-11-36I23, genomic survey sequence.//2.6e-31:176:97//AQ045400

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.3e-166:791:98//AB014548

F-PLACE1006262//342E3. TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447

F-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320

F-PLACE1006318

F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454

30 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721

F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504

F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559

F-PLACE1006368//X.laavis mRNA for KLP2 protein.//3.0e-25:376:68//X94082

40 F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//2.0e-146:711:97//AC004232

F-PLACE1006382

F-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-110:539:97//AF062085

F-PLACE1006412//Homo sapiens BAC clone GS588C18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029

50 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//A

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F069735
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129
 F-PLACE1006445//HS_3071_A1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ103347
 F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496
 F-PLACE1006470//T.brucei kinetoplast maxicircle variable region DNA.//0.99:250:59//Z15118
 F-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977
 F-PLACE1006488//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744
 F-PLACE1006492
 F-PLACE1006506
 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083
 F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355
 F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510
 F-PLACE1006540
 F-PLACE1006552//P.falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998
 F-PLACE1006598//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670
 F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems HumanBAC library) complete sequence.//0.98:514:59//AC004470
 F-PLACE1006626//H.sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589
 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015
 F-PLACE1006640//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276
 F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688

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F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-I (b3GT1) gene, complete cds.//0.00011:184:64//AF029790
 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP)mRNA, complete cds.//0.0013:380:62//U67916
 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 22q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN), ESTs and STS.//1.5e-78:520:86//Z98048
 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.9e-135:378:99//AC005626
 F-PLACE1006760//CIT-HSP-2336013. TR CIT-HSP Homo sapiens genomic clone 2336013, genomic survey sequence.//0.018:147:66//AQ039246
 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426
 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487
 F-PLACE1006792//HS_3165_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559
 F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513
 F-PLACE1006800//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272
 F-PLACE1006805//paramecium species 1, 168 nt dna dimer: replication init. region.//9.1e-09:369:62//K00915
 F-PLACE1006815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033
 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230
 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350
 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559
 F-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378
 F-PLACE1006878
 F-PLACE1006883//Mycobacterium tuberculosis H37Rv c

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complete genome; segment 138/162.//1.0:236:62//Z95120

F-PLACE1006901//Mus musculus t complex testis-specific protein (Tctex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672

F-PLACE1006904

F-PLACE1006917//H.sapiens CpG island DNA genomic Msel fragment, clone 79g10, forward read cpg79g10.f tla.//1.3e-21:131:98//Z63175

F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063

F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308

F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447

F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//U23921

F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.6e-06:651:58//AJ223323

F-PLACE1006962//H.sapiens irlb mRNA.//7.1e-15:202:71//X63417

F-PLACE1006966//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594

F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188

F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305

F-PLACE1007021//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//5.1e-17:285:70//AC005777

F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat*.//6.2e-131:775:89//Z82899

F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895

F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214_0_1, complete sequence.//1.3e-131:652:97//AC005224

F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with abeta-galacturonidase LIKE pseudogene. Contains a membrane

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protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368

F-PLACE1007105//Mus musculus muskellin mRNA, complete cds.//4.1e-124:687:91//U72194

F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:586:56//AC005139

F-PLACE1007112//HS_2234_B2_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, genomic survey sequence.//0.26:200:62//AQ087801

F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112

F-PLACE1007140//QN1 orf [Coturnix coturnix, japonica, K2 neuroretinal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151

F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.011:329:61//AC005140

F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//0.0036:180:63//M62899

F-PLACE1007238//FMR1 {CGG repeats} [human, Fragile X syndrome patient, Genomic, 429 nt].//2.8e-08:269:63//S74494

F-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.3e-57:405:87//D50495

F-PLACE1007242//HS_3006_A1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, genomic survey sequence.//0.088:191:59//AQ089443

F-PLACE1007243//Human transporter protein (gl7) mRNA, complete cds.//7.9e-12:245:66//U49082

40 F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:677:98//Y15908

F-PLACE1007274//HS_3003_A1_D08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, genomic survey sequence.//7.4e-49:345:85//AQ294154

F-PLACE1007276//Fugu rubripes GSS sequence, clone 014010aG11, genomic survey sequence.//0.0052:228:62//AL024982

F-PLACE1007282//F.rubripes GSS sequence, clone 019007aB3, genomic survey sequence.//0.024:289:58//AL0

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F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, complete sequence. //0.0048:185:69//AC002492

F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete cds. //0.069:761:57//AB009080

F-PLACE1007317

F-PLACE1007342

F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds. //5.4e-120: 567:98//AF096870

F-PLACE1007367//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //1.2e-59:613:75//AC005077

F-PLACE1007375//Caenorhabditis elegans cosmid D2092. //1.8e-12:193:70//U88167

F-PLACE1007386

F-PLACE1007402//HS_2170_A2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, genomic survey sequence. //5.6e-06:162:67//AQ125590

F-PLACE1007409//Homo sapiens mitoxantrone resistance protein 2 mRNA, complete sequence. //1.6e-25:165:93//AF093772

F-PLACE1007416

F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence. //4.9e-34:764:62//AC003973

F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds. //4.1e-17:374:64//AF041433

F-PLACE1007454//Homo sapiens (clone si53) mRNA fragment. //8.1e-52:317:93//L40391

F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence. //0.0019:280:64//AL031117

F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345C4 -complete genomic sequence, complete sequence. //2.5e-24:362:71//AC002302

F-PLACE1007484

F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) mRNA, complete cds. //3.8e-14:293:63//AF017370

F-PLACE1007507//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence. //4.6e-10:152:75//AL031311

F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence. //3.6e-139:477:98//AC004231

F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence. //0.0055:395:59//AF015461

F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxidase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and apocytochrome b (cyt b) genes, complete cds, and complete 9S rRNA gene and partial 12SrRNA gene. //0.0013:550:58//U11682

F-PLACE1007537//H. sapiens CpG island DNA genomic Msel fragment, clone 198g6, reverse read cpg198g6.r tla. //0.98:121:67//Z60280

F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence. //2.3e-10:141:75//U31508

F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds. //3.1e-69:733:71//AB014561

F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule. //0.022:393:61//X03240

F-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 545L17, WORKING DRAFT SEQUENCE. //3.6e-114:565:97//AL031665

F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic clone 2371G14, genomic survey sequence. //2.0e-22:304:70//AQ111183

F-PLACE1007618//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence. //1.0:386:59//AC005245

F-PLACE1007621

F-PLACE1007632//Homo sapiens 12p13.3 PAC RPCI5-940 J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //1.0e-88:276:96//AC006064

F-PLACE1007645//Bovine elastin mRNA, partial cds. //2.1e-07:110:79//M26132

F-PLACE1007649

F-PLACE1007677//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE. //1.2e-21:567:64//AL023755

F-PLACE1007688//Pseudorabies virus immediate-early gene. //2.2e-05:287:66//X15120

F-PLACE1007690//Caenorhabditis elegans cosmid R07G3. //0.40:122:70//U23452

F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment. //0.85:117:71//L40483

F-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE. //0.0035:75:88//AL031662

F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds. //1.3e-147:709:97//AF061243

F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence. //1.0:510:58//AB005231

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F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HML6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-136:516:89//U86698
 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//7.9e-155:728:98//AB014585
 F-PLACE1007737//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3unordered pieces.//5.8e-22:806:60//AC005484
 F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-06:510:56//AC005504
 F-PLACE1007746//HS_2268_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, genomic surveysequence.//0.10:171:63//AQ124780
 F-PLACE1007791//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MALIP6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749
 F-PLACE1007807//Homo sapiens chromosome 17, clone hRPK.879_D_6, complete sequence.//1.0e-120:743:87//AC005273
 F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//1.0e-113:739:86//AC003658
 F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic clone 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438
 F-PLACE1007843//F.rubripes GSS sequence, clone 162 K02bC12, genomic survey sequence.//1.6e-10:148:72//AL006903
 F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-177:844:98//AF000010
 F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90//M77174
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//3.9e-189:894:98//AB018309
 F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271
 F-PLACE1007877
 F-PLACE1007897
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//2.3e-154:755:97//AB007956
 F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, WORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097
 F-PLACE1007954//Homo sapiens BAC clone NH0414C23 f 50

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rom Y, complete sequence.//2.1e-61:522:79//AC006157
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//2.7e-171:813:98//AF084530
 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//2.5e-153:730:98//AF079529
 F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//3.4e-32:383:74//U13262
 F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198:96//Z94758
 F-PLACE1008000//Mus musculus veli 3 mRNA, complete cds.//1.5e-118:706:88//AF087695
 F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4unordered pieces.//6.4e-163:786:98//AC005628
 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625:84//L31840
 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165:65//Z35719
 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251:64//Z68883
 F-PLACE1008095//RPCI11-21F19.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21F19, genomic survey sequence.//1.5e-30:166:99//B85883
 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondria 1 protein, partial cds.//7.5e-06:414:60//AF069163
 F-PLACE1008122//S.cerevisiae chromosome XV reading frame ORF YOL125w.//0.046:477:59//Z74867
 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290121 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446:57//AC004586
 F-PLACE1008132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111:93//Z82199
 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866:73//D14849
 F-PLACE1008181//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727:56//AL034397
 F-PLACE1008198//HS_3073_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic surveysequence

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e. //2.3e-12:94:92//AQ171450
 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces. //2.5e-162:791:97//AC005069
 F-PLACE1008209
 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds. //0.65:174:66//M26332
 F-PLACE1008244//CIT-HSP-2337B4. TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence. //6.7e-28:165:95//AQ039317
 F-PLACE1008273//B. primigenius mRNA for coat protein gamma-cop. //2.8e-71:709:71//X92987
 F-PLACE1008275//D. discoideum actin A-13 gene, 5' flank. //0.12:131:64//M29123
 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence. //0.011:96:73//AC005913
 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds. //8.2e-86:672:77//AF078779
 F-PLACE1008329//HS_2027_A1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence. //8.7e-09:116:81//AQ244432
 F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence. //2.2e-141:670:98//AC005176
 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces. //2.1e-27:157:78//AC005000
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds. //1.1e-137:659:98//AB014579
 F-PLACE1008368//CIT-HSP-2311C9. TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence. //7.1e-08:398:60//AQ016352
 F-PLACE1008369//HS_2251_B1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence. //2.1e-35:217:93//AQ066512
 F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence. //1.4e-11:403:64//AC005856
 F-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE. //3.7e-144:681:99//AL034417
 F-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces. //2.8e-45:257:96//AC004604
 F-PLACE1008402//Homo sapiens mRNA for p115, complete

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te cds. //4.3e-148:711:98//D86326
 F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.089:672:56//AC004688
 F-PLACE1008424
 F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11. //1.0e-88:331:84//AB020864
 10 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987S K-384D8 complete sequence. //0.55:530:58//U62317
 F-PLACE1008437//CIT-HSP-2376H4. TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence. //3.3e-78:349:94//AQ112479
 F-PLACE1008455//HS_2064_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence. //4.7e-59:471:81//AQ246589
 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence. //8.9e-43:307:73//AC004526
 F-PLACE1008465//CIT-HSP-2163F24. TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence. //8.9e-41:210:99//B90014
 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds. //0.00013:516:58//AB003494
 F-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING DRAFT SEQUENCE. //1.3e-161:778:98//AL031778
 30 F-PLACE1008531//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds. //1.1e-78:191:100//AF045555
 F-PLACE1008532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE. //3.8e-24:257:70//Z93097
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence. //1.0e-13:215:71//AC004997
 40 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome Xq21.1. //0.66:263:64//Z9571
 F-PLACE1008584//Homo sapiens cosmid clone U39B3 from Xp22.1-22.2, complete sequence. //1.1e-19:315:68//U73023
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds. //1.2e-173:812:98//AB018334
 F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //3.9e-09:198:71//AC005077
 50 F-PLACE1008625//Homo sapiens chromosome 5, PAC clone

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ne 45L14 (LBNL H91), complete sequence.//0.68:568:59//AC005373
 F-PLACE1008626//HS_3221_A2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147:82//AQ180967
 F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586:88//Y12836
 F-PLACE1008629//CIT-HSP-201214.TR CIT-HSP Homo sapiens genomic clone 201214, genomic survey sequence.//0.00085:203:66//B53732
 F-PLACE1008630//Sequence 26 from Patent W09517522.//9.7e-05:97:80//A45356
 F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23:299:64//D38595
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622:99//AF044333
 F-PLACE1008693//CIT-HSP-2346F2.TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89:76//AQ060732
 F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420:97//AF038406
 F-PLACE1008715//CIT-HSP-2294K20.TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349:98//AQ007199
 F-PLACE1008748//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.14:347:59//AC004260
 F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems HumanBAC library) complete sequence.//7.9e-25:244:71//AC003037
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503:97//AF060543
 F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370:61//AF001549
 F-PLACE1008807//CIT-HSP-2334B19.TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220:65//AQ036643
 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470:97//AF030933
 F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504:89//AF032668
 F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains prote

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in synthesis factor (eIF-4C), D1F15S1A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212:74//AL021920
 F-PLACE1008854
 F-PLACE1008867//Human DNA sequence from clone J428 A131, WORKING DRAFT SEQUENCE.//4.7e-77:477:84//Z82209
 F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699:70//AC005539
 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164:68//M63660
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753:98//AB018308
 F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:400:63//AC002042
 F-PLACE1008934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022312
 F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete cds.//4.3e-41:282:87//L15309
 F-PLACE1008947//Pseudorabies virus with upstream and downstream sequences.//5.9e-15:710:60//M34651
 F-PLACE1009020//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//1.9e-21:167:86//AQ253727
 F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117
 F-PLACE1009039//HS_2034_A2_F08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, genomic survey sequence.//0.17:252:59//AQ230137
 F-PLACE1009045//HS_3185_B2_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, genomic survey sequence.//1.9e-34:260:86//AQ172861
 F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit gene, 5' flank and exon 1.//4.7e-70:463:80//D00766
 F-PLACE1009050//Homo sapiens 12q13.1 PAC RPC13-197 B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.63:280:61//AC004241
 F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting protein X), complete CDS.//5.9e-113:725:85//AJ005073
 F-PLACE1009090//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 1045J21, WORKING DRAFT SEQUENCE. //9.1e-27:222:84//AL021919
 F-PLACE1009091//Homo sapiens clone DJ0968I16, complete sequence. //0.027:630:58//AC006016
 F-PLACE1009094
 F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cds. //2.1e-85:726:76//M36515
 F-PLACE1009110
 F-PLACE1009111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 138B7, WORKING DRAFT SE 10
 QUENCE. //6.0e-12:362:64//Z98752
 F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3(XRCC3) mRNA, complete cds. //3.4e-138:671:97//AF035586
 F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds. //3.6e-23:718:59//D25215
 F-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS *** from clone 1014D13, WORKING DRAFT SE 10
 QUENCE. //6.1e-142:684:98//AJ011929
 F-PLACE1009155//Homo sapiens genomic DNA, chromoso 20
 me 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE. //4.3e-36:227:77//AP000031
 F-PLACE1009158//H. sapiens genomic sequence for ERC C2 gene 3' region involved in DNA excision repair. //1.0:173:60//X52222
 F-PLACE1009166
 F-PLACE1009172//Human BAC clone 7E17 from 12q, complete sequence. //4.0e-35:257:85//AC002070
 F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC G SHB-531I17 (Genome Systems Human BAC Library) comp 30
 lete sequence. //2.9e-19:288:72//AC004805
 F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence. //0.053:388:60//AB008266
 F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxCl) mRNA, complete cds. //1.8e-50:317:89//AF061242
 F-PLACE1009190//RPCI11-81N5.TJ RPCI11 Homo sapiens genomic clone R-81N5, genomic survey sequence. //0.91:114:67//AQ281881
 F-PLACE1009200//CITBI-E1-2509J16.TF CITBI-E1 Homo sapiens genomic clone 2509J16, genomic survey sequence. //2.8e-44:175:83//AQ262198
 F-PLACE1009230//H. sapiens gene for pregnancy specific beta-1 glycoprotein. //1.1e-106:495:88//X63203
 F-PLACE1009246//HS_3058_B1_A06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, genomic survey sequence. //0.10:175:68//AQ185945
 F-PLACE1009298//Mus musculus maternal-embryonic 3 50

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(Mem3) mRNA, complete cds. //1.8e-94:575:89//U47024
 F-PLACE1009308//Human clone mcag32 chromosome 7 CT G repeat region. //0.0017:350:62//U23862
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds. //3.0e-06:411:59//U83192
 F-PLACE1009328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191P20, WORKING DRAFT S
 EQUENCE. //5.7e-138:830:86//AL034399
 F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain. //0.071:253:62//D87015
 F-PLACE1009338//RPCI11-74N24.TV RPCI11 Homo sapiens genomic clone R-74N24, genomic survey sequence. //2.4e-34:180:100//AQ268811
 F-PLACE1009368
 F-PLACE1009375
 F-PLACE1009388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1014D13, WORKING DRAFT SE 10
 QUENCE. //2.0e-37:288:84//AL022311
 F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cds. //4.3e-78:730:74//M27878
 F-PLACE1009404//SmD homolog [mice, liver, mRNA Partial, 199 nt]. //0.16:95:71//S71494
 F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence. //1.6e-150:701:99//AC005919
 F-PLACE1009434//Mus musculus clone OST431, genomic survey sequence. //2.9e-73:442:88//AF046700
 F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome; segment 148/162. //0.012:582:56//AL022022
 F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230)mRNA, complete cds. //4.6e-21:146:93//AF012872
 F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequence. //2.9e-31:264:81//AF046660
 F-PLACE1009468//Sequence 1 from patent US 5580968. //1.9e-83:567:84//I30536
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence. //1.9e-142:704:97//AC004531
 F-PLACE1009477//Human 11p14.3 PAC clone pDJ939m16, complete sequence. //2.2e-09:235:68//AC004601
 F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence. //2.9e-83:171:92//U91321
 F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unk

nown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence. //3.8e-69:175:92//Z94160

F-PLACE1009539//Mus musculus synaptotagmin 2 isoform alpha mRNA, complete cds. //7.0e-26:237:78//AF041862

F-PLACE1009542//Human DNA sequence from clone 1039 K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, genes similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence. //3.1e-10:126:79//AL031587

F-PLACE1009571//RPC11-60K12.TK RPC11 Homo sapiens genomic clone R-60K12, genomic survey sequence. //1.4e-05:68:91//AQ195869

F-PLACE1009581

F-PLACE1009595//Homo sapiens chromosome 5, P1 clone 1029A7 (LBNL H15), complete sequence. //6.6e-19:309:70//AC003959

F-PLACE1009596//Rattus norvegicus platelet-activating factor acetylhydrolase beta subunit (PAF-AH beta) gene, complete cds. //9.0e-09:485:59//AF016049

F-PLACE1009607//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE. //4.9e-43:714:66//Z83824

F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.017:655:57//AC004157

F-PLACE1009621

F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genomic survey sequence. //2.7e-15:100:98//B33248

F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.63:130:67//AC005308

F-PLACE1009639//S.pombe chromosome II cosmid c24E9. //0.86:509:58//AL021816

F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds. //1.4e-171:816:98//AB011159

F-PLACE1009665//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence. //3.4e-67:437:87//AC005177

F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds. //2.5e-147:701:98//AF062534

F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence. //1.5e-98:228:100//AC006011

F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence. //2.2e-130:736:91//AC000109

F-PLACE1009731//M.musculus mRNA for immunity assoc

iated protein 38. //1.1e-13:311:64//Y08026

F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds. //4.2e-125:602:98//AF046024

F-PLACE1009794

F-PLACE1009798//Human DNA sequence from clone 1189 B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence. //1.3e-73:271:84//AL030996

F-PLACE1009845

F-PLACE1009861//B.tauris cathepsin B mRNA, 3' end. //0.00023:147:65//M64620

F-PLACE1009879//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE. //4.9e-27:725:63//AL034397

F-PLACE1009886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE. //8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence. //0.0044:232:60//AQ251431

F-PLACE1009908//S.pombe chromosome I cosmid c3F10. //1.5e-19:559:59//Z69369

F-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid. //5.9e-48:304:87//M63005

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces. //2.4e-51:481:78//AC004529

F-PLACE1009925//nbxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0027C22r, genomic survey sequence. //0.98:220:67//AQ272066

F-PLACE1009935//Sequence 16 from patent US 5552281. //0.030:152:67//I25655

F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces. //2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS_3178_B1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence. //4.9e-23:142:95//AQ150311

F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence. //0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchori

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ng protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to *C. elegans* Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//*M. musculus* Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692

F-PLACE1010069//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925

F-PLACE1010089//HS_3111_A1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=I, genomic survey sequence.//4.8e-07:124:78//AQ101268

F-PLACE1010096//*R. norvegicus* mRNA for 100 kDa protein.//1.2e-108:700:85//X64411

F-PLACE1010102//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome Xq22.//6.5e-25:488:63//Z93928

F-PLACE1010134//*S. pombe* chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164

F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-83:409:98//AJ222636

F-PLACE1010152//CIT-HSP-2381F24.TF CIT-HSP Homo sapiens genomic clone 2381F24, genomic survey sequence.//1.5e-28:163:98//AQ196757

F-PLACE1010181//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//2.4e-15:197:72//AC004973

F-PLACE1010194//*Ictalurus punctatus* tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967

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F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829

F-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033377

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917

F-PLACE1010270//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710

F-PLACE1010274//*Caenorhabditis elegans* cosmid C01A2, complete sequence.//0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI3-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005

F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//*Apis mellifera ligustica* complete mitochondrial genome.//2.8e-08:384:64//L06178

F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

F-PLACE1010362//*Mycobacterium tuberculosis* H37Rv complete genome; segment 155/162.//0.94:398:57//AL022121

F-PLACE1010364//*Caenorhabditis elegans* DNA *** SEQUENCING IN PROGRESS *** from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//AL020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//0.066:88:76//AC004675

F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//*Bos taurus* C5-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081

F-PLACE1010492
 F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq 28.//0.022:405:60//U82695
 F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417
 F-PLACE1010547//Human DNA sequence from clone 790B 6 on chromosome 20p11.22-12.2. Contains STSs and C SSs, complete sequence.//1.0:283:61//AL031677
 F-PLACE1010562//RPCI11-65I16.TK RPCI11 Homo sapiens genomic clone R-65I16, genomic survey sequence.//0.017:216:67//AQ200831
 F-PLACE1010579//Homo sapiens full length insert cDNA YI23D12.//3.9e-19:147:89//AF075014
 F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186
 F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308
 F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558
 F-PLACE1010624//Streptomyces coelicolor cosmid 5A 7.//1.4e-05:518:61//AL031107
 F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846
 F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-259H10, complete sequence.//2.5e-17:187:80//AC004682
 F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence.//0.21:159:64//AB016872
 F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069
 F-PLACE1010661
 F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960
 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376
 F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583
 F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS_2013_B2_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864
 F-PLACE1010743//R.norvegicus mRNA for myr5.//1.7e-87:582:85//X77609
 F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//4.7e-45:235:99//AC005921
 F-PLACE1010771//M.musculus HCNGP mRNA.//1.6e-135:801:88//X68061
 F-PLACE1010786//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence.//0.35:334:60//AL010221
 F-PLACE1010800//RPCI11-79H17.TV RPCI11 Homo sapiens genomic clone R-79H17, genomic survey sequence.//5.8e-18:168:82//AQ284252
 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence.//1.6e-30:693:63//AC004384
 F-PLACE1010811//RPCI11-51N5.TK RPCI11 Homo sapiens genomic clone R-51N5, genomic survey sequence.//8.3e-11:142:78//AQ052380
 F-PLACE1010833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//7.3e-40:147:88//AL031283
 F-PLACE1010856//M.musculus mRNA for utrophin.//7.3e-17:150:86//Y12229
 F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.4e-94:422:95//AB020868
 F-PLACE1010870//M.musculus mRNA for ZT3 zinc finger factor.//1.3e-93:530:90//Z67747
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.1e-147:694:98//AB011182
 F-PLACE1010891
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//3.9e-26:394:68//AC003997
 F-PLACE1010900
 F-PLACE1010916//HS_2242_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence.//1.0e-78:391:97//AQ146687
 F-PLACE1010917
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.11:629:56//AC004688
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//9.5e-138:653:98//AB011126

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F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds.//5.6e-90:437:98//AF064243
 F-PLACE1010944//Homo sapiens full length insert cDNA clone ZD38E12.//1.4e-09:208:68//AF086247
 F-PLACE1010947
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence.//2.1e-29:190:91//B98965
 F-PLACE1010960//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 4-52, complete sequence.//0.00074:421:60//AL010226
 F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence.//1.8e-84:412:99//AQ240696
 F-PLACE1011026//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-20, complete sequence.//0.00037:257:64//AL008972
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (LBNL H176), complete sequence.//3.8e-06:315:65//AC005348
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds.//1.5e-56:286:98//U70669
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds.//1.3e-24:278:76//M20636
 F-PLACE1011054//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 981L23, WORKING DRAFT SEQUENCE.//3.8e-27:196:84//AL031686
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds.//5.4e-06:182:67//U77049
 F-PLACE1011057//protein kinase PRK2 [human, DX3 B-cell myeloma cell line, mRNA, 3255 nt].//3.2e-31:169:100//S75548
 F-PLACE1011090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//5.1e-80:479:89//AL031687
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//2.3e-24:192:84//L14684
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c.//1.4e-14:346:60//Z28249
 F-PLACE1011133//T7E9-T7.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence.//0.010:345:60//B19698
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00013:95:76//AQ109305
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.7e-111:692:87//AC004893

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F-PLACE1011165//H.sapiens galactokinase (CK2) mRNA, complete cds.//8.4e-31:194:92//M84443
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-249B10, complete sequence.//3.1e-43:447:72//AC002288
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyltransferase mRNA, complete cds.//3.3e-124:584:99//AF038664
 F-PLACE1011214//HS_2046_A2_B01_MR CIT Approved Human Genomic Sperm Library D-Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence.//2.0e-39:346:81//AQ305965
 F-PLACE1011219
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence.//2.4e-20:119:100//AQ279801
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds.//4.4e-146:675:99//AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.7e-42:212:84//AC005014
 F-PLACE1011273//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y37D8, WORKING DRAFT SEQUENCE.//1.0:214:60//Z92819
 F-PLACE1011291//RPCI11-16P9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-16P9, genomic survey sequence.//8.0e-08:66:98//B81770
 F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LANL), complete sequence.//0.027:135:67//AC004647
 F-PLACE1011310//H.sapiens CpG island DNA genomic Msel fragment, clone 53c10, reverse read cpG53c10.rtlb.//1.4e-05:57:100//Z61496
 F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds.//0.077:193:60//L02290
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-6-phosphate mutase mRNA, complete cds.//3.1e-150:699:99//AF102265
 F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388_F_14, complete sequence.//2.4e-38:186:83//AC005375
 F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds.//6.0e-35:689:63//AF023919
 F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.0e-88:584:86//AJ010310
 F-PLACE1011399//paramecium species 7, 325 mt dna dimer: replication init. region.//0.00011:255:63//K00919
 F-PLACE1011419//Homo sapiens chromosome 21 PAC LLN

- LP704G1150Q13. //0.067:337:62//AJ006996
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds. //4.6e-157:743:98//AB011102
 F-PLACE1011452//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE. //1.1e-53:557:73 //AJ011929
 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence. //3.5e-71:498:80//AC004605
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds. //4.8e-151:703:99//AB018255
 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //5.2e-145:675:99//AF065482
 F-PLACE1011492//Ray (T. californica) acetylcholine receptor beta-subunit mRNA. //1.0:448:59//J00964
 F-PLACE1011503
 F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence. //3.8e-147:692:99//AC004968
 F-PLACE1011563//R. norvegicus mRNA for leucocyte common antigen-related protein (3941 bp). //0.00036:296:61//X83546
 F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence. //1.1e-38:315:82//AC004984
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds. //1.3e-65:268:86//AF054180
 F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence. //2.0e-82:188:96//AC004477
 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214_0_1, complete sequence. //1.8e-153:752:97//AC005224
 F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence. //4.8e-05:190:67//AE000660
 F-PLACE1011643//Alcaligenes eutrophus phaP gene. //0.16:466:59//X85729
 F-PLACE1011646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE. //9.1e-19:156:76//AL033383
 F-PLACE1011649
 F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds. //6.4e-09:172:74//AF037062
 F-PLACE1011664//D. melanogaster crn mRNA. //1.1e-52:650:68//X58374
 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.11:443:58//AC005507
 F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence. //0.31:127:71//AL008719
 F-PLACE1011719//Human BAC clone RC369K23 from 7q31, complete sequence. //4.6e-52:461:77//AC002487
 F-PLACE1011725
 F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.011:320:62//AC004737
 F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.00031:544:59//AC004157
 F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence. //2.4e-115:682:90//AC004003
 F-PLACE1011778//RPCI11-22D17.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22D17, genomic survey sequence. //2.7e-114:611:93//AQ008944
 F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1, genomic survey sequence. //2.3e-17:120:94//AQ042330
 F-PLACE1011858//Gallus domesticus filamin mRNA, complete cds. //4.1e-24:565:64//U00147
 F-PLACE1011874//Homo Sapiens Chromosome X clone bW XD312, complete sequence. //2.5e-141:678:98//AC004478
 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds. //1.6e-108:526:98//AB011152
 F-PLACE1011891//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING DRAFT SEQUENCE. //0.0014:330:62//AL021392
 F-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds. //1.4e-89:678:82//U61969
 F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds. //0.069:246:61//U81400
 F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds. //1.2e-138:664:98//AF059617
 F-PLACE1011962//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence. //2.4e-07:154:74//AQ175369
 F-PLACE1011964//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE. //3.7e-22:369:69//AL023799
 F-PLACE1011982//HS-1041-A1-B01-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Pl

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ate=CT 823 Col=1 Row=C, genomic survey sequence.//
O.44:309:58//B36529
F-PLACE1011995//Homo sapiens Xq28 BAC RPCI11-382P7
(Roswell Park Cancer Institute Human BAC Library)
complete sequence.//8.8e-53:687:71//AC006054
F-PLACE1012031//Homo sapiens mRNA for KIAA0713 pro
tein, partial cds.//1.2e-146:690:98//AB018256
F-PLACE2000003//Homo sapiens chromosome 17, clone
hRPK.318_A.15, complete sequence.//1.7e-62:293:88/
/AC005837
F-PLACE2000006//Homo sapiens chromosome 12p13.3 cl
one RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unorder
ed pieces.//1.4e-116:261:91//AC006057
F-PLACE2000007
F-PLACE2000011//Homo sapiens chromosome 19, cosmid
F20887, complete sequence.//5.2e-102:489:99//AC00
5578
F-PLACE2000014//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 1111N9, WORKING DRAFT S
EQUENCE.//0.0095:307:62//AL022574
F-PLACE2000015//Homo sapiens clone RG140B11, WORKI
NG DRAFT SEQUENCE, 1 unordered pieces.//2.0e-36:31
6:81//AC005069
F-PLACE2000017//HS_3042_A1_F08_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3042 Col=15 Row=K, genomic surveysequenc
e.//1.0:184:61//AQ098074
F-PLACE2000021//Homo sapiens TRF1-interacting anky
rin-related ADP-ribosepolymerase mRNA, complete cd
s.//4.6e-84:844:72//AF082556
F-PLACE2000030//Human Chromosome 11 Cosmid cSRL16b
6, complete sequence.//2.3e-22:233:77//U73638
F-PLACE2000033//C.capitata mRNA for chorion protei
n sl8.//0.0019:342:62//Y08913
F-PLACE2000034//Rattus norvegicus transmembrane re
ceptor Robo1 mRNA, complete cds.//2.8e-13:335:63//
AF041082
F-PLACE2000039//Rattus norvegicus cytoplasmic dyne
in heavy chain (MAP 1C), mRNA, complete cds.//7.7e
-84:489:90//L08505
F-PLACE2000047//Homo sapiens ccr2b, (ccr2), ccr2a
(ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete
cds, and lactoferrin (lactoferrin) gene, partial
cds, complete sequence.//5.0e-28:327:76//U95626
F-PLACE2000050//Homo sapiens chromosome 17, clone
HRPC41C23, complete sequence.//1.1e-32:527:68//AC0
03101
F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sa
piens genomic clone 2346L20, genomic survey sequen
ce.//1.1e-05:89:83//AQ059010

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F-PLACE2000062//Human membrane-associated lectin t
ype-C mRNA.//9.0e-113:662:86//M98457
F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202)
mRNA, complete cds.//2.2e-133:631:98//AF027219
F-PLACE2000097//Homo sapiens chromosome 12p13.3 cl
one RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unor
dered pieces.//1.6e-16:119:93//AC005910
F-PLACE2000100//HS_3184_A1_D06_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3184 Col=11 Row=G, genomic surveysequenc
e.//1.5e-80:409:97//AQ150004
F-PLACE2000103//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 20208, WORKING DRAFT SE
QUENCE.//1.0e-172:830:98//AL031848
F-PLACE2000111//Homo sapiens DNA, trinucleotide re
peats region.//1.0:200:64//AB018491
F-PLACE2000115
F-PLACE2000124//Homo sapiens Chromosome 16 BAC clo
ne CIT987SK-A-67A1, complete sequence.//6.2e-43:36
2:80//AC004531
F-PLACE2000132//RPCI11-79F15.TV RPCI11 Homo sapien
s genomic clone R-79F15, genomic survey sequence./
/5.4e-35:206:94//AQ284166
F-PLACE2000136//Human BAC clone 7E17 from 12q, com
plete sequence.//2.7e-12:814:59//AC002070
F-PLACE2000140//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 11703, WORKING DRAFT SE
QUENCE.//3.6e-165:799:97//AL020995
F-PLACE2000164//Canine histamine H2 receptor gene,
complete cds.//0.10:392:56//M32701
F-PLACE2000170
F-PLACE2000172//Homo sapiens PAC clone DJ0811017 f
rom 7q21-22, complete sequence.//3.9e-91:552:88//AC
006005
F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BA
C Clone b437g10 In BCRL2-CGT Region, complete sequ
ence.//0.98:201:64//AC004032
F-PLACE2000187
F-PLACE2000216
F-PLACE2000223//RPCI11-12L17.TP RPCI-11 Homo sapie
ns genomic clone RPCI-11-12L17, genomic survey seq
uence.//0.00039:325:58//B75888
F-PLACE2000235//Human Chromosome 16 BAC clone CIT9
87SK-254P9, complete sequence.//7.5e-55:237:78//AC
003003
F-PLACE2000246//Homo sapiens chromosome 3p clone R
PCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered
pieces.//2.4e-92:236:94//AC005902
F-PLACE2000264//Human DNA sequence from clone 3910
22 on chromosome 6p21.2-21.31 Contains pseudogenes

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similar to ribosomal protein, ESTs, GSSs, complete sequence. //1.4e-32:331:78//AL031577
 F-PLACE2000274//Anthracidaris crassispina mRNA for B2HC, partial cds. //8.5e-48:765:66//AB012308
 F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds. //8.3e-08:662:58//U52064
 F-PLACE2000305//Homo sapiens clone DJ1129L24, WORKING DRAFT SEQUENCE, 5unordered pieces. //2.4e-08:95:81//AC006021
 F-PLACE2000317//HS_3183_B2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L, genomic survey sequence. //2.5e-71:346:99//AQ172747
 F-PLACE2000335//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3unordered pieces. //3.7e-14:402:65//AC004952
 F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SHVT) mRNA, complete cds. //4.5e-77:555:82//AF026554
 F-PLACE2000342//Suid herpesvirus 1 UL5 gene, partial cds, UL6 and UL7 genes, complete cds, UL8 gene, partial cds. //1.8e-14:259:71//U66829
 F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmids R32543, , and F15613 containing ZNF gene family member, genomic sequence, complete sequence. //6.0e-34:376:74//AC003006
 F-PLACE2000359//RPCI11-23J20.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-23J20, genomic survey sequence. //8.4e-21:288:69//AQ013849
 F-PLACE2000366//Human Tigger1 transposable element, complete consensus sequence. //5.0e-114:692:80//U49973
 F-PLACE2000371//Homo sapiens 12p13.3 PAC RPCI1-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //0.38:356:58//AC005182
 F-PLACE2000373//RPCI11-49C18.TJ RPCI11 Homo sapiens genomic clone R-49C18, genomic survey sequence. //0.064:132:68//AQ051776
 F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence. //1.6e-130:776:88//AC003658
 F-PLACE2000394//Homo sapiens chromosome 18 BAC RPCI11-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //5.4e-113:808:83//AC005909
 F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene. //0.87:286:63//X06967
 F-PLACE2000399

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F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence. //2.9e-59:532:68//Z36238
 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds. //0.44:553:56//U89984
 F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds. //1.4e-56:303:86//M13792
 F-PLACE2000425//HS_3047_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=0, genomic survey sequence. //2.8e-42:224:97//AQ126949
 F-PLACE2000427
 F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence. //1.1e-19:363:67//AC005821
 F-PLACE2000435//HS_3036_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence. //3.1e-06:184:66//AQ096999
 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence. //4.6e-23:550:62//AL021492
 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence. //1.0e-78:604:80//AC006025
 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence. //8.2e-05:330:63//AC002300
 F-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //5.7e-168:816:97//AC005740
 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence. //4.3e-33:296:79//AC002037
 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11unordered pieces. //3.4e-59:598:74//AC005057
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds. //7.6e-49:361:84//U81602
 F-PLACE3000009//Human placenta (Diff48) mRNA, complete cds. //3.0e-58:713:69//U49187
 F-PLACE3000020//R. norvegicus type III adenylyl cyclase mRNA, complete cds. //6.1e-103:600:89//M55075
 F-PLACE3000029
 F-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme. //4.4e-115:718:86//Y17267
 F-PLACE3000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence. //1.8e-17:250:74//AC005368
 F-PLACE3000103//Caenorhabditis elegans cosmid C13F10. //4.6e-07:408:61//U97006

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F-PLACE3000119//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces. //1.5e-58:291:86//AC004670

F-PLACE3000121//Rattus norvegicus rsec15 mRNA, complete cds. //8.1e-81:837:71//AF032668

F-PLACE3000124//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence. //1.8e-48:330:79//AC005695

F-PLACE3000136

F-PLACE3000142//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE. //0.011:294:62//AL033520

F-PLACE3000145//Gallus gallus tensin mRNA, 3' end. //6.9e-52:659:68//L06662

F-PLACE3000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence. //5.1e-37:305:81//AL031053

F-PLACE3000148//Homo sapiens chromosome Y, clone 475I1, complete sequence. //4.7e-32:766:63//AC004474

F-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence. //7.4e-173:822:98//AC005277

F-PLACE3000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence. //2.2e-81:783:74//AC003682

F-PLACE3000157

F-PLACE3000158//, complete sequence. //1.0e-180:845:97//AC005500

F-PLACE3000160//CIT978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence. //0.080:259:59//B50878

F-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence. //9.8e-158:749:98//AC006130

F-PLACE3000194

F-PLACE3000197//F.rubripes GSS sequence, clone 075N04bB7, genomic survey sequence. //1.4e-08:164:68//AL003352

F-PLACE3000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE. //0.0019:277:58//Z82207

F-PLACE3000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence. //6.6e-21:312:67//AC005013

F-PLACE3000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds. //1.0:279:61//L23982

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F-PLACE3000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces. //9.3e-43:383:79//AC004086

F-PLACE3000220//RPCI11-54B4.TV RPCI11 Homo sapiens genomic clone R-54B4, genomic survey sequence. //2.4e-36:381:76//AQ082056

F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces. //7.2e-135:721:91//AC005231

F-PLACE3000226

10 F-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence. //3.3e-80:498:78//U95626

F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence. //2.6e-54:254:92//Z98046

F-PLACE3000244//M.musculus mRNA for 200 kD protein. //1.4e-139:850:86//X80169

F-PLACE3000254//Ateline herpesvirus 3 complete genome. //1.3e-10:399:61//AF083424

F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence. //1.8e-21:350:68//AF001548

F-PLACE3000276//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence. //5.7e-45:376:81//AQ231147

F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence. //1.6e-138:650:99//AC005328

F-PLACE3000310

F-PLACE3000320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //1.9e-41:379:77//AL034379

40 F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence. //3.3e-35:419:68//AC005822

F-PLACE3000331//CIT-HSP-2347D24.TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence. //2.7e-20:119:99//AQ061543

F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and Bch0 (bch0) gene, partial cds. //0.99:310:58//AF017642

50 F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC

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I4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //7.5e-159:752:98//ACO06055

F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TA01 mRNA, complete cds. //2.3e-107:592:92//AF084205

F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence. //2.1e-37:480:70//Z83732

F-PLACE3000353

F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence. //0.00011:373:60//AC005969

F-PLACE3000363

F-PLACE3000365//Human DNA sequence from PAC 227P1 7, between markers DXS6791 and DXS8038 on chromosome X contains CpG island, EST. //0.074:279:61//Z81007

F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat. //2.8e-118:653:92//Z92545
F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence. //2.2e-25:288:71//AC005154

F-PLACE3000399//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE. //2.3e-69:303:86//Z97630

F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence. //0.0063:435:58//Z93239

F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces. //5.8e-25:292:73//AC006023

F-PLACE3000402//RPCI11-20D6.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-20D6, genomic survey sequence. //1.1e-10:154:74//AQ008761

F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence. //2.9e-41:515:72//AC005701

F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-179E11, genomic survey sequence. //2.8e-91:540:89//B03443

F-PLACE3000413

F-PLACE3000416//F19L8-Sp6 IGF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence. //0.018:664:55//B11305

F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, com

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plete sequence. //1.1e-16:284:70//AL022719

F-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE. //3.6e-146:732:96//AL031284

F-PLACE3000475//HS_2164_A2_H10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=0, genomic survey sequence. //1.5e-07:159:71//AQ132983

10 F-PLACE3000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs. //2.9e-11:213:70//Z83843

F-PLACE4000009//Sequence 93 from patent US 5616500. //9.9e-08:692:60//I39845

F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds. //1.1e-116:331:100//AB018352

F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence. //5.0e-05:244:63//AC004131

20 F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence. //1.2e-37:385:74//AC005926

F-PLACE4000052//M.musculus abc1 mRNA. //1.5e-110:671:88//X75926

F-PLACE4000063

F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation. //3.7e-12:114:85//X74311

30 F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence. //0.11:245:60//AQ108342

F-PLACE4000100//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE. //2.9e-19:384:65//AL031848

F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds. //1.2e-145:684:99//AB007931

F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds. //3.7e-62:541:78//AF091234

40 F-PLACE4000129

F-PLACE4000131//HS_3139_B2_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence. //2.3e-14:221:70//AQ183207

F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5(IV) Chain Precursor. Contains GSSs, complete sequence. //0.28:412:58//AL031622

50 F-PLACE4000156//Human zinc finger protein ZNF136./

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/7.2e-88:764:76//U09367
 F-PLACE4000192
 F-PLACE4000211
 F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158
 F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430
 F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//A 10 C003973
 F-PLACE4000247
 F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673
 F-PLACE4000252
 F-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200
 F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71 20 //AF084259
 F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667
 F-PLACE4000270
 F-PLACE4000300
 F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075
 F-PLACE4000323//HS_2165_B1_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036
 F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M1 0296
 F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401
 F-PLACE4000367
 F-PLACE4000369
 F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661
 F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649
 F-PLACE4000392//Rattus norvegicus polymorphic marker D20UIA1 sequence.//1.2e-05:222:68//AF054088
 F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds.//9.6e-46:605:71//AB014540 50

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F-PLACE4000411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984
 F-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200
 F-PLACE4000445//HS-1053-B1-D02-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346
 F-PLACE4000450
 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//2.3e-07:273:65//AC005065
 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//4.1e-34:351:70//AC005821
 F-PLACE4000489//HS_3012_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537
 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-106 3M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865
 F-PLACE4000521//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929
 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch2-C, partial cds.//4.0e-124:686:90 //U47645
 F-PLACE4000548 30
 F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747
 F-PLACE4000581
 F-PLACE4000590//Homo sapiens chromosome Y, clone 475I1, complete sequence.//3.6e-20:747:59//AC004474
 F-PLACE4000593//Caenorhabditis elegans cosmid F25D 7, complete sequence.//5.6e-16:326:65//Z78418
 F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.7e-163:78 40 5:97//AC005281
 F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3unordered pieces.//8.7e-74:707:74//AC006039
 F-PLACE4000650
 F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267
 F-PLACE4000670//Sequence 13 from patent US 571238 1.//1.0:311:59//I82816
 F-SKNMC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577

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F-SKNMC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312
 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.6e-147:706:98//AB014554
 F-SKNMC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//ARO20616
 F-SKNMC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797
 F-THYR01000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561
 F-THYR01000026//Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NC F4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637
 F-THYR01000034//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353
 F-THYR01000035//Human Chromosome X clone bWXD187, complete sequence.//1.2e-39:303:83//AC004383
 F-THYR01000040
 F-THYR01000070//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383
 F-THYR01000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557
 F-THYR01000085
 F-THYR01000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606
 F-THYR01000107
 F-THYR01000111//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403
 F-THYR01000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//1.4e-127:816:85//U49055
 F-THYR01000124//H.sapiens CpG island DNA genomic Msel fragment, clone 72a7, forward read cpg72a7.ft1a.//9.5e-26:169:94//Z62724
 F-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142
 F-THYR01000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096
 F-THYR01000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a p

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utative Homeobox (pseudo?) gene, ESTs and anSTS, complete sequence.//1.2e-21:335:71//AL023574
 F-THYR01000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331
 F-THYR01000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419
 F-THYR01000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207
 F-THYR01000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214
 F-THYR01000190//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//0.38:184:64//AC005746
 F-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698
 F-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552
 F-THYR01000206//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134
 F-THYR01000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157
 F-THYR01000241//Callus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186
 F-THYR01000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156
 F-THYR01000253//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC006055
 F-THYR01000270
 F-THYR01000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664
 F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068
 F-THYR01000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894
 F-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233
 F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333
 F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091

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F-THYR01000368//Caenorhabditis elegans cosmid W09C3, complete sequence.//0.97:206:60//Z82080

F-THYR01000381//Arthrobacter sp. glcI gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668

F-THYR01000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019

F-THYR01000394//HS_2061_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672

F-THYR01000395//Drosophila melanogaster ring canel protein and ORF2 mRNA, complete cds.//4.3e-15:512:59//L08483

F-THYR01000401

3.2e-116:504:80//AF051908

F-THYR01000438//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-09:539:59//AC005308

F-THYR01000452//RPCI11-1C19.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1C19, genomic survey sequence.//0.27:132:64//B49573

F-THYR01000471//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.3e-38:332:81//AC005229

F-THYR01000484//Homo sapiens BAC378, complete sequence.//2.2e-37:254:76//U85196

F-THYR01000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740

F-THYR01000501//H.sapiens Staf50 mRNA.//9.8e-74:615:77//X82200

F-THYR01000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056

F-THYR01000505

F-THYR01000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563

F-THYR01000569//HS_2178_B2_E03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499

F-THYR01000570

F-THYR01000585//Homo sapiens protein associated wi

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th Myc mRNA, complete cds.//7.4e-167:808:97//AF075587

F-THYR01000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323

F-THYR01000602//HS_3037_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057

10 F-THYR01000605//Homo sapiens map 2p11.2; 83cM from GATA85A06 repeat region, complete sequence.//1.0:84:70//AF067777

F-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546

F-THYR01000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474

20 F-THYR01000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559

F-THYR01000658//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//1.1e-68:468:84//AC005696

F-THYR01000662//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0072:141:70//AB016874

F-THYR01000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437

30 F-THYR01000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778

F-THYR01000684//Fugu rubripes cosmid 165K09 DNA for GRW7, TRIP, Sand, PRGFR3 genes.//6.6e-13:236:69//AJ010317

F-THYR01000699//RPCI11-50D4.TK RPCI11 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641

F-THYR01000712//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//5.2e-17:290:67//AC005053

F-THYR01000715//Bovine herpesvirus type 1 early-in intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320

F-THYR01000734//HS_3233_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143

F-THYR01000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871

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F-THYR01000756//M.musculus mRNA for Gal beta1, 3GalNAc alpha2,3-sialyltransferase.//0.00034:349:60//X73523

F-THYR01000777//S.griseus str0 gene and sts gene cluster.//8.2e-05:625:59//Y08763

F-THYR01000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373

F-THYR01000787//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986

F-THYR01000793

F-THYR01000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422

F-THYR01000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468

F-THYR01000815//Homo sapiens chromosome 5, BAC clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914

F-THYR01000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053

F-THYR01000843

F-THYR01000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782

F-THYR01000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:64//AF008573

F-THYR01000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477

F-THYR01000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720

F-THYR01000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015

F-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//9.2e-178:839:98//AF079529

F-THYR01000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836

F-THYR01000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229

F-THYR01000952

F-THYR01000974//HS_3238_B2_F01_MR CIT Approved Hum

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an Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//2.4e-26:154:96//AQ219846

F-THYR01000975//Plasmodium falciparum TopoII gene.//0.32:491:58//X79345

F-THYR01000983//Mv9A3 exon amplification products from BACs in Mv9A region Mus musculus genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457

F-THYR01000984//CIT-HSP-2167017.TR CIT-HSP Homo sapiens genomic clone 2167017, genomic survey sequence.//0.00015:186:66//B91313

F-THYR01000988//Human Chromosome 11q12.2 PAC clone pDJ756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588

F-THYR01001003

F-THYR01001031//Homo sapiens chromosome 17, clone hRPC.859_0_20, complete sequence.//1.1e-55:543:72//AC003695

F-THYR01001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799

F-THYR01001062//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320

F-THYR01001093//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//4.9e-34:353:76//AC006241

F-THYR01001100//Human DNA-binding protein mRNA, 3' end.//1.1e-72:742:74//L14787

F-THYR01001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522

F-THYR01001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 671014, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595

F-THYR01001133//Homo sapiens PAC clone DJ1200I23 from 7p15, complete sequence.//4.0e-35:349:76//AC004996

F-THYR01001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486

F-THYR01001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178

F-THYR01001173

F-THYR01001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953

F-THYR01001189//HS_3171_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl

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one Plate=3171 Col=20 Row=L, genomic surveysequence. //1.8e-28:246:83//AQ302330
 F-THYR01001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds. //4.9e-39:657:64//U34925
 F-THYR01001213//, complete sequence. //1.7e-45:257:84//AC005300
 F-THYR01001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE. //1.5e-40:274:87//AP000036
 F-THYR01001271//Streptomyces coelicolor cosmid 1A6. //0.033:364:61//AL023496
 F-THYR01001287//Drosophila melanogaster cosmid clone 86E4. //9.6e-49:586:69//AL021086
 F-THYR01001290//HS_2045_B1_H09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic surveysequence. //4.4e-13:156:78//AQ248237
 F-THYR01001313//S. lavendulae bla gene for beta-lactamase, complete cds. //1.0:229:64//D12693
 F-THYR01001320//Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-CGT Region, complete sequence. //1.1e-88:672:82//AC002472
 F-THYR01001321//Human PAC clone DJ527C21 from Xq23, complete sequence. //1.2e-115:740:87//AC000114
 F-THYR01001322//HS_3205_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic surveysequence. //0.00031:285:61//AQ304025
 F-THYR01001347//Homo sapiens mRNA for KIAA0745 protein, partial cds. //2.2e-43:638:64//AB018288
 F-THYR01001363//Homo sapiens PAC clone DJ0845I21 from 7q11.21-q11.23, complete sequence. //1.0e-09:189:74//AC004905
 F-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence. //7.6e-168:821:97//AC005660
 F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds. //2.3e-155:740:97//AB014607
 F-THYR01001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence. //3.2e-07:138:73//AC005239
 F-THYR01001403//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces. //3.6e-70:360:86//AC005845
 F-THYR01001405//Bos taurus mRNA for NDP52, complete cds. //2.6e-14:559:63//AB008852
 F-THYR01001406//Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds. //1.0e-91:631:82//AF064635

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F-THYR01001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence. //5.5e-42:509:71//AC006126
 F-THYR01001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118122) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE. //2.7e-31:172:81//AJ002553
 F-THYR01001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces. //1.0:98:70//AC000384
 F-THYR01001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds. //1.9e-58:653:71//U87265
 F-THYR01001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces. //7.5e-42:357:80//AC006001
 F-THYR01001487//H. sapiens DNA sequence. //0.92:160:64//Z22449
 F-THYR01001534//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces. //4.8e-47:266:80//AC004666
 F-THYR01001537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE. //1.3e-79:479:89//AL031687
 F-THYR01001541//Human DNA sequence from clone 399M14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence. //0.0034:106:77//Z96074
 F-THYR01001559//Rattus norvegicus simple sequence repeat D18Mco6. //1.6e-09:351:63//AF006056
 F-THYR01001570//RPCI11-49B23. TJ RPCI11 Homo sapiens genomic clone R-49B23, genomic survey sequence. //1.4e-65:384:91//AQ052105
 F-THYR01001573//Homo sapiens clone 24778 unknown mRNA. //8.2e-104:546:95//AF070572
 F-THYR01001584//CIT-HSP-2365J21. TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence. //1.3e-24:180:88//AQ080498
 F-THYR01001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE. //8.7e-145:779:93//AL023808
 F-THYR01001602//Homo sapiens chromosome 17, clone hRPK.786_0_4, complete sequence. //2.9e-26:393:68//AC005863
 F-THYR01001605//Dictyostelium discoideum filopodin (talA) gene, complete cds. //0.0012:436:58//U14576
 F-THYR01001617//Homo sapiens full length insert cDNA clone ZD69D05. //8.6e-43:342:82//AF086381
 F-THYR01001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces. //6.2e-15:318:66//AC004950

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F-THYR01001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827
 F-THYR01001661
 F-THYR01001671//Homo sapiens mRNA for 2'-5' oligo adenylate synthetase 59kDa isoform.//2.5e-164:780:98//AJ225089
 F-THYR01001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071
 F-THYR01001703//S.coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857
 F-THYR01001706//Homo sapiens BAC clone RG281B09 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745
 F-THYR01001721//, complete sequence.//9.9e-134:770:91//AC005500
 F-THYR01001738//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327
 F-THYR01001745
 F-THYR01001746
 F-THYR01001772//HS_3069_B1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021
 F-THYR01001793//B.taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626
 F-THYR01001809
 F-THYR01001828//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526
 F-THYR01001854//Homo sapiens chromosome 17, clone hC1754K19, complete sequence.//7.9e-07:445:59//AC03664
 F-THYR01001895
 4.4e-13:248:68//AB012576
 F-THYR01001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058
 F-VESEN1000122//HS_3075_B1_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749
 F-Y79AA1000013
 F-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027
 F-Y79AA1000037//Human prot-oncogene (BMI-1) mRNA, complete cds.//2.4e-19:230:66//L13689

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F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521
 F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:117:83//Z72005
 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-10:381:64//U92893
 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//1.4e-165:732:99//AL031864
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.//9.1e-20:339:65//AC005115
 F-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33unordered pieces.//3.7e-72:397:93//AC004854
 F-Y79AA1000230
 20 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cds.//8.5e-151:833:90//AF053232
 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosphatase(SAcP-1) gene, complete cds.//0.0099:547:58//U78522
 F-Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.//4.0e-11:424:62//AF035207
 F-Y79AA1000313
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//5.9e-07:173:69//B55085
 F-Y79AA1000342//RPCI11-57J6.TK.1 RPCI11 Homo sapiens genomic clone R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.7e-69:694:71//X92987
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8e-98:535:92//X84692
 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3unordered pieces.//1.6e-21:129:85//AC005484
 F-Y79AA1000368//H.sapiens CpG island DNA genomic Msel fragment, clone 12f1, reverse read cpg12f1.rt1c.//0.00016:53:98//Z56610
 F-Y79AA1000405//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL031747
 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome X.//1.0e-25:235:80//Z86061
 F-Y79AA1000420//H.sapiens CpG island DNA genomic Msel fragment, clone 82c3, forward read cpg82c3.ft1

- a. //2.0e-36:194:98//Z63378
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds. //8.5e-121:696:89//U41736
 F-Y79AA1000480//HS_2175_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=0, genomic surveysequence. //2.5e-26:178:89//AQ307693
 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUENCE, 23unordered pieces. //0.67:111:72//AC004980
 F-Y79AA1000539//HS_2237_B2_F10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, genomic surveysequence. //1.2e-14:168:77//AQ153503
 F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUENCE, 8unordered pieces. //0.94:127:67//AC005193
 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C). //1.7e-114:776:84//X14972
 F-Y79AA1000574//M.musculus tex23 mRNA (5' region). //1.8e-23:291:75//X80424
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence. //8.6e-153:755:97//AF091080
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, completecds. //5.2e-135:644:98//AF060503
 F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1. //6.9e-148:902:86//X69942
 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assembly factor, complete cds. //4.8e-180:850:98//AB018080
 F-Y79AA1000748//Caenorhabditis elegans cosmid F25B5. //0.00019:308:60//U23172
 F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein. //1.7e-40:513:68//AJ003023
 F-Y79AA1000774
 F-Y79AA1000782
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds. //3.5e-177:847:97//AF098799
 F-Y79AA1000794//H.sapiens CpG island DNA genomic Msel fragment, clone 45a4, forward read cpg45a4.ft1a. //2.5e-13:104:92//Z61120
 F-Y79AA1000800//Homo sapiens CABA-B receptor mRNA, complete cds. //0.98:244:60//AF056085
 F-Y79AA1000802
 F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence. //9.3e-76:528:85//U73642
 F-Y79AA1000824//RPCI11-26B4.TP RPCI-11 Homo sapiens genomic clone RPCI-11-26B4, genomic survey sequence. //4.4e-14:99:95//B84538
 F-Y79AA1000827//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE. //1.5e-08:249:69//AL022315
 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin. //1.8e-103:603:89//X04757
 F-Y79AA1000850
 F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat. //0.038:468:59//Z82203
 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds. //9.7e-150:865:89//AF071314
 F-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit(eIF-2B gamma) mRNA, complete cds. //6.4e-122:717:88//U38253
 F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics mouse BAC library) complete sequence. //1.0:155:63//AC002397
 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1. //4.3e-06:130:73//U88165
 F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds. //2.4e-44:428:77//U05823
 F-Y79AA1001023
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds. //2.3e-13:90:100//U63329
 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds. //2.6e-28:772:60//D43682
 F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, complete sequence. //9.4e-36:292:82//AC004701
 F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces lividans, Genomic, 1146 nt]. //0.17:537:59//S64314
 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase -2, complete cds. //0.17:231:64//D88452
 F-Y79AA1001078
 F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete cds. //3.1e-63:529:77//D26173
 F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces. //1.3e-23:228:76//AC005015
 F-Y79AA1001167
 F-Y79AA1001177//M.musculus mRNA for NfiX1-protein. //4.0e-10:398:64//Y07688
 F-Y79AA1001185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE. //1.1e-113:666:90//Z93015
 F-Y79AA1001211//HS_3124_B2_H08_MR CIT Approved Human

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an Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic surveysequence. //5.5e-12:87:96//AQ187492

F-Y79AA1001216

F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. //0.028:188:67//AL021841

F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogenase mRNA, complete cds. //3.5e-24:731:60//M36263

F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110i133Q7 (RZPD Berlin)). //1.2e-133:441:97//AJ005892

F-Y79AA1001281//HS_2241_B2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, genomic surveysequence. //5.0e-27:169:94//AQ217497

F-Y79AA1001299//Human Ini1 mRNA, complete cds. //6.7e-115:323:93//U04847

F-Y79AA1001312

F-Y79AA1001323

F-Y79AA1001384

F-Y79AA1001391//Mus musculus transcription factor HoxA13 (Hoxa13) gene, complete cds. //5.8e-42:245:74//U59322

F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequence. //7.8e-18:636:58//Z48583F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer

Institute Human PAC Library) complete sequence. //1.2e-110:738:85//AC005924

F-Y79AA1001493//H. sapiens DNA sequence. //2.0e-27:254:82//Z22497

F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence. //1.1e-158:804:95//AL034430

F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds. //1.7e-100:820:78//D14336

F-Y79AA1001541//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic surveysequence. //5.1e-28:218:86//AQ150183

F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complete sequence. //5.4e-21:167:86//AC004151

F-Y79AA1001555//R. norvegicus mRNA for drebrin A. //0.88:463:59//X59267

F-Y79AA1001581//FMR1 {CGG repeats} [human, Fragile 50

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X syndrome patient, Genomic, 429 nt]. //0.00051:252:65//S74494

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds. //7.2e-33:375:76//M26434

F-Y79AA1001594

F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence. //4.2e-06:338:66//AF064861

F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds. //0.024:520:57//AB014583

F-Y79AA1001647//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE. //0.014:331:61//Z92860

F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence. //0.99:273:63//Z84468

F-Y79AA1001679//O. cuniculus lambda-crystallin mRNA A, complete cds. //1.2e-97:682:81//M22743

F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4]. //5.6e-05:426:59//S37712

F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyprotein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds. //1.0:437:60//D32136

F-Y79AA1001705//M. musculus fkh-5 gene. //0.18:153:64//X71943

30 F-Y79AA1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE. //5.4e-76:191:98//AL022240

F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE. //0.99:227:63//AP000017

F-Y79AA1001805//H. sapiens CpG island DNA genomic Msel fragment, clone 13d12, reverse read cpg13d12.r1c. //2.6e-13:88:100//Z64565

F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds. //3.7e-130:775:88//U74297

F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence. //8.3e-17:218:76//AQ012369

F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds. //4.2e-10:378:62//AB002388

F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKrl) mRNA, complete cds. //6.9e-41:441:71//U41164

F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, com

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plete cds.//0.00017:412:62//AF029779
 F-Y79AA1001875//CIT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654
 F-Y79AA1001923//H.sapiens CpG island DNA genomic Msel fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186
 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ0261184
 F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
 F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
 F-Y79AA1002089
 F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
 F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
 F-Y79AA1002115
 F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
 F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
 F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
 F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
 F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
 F-Y79AA1002211//Homo sapiens chromosome 17, clone HRP1067M6, complete sequence.//1.0e-06:241:67//AC003043
 F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045

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F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
 F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555
 F-Y79AA1002298//Human density enhanced phosphatase -1 mRNA, complete cds.//0.036:278:62//U10886
 10 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
 F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
 F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101
 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
 20 F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.0e-159:411:100//AC005920
 F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662
 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//4.4e-90:529:88//U49385
 F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196
 30 F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
 F-Y79AA1002482//Homo sapiens full length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
 40 F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27, 28, 29, 30, 31].//0.93:215:60//X94677
 【1124】 同源性検索結果データ 3.
 3'末端クローン配列に対するESTとSTSを除いたGenBank 同源性検索結果データ
 各データは、クローン配列名、トップヒットデータのDefinition、P値:比較配列の長さ (base):同源性(%), トップヒットデータのAccession No.の順に//で区切って記載した。なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。同源性のスコアのP値が1より大であった場合はデータは示さ

ない。

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein
1 mRNA, complete cds.//3.6e-60:504:78//L16953
R-HEMBA1000030//F.rubripes GSS sequence, clone 063
K10bD3, genomic survey sequence.//0.28:117:68//Z888
64
R-HEMBA1000042//RPC11-77G23.TV RPC11 Homo sapien
s genomic clone R-77G23, genomic survey sequence.//
/1.3e-56:292:97//AQ268240
R-HEMBA1000046//Homo sapiens chromosome X map Xq2
8, complete sequence.//9.8e-56:401:82//U82696
R-HEMBA1000050//Human cosmid insert containing pol
ymorphic marker DXS455.//0.0010:175:68//L31948
R-HEMBA1000076//Homo sapiens clone DJ1021120, WORK
ING DRAFT SEQUENCE, 6unordered pieces.//4.9e-41:36
4:79//AC005520
R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5
(Genome Systems Human BAC library) complete sequen
ce.//4.7e-30:229:84//AC003684
R-HEMBA1000129//Homo sapiens chromosome 17, clone
HCIT48C15, complete sequence.//2.4e-93:503:93//AC0
03104
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 pro
tein, partial cds.//6.5e-99:514:94//AB018340
R-HEMBA1000150//Homo sapiens clone RG086D03, WORKI
NG DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:28
9:83//AC005060
R-NNNNNNNNNNNN//Homo sapiens scaffold attachment f
actor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64/
/L43631
R-HEMBA1000158
R-NNNNNNNNNNNN
R-HEMBA1000180//Plasmodium falciparum encoding Pfg
27/25.//0.073:292:56//X84904
R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORK
ING DRAFT SEQUENCE, 7unordered pieces.//5.3e-40:28
6:85//AC006146
R-HEMBA1000193
R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon
9.//2.0e-24:137:99//Y17126
R-HEMBA1000213//Caenorhabditis elegans cosmid C44C
8.//0.025:192:68//AF100655
R-HEMBA1000216//Human Chromosome 16 BAC clone CIT9
87SK-A-815A9, complete sequence.//2.5e-31:269:79//A
F001548
R-NNNNNNNNNNNN
R-HEMBA1000231//Human DNA sequence from PAC 212P9
on chromosome 1p34.1-1p35. Contains delta opiate r
eceptor, CpG island, CA repeat.//4.3e-24:400:68//
AL009181

R-HEMBA1000243//Homo sapiens chromosome 17, Neurof
1bromatosis 1 locus, complete sequence.//1.3e-19:3
19:69//AC004526
R-HEMBA1000244
R-HEMBA1000251//Meloidogyne hapla mitochondrial CO
II gene, 3' end of cds; transfer RNA-His gene; 16S
ribosomal RNA gene; ND3 gene, complete cds; cytoch
rome b (cytb) gene, 5' end of cds.//0.16:338:60//L
76262
R-HEMBA1000264//Homo sapiens genomic DNA, chromoso
me 21q22.2 (Down Syndrome region), segment 5/15, W
ORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012
R-NNNNNNNNNNNN//Homo sapiens Xp22 BAC GSHB 526D21
(Genome Systems HumanBAC library) complete sequenc
e.//3.5e-10:238:70//AC003037
R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.
//0.71:344:60//AF007270
R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4
and RPC11-164K3 complete sequence.//4.8e-33:267:8
2//AC003046
R-HEMBA1000290//Homo sapiens chromosome 17, clone
HRPC837J1, complete sequence.//2.2e-15:249:69//AC0
04223
R-HEMBA1000302//CIT-HSP-2173N10. TF CIT-HSP Homo sa
piens genomic clone 2173N10, genomic survey sequen
ce.//1.0:215:61//B95105
R-NNNNNNNNNNNN//Mus musculus Plenty of SH3s (POSH)
mRNA, complete cds.//1.0e-77:551:82//AF030131
R-NNNNNNNNNNNN//Rattus norvegicus Ca2+-dependent a
ctivator protein (CAPS) mRNA, complete cds.//2.0e-
96:546:90//U16802
R-HEMBA1000307//Mus musculus mRNA for CDV-1 protei
n.//3.8e-36:315:68//Y10496
R-NNNNNNNNNNNN//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC181 genomic sequence, WORKING DRAFT SEQU
ENCE, 8 unordered pieces.//0.078:379:59//AC005505
R-HEMBA1000338//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 620E11, WORKING DRAFT S
EQUENCE.//2.0e-33:399:72//AL031667
R-HEMBA1000351//Homo sapiens complete genomic sequ
ence between D16S3070 and D16S3275, containing Fami
lial Mediterranean Fever gene disease.//1.7e-39:27
2:87//AJ003147
R-HEMBA1000355//Human primary Alu transcript.//0.0
045:67:85//U67829
R-HEMBA1000357//Homo sapiens (subclone 9_h8 from P
1 H16) DNA sequence.//8.7e-93:426:88//L42086
R-HEMBA1000366//Homo sapiens PAC clone DJ0942I16 f
rom 7q11, complete sequence.//1.7e-12:130:83//AC00
6012

3467

R-HEMBA1000369//Human DNA sequence from clone 1039 K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, genes similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587

R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//3.7e-66:410:89//AC006116

R-HEMBA1000387//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993

R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053

R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582

R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575

R-HEMBA1000411

R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465

R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233

R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93:526:90//Z95400

R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826

R-HEMBA1000442//E.caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733

R-HEMBA1000456//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226

R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein Glp(AtG1), putative nuclear DNA-binding protein G2p (AtG2), Eml protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), putative acyl-coA dehydrogenase (AtG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236

R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839

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R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220

R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104

R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500

R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278

R-HEMBA1000491

10 R-HEMBA1000504//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014

R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858

R-HEMBA1000508//Human DNA sequence from cosmid V21OE9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280

20 R-HEMBA1000518//RPCI11-6022.TV RPCI-11 Homo sapiens genomic clone RPCI-11-6022, genomic survey sequence.//0.0035:293:61//B49544

R-HEMBA1000519

R-HEMBA1000520//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232

R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782

30 R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638

R-HEMBA1000540//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC Library) complete sequence.//6.9e-87:552:87//AC004103

R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555

R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381

R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762

R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368

50 R-HEMBA1000568//RPCI11-49P8.TK.1 RPCI11 Homo sapie

3469

ns genomic clone R-49P8, genomic survey sequence. /
/1.7e-101:498:97//AQ116293
R-nnnnnnnnnnnnn
R-HEMBA1000575//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 754E20, WORKING DRAFT S
EQUENCE. //1.3e-47:458:75//AL022335
R-HEMBA1000588//Mus musculus FLI-LRR associated pr
oteins-1 mRNA, complete cds. //2.9e-62:447:81//AF0455
73
R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-as
sociated protein. //1.2e-111:591:94//AJ007509
R-HEMBA1000592//Plasmodium falciparum DNA *** SEQU
ENCING IN PROGRESS *** from contig 4-10, complete s
equence. //3.5e-09:421:60//AL010216
R-HEMBA1000594//Homo sapiens clone RG004N09, WORKI
NG DRAFT SEQUENCE, 5 unordered pieces. //1.1e-15:42
1:66//AC005044
R-HEMBA1000604//HS_2220_A1_G10_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2220 Col=19 Row=M, genomic survey sequenc
e. //1.0e-51:306:92//AQ151991
R-HEMBA1000608
R-HEMBA1000622//H.sapiens CpG island DNA genomic M
sel fragment, clone 155e4, reverse read cpg155e4.r
tla. //4.5e-16:105:98//Z56962
R-HEMBA1000636//Homo sapiens genomic DNA, chromoso
me 21q22.2 (Down Syndrome region), segment 1/15, W
ORKING DRAFT SEQUENCE. //4.8e-62:421:86//AP000008
R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 pro
tein, partial cds. //1.2e-97:443:97//AB014590
R-HEMBA1000655//Homo sapiens chromosome 19, cosmid
R26349, complete sequence. //9.8e-61:311:90//AC005
953
R-HEMBA1000657
R-HEMBA1000662
R-HEMBA1000673//Human DNA sequence from PAC 448E20
on chromosome Xq26.1 contains ESTs and STS. //1.0e-
13:351:63//Z97196
R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORK
ING DRAFT SEQUENCE, 4 unordered pieces. //1.2e-50:29
8:79//AC005377
R-HEMBA1000686//HS_3018_B1_H10_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3018 Col=19 Row=P, genomic survey sequenc
e. //0.00048:210:62//AQ093513
R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKI
NG DRAFT SEQUENCE, 7 unordered pieces. //9.7e-54:31
7:88//AC005000
R-HEMBA1000705//Glossonotus univittatus 12S mitoch
ondrial ribosomal RNA, small subunit, mitochondrial

3470

gene, partial sequence. //0.080:138:65//U77850
R-HEMBA1000719//Rattus norvegicus mRNA for TESK1,
complete cds. //0.96:291:58//D50864
R-HEMBA1000722
R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 f
rom 7q33-q36, complete sequence. //4.4e-26:284:77//A
C005531
R-HEMBA1000727//Plasmodium falciparum DNA *** SEQU
ENCING IN PROGRESS *** from contig 4-89, complete s
equence. //9.1e-05:351:60//AL010266
R-HEMBA1000747//Homo sapiens DNA sequence from PAC
124C6 on chromosome 6q21. Contains genomic marker
D6S1603, ESTs, GSSs and a STS with a CA repeat po
lymorphism, complete sequence. //2.5e-16:123:93//AL
021326
R-HEMBA1000749//Human Chromosome 16 BAC clone CIT9
87SK-327024, complete sequence. //2.8e-32:298:79//AC
003108
R-HEMBA1000752//Human DNA sequence from PAC 50A13
on chromosome Xp11. Contains ATP SYNTHASE LIPID BI
NDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G
2, ATP5G3) like pseudogene, ESTs and STSs. Contain
s polymorphic CA repeat. //2.8e-90:542:90//Z92545
R-HEMBA1000769//Homo sapiens P1 clone GSP13996 fro
m 5q12, complete sequence. //2.7e-36:405:75//AC0050
31
R-HEMBA1000773//HS_3050_A2_B08_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3050 Col=16 Row=C, genomic survey sequenc
e. //0.00053:268:60//AQ105619
R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 f
rom 7q31-q32, complete sequence. //4.7e-46:338:85//A
C004690
R-HEMBA1000791//ALU WARNING: Human Alu-Sc subfa
mily consensus sequence. //5.3e-47:279:91//U14571
R-HEMBA1000817//Sequence 1 from Patent WO 8904839.
//0.86:148:67//I09339
R-HEMBA1000822//T.brucei kinetoplast maxicircle va
riable region DNA. //0.00061:246:61//Z15118
R-HEMBA1000827//Homo sapiens Ser/Arg-related nucle
ar matrix protein (SRM160) mRNA, complete cds. //6.
9e-43:228:98//AF048977
R-HEMBA1000843//Homo sapiens DNA sequence from clo
ne 511B24 on chromosome 20q11.2-12. Contains the T
OP1 gene for Topoisomerase I, the PLCG1 gene for 1-
Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase
Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase
C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a
probable Zinc Finger Homeobox protein and a 60S
Ribosomal Protein L23 LIKE pseudogene. Contain

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s a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC I4-617A9 (Roswell ParkCancer Institute Human PAC L library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT987SK-A-180G2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from 7q31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-2373I4.TR CIT-HSP Homo sapiens genomic clone 2373I4, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T.pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPCI11-68E14.TK RPCI11 Homo sapiens genomic clone R-68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RC350L10, WORKING DRAFT SEQUENCE, 15unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//T5N8TFB TAMU Arabidopsis thaliana genomic clone T5N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RC339C12, WORKING DRAFT SEQUENCE, 10unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 conta

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ining MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPCI11-54D1.TJ RPCI11 Homo sapiens genomic clone R-54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-05:306:63//AC004888

R-HEMBA1000986//Homo sapiens clone RC031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPCI11-22017.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O.sativa osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

R-HEMBA1001020//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

40 R-HEMBA1001024//Homo sapiens BAC clone 393I22 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-nnnnnnnnnnnnn//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPCI3-521 E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

3473

R-HEMBA1001052//Rabbit alpha-1-globin gene to the alpha-1-globin pseudogene region. //2.4e-24:279:74//X04751

R-HEMBA1001060//HS_2056_B1_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence. //4.1e-14:137:83//AQ245004

R-HEMBA1001071//M.musculus COL3A1 gene for collagen alpha-1. //6.9e-38:513:70//X52046

R-HEMBA1001077//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE. //1.9e-22:507:61//AL022318

R-HEMBA1001080

R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces. //2.2e-43:317:83//AC004586

R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7. //0.46:301:60//AF067607

R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence. //5.3e-98:501:96//AC005105

R-HEMBA1001099

R-HEMBA1001109//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE. //3.1e-39:335:80//AL033527

R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2. //9.8e-11:122:81//U81833

R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence. //0.0024:284:63//Z98551

R-HEMBA1001123//Human NFE genomic fragment. //3.6e-26:318:72//M98511R-HEMBA1001133

R-HEMBA1001137//Homo sapiens full length insert cDNA clone ZD29F04. //4.2e-88:426:98//AF086241

R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //4.0e-41:304:84//AC005077

R-HEMBA1001172//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE. //3.7e-36:261:85//Z98304

R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence. //1.0:219:58//AE001398

R-HEMBA1001197

R-HEMBA1001208//HS_2233_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence. //0.083:174:68//AQ170789

R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces. //5.1e-59:553:75//AC005377

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R-HEMBA1001235//RPC111-50E6.TJ RPC111 Homo sapiens genomic clone R-50E6, genomic survey sequence. //2.6e-08:97:76//AQ052666

R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1. //2.4e-05:319:63//U58761

R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds. //1.5e-24:439:66//U89905

R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence. //9.9e-21:537:63//AC004491

R-nnnnnnnnnnnnn//Homo sapiens chromosome 17, clone HCIT75G16, complete sequence. //0.022:169:65//AC003042

R-HEMBA1001286

R-HEMBA1001289

R-HEMBA1001294//HS_3219_A2_G01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence. //0.24:251:63//AQ189882

R-HEMBA1001299//Homo sapiens, clone hRPK.12_A_1, complete sequence. //1.3e-38:381:76//AC006222

R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell. //4.1e-28:114:92//E12258

R-HEMBA1001303//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE. //0.00011:382:58//AL031744

R-HEMBA1001310

R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //4.2e-09:491:58//AC005504

R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule. //8.3e-06:485:60//X03240

R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with abeta-galacturonidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence. //2.2e-14:277:69//AL021368

R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //0.15:360:61//AL024509

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R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216
 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//7.1e-45:252:94//AC006238
 R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.4e-113:569:97//AC006241
 R-HEMBA1001375//Homo sapiens full length insert cDNA clone ZE09H03.//2.8e-89:428:99//AF086542
 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865
 R-HEMBA1001383
 R-HEMBA1001387
 R-HEMBA1001388//Homo sapiens clone RC189J21, WORKING DRAFT SEQUENCE, 15unordered pieces.//8.9e-06:108:83//AC005073
 R-HEMBA1001391//Yeast mitochondrial aap1 gene for ATPase subunit 8.//7.3e-08:500:59//X00960
 R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050
 R-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380
 R-HEMBA1001407
 R-HEMBA1001411//Yeast (S.cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981
 R-HEMBA1001413
 R-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732
 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7unordered pieces.//6.3e-37:302:81//AC006146
 R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054
 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527
 R-HEMBA1001442//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950

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R-HEMBA1001446//HS_3207_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385
 R-HEMBA1001450//Homo sapiens BAC clone RC114B19 from 7q31.1, complete sequence.//0.0043:266:63//AC005065
 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from 7q31, complete sequence.//7.1e-25:210:82//AC004855
 R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//2.7e-08:316:62//AC005324
 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//0.57:219:60//AC005208
 R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12unordered pieces.//9.3e-50:252:80//AC004840
 R-HEMBA1001478
 R-HEMBA1001497
 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337
 R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS.//1.9e-79:529:86//Z98753
 R-HEMBA1001517//Homo sapiens BAC clone RC459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549
 R-HEMBA1001522
 R-HEMBA1001526//Human DNA sequence from cosmid 444 G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs and CpG islands.//5.6e-08:265:67//Z98258
 R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 20q12-13.1. Contains adenosine deaminase (ADA), placental protein Diff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053
 R-HEMBA1001557
 R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383
 R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//I77040
 R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453
 R-HEMBA1001579//Plasmodium falciparum 3D7 chromoso

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me 12 PFYAC357 genomicsequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506
 R-HEMBA1001581//P.falciparum complete gene map of plastid-like DNA (IR-B).//2.3e-07:491:58//X95276
 R-HEMBA1001585//Caenorhabditis elegans cosmid C06A 6.//0.68:224:62//U41012
 R-HEMBA1001589
 R-HEMBA1001595//CIT-HSP-2349G19.TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence.//8.0e-69:337:99//AQ060483
 R-HEMBA1001608//Homo sapiens chromosome 17, clone HCIT462L7, complete sequence.//9.5e-59:514:78//AC005177
 R-HEMBA1001620//S.polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase.//4.5e-12:289:65//Z11693
 R-nnnnnnnnnnnn//HS_2195_A1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic surveysequence.//5.8e-09:358:58//AQ292688
 R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds.//0.77:225:59//U04270
 R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 6p21. Contains ETS related protein TEL like and CS2 like genes, ESTs and an STS.//6.0e-49:404:79//Z84484
 R-nnnnnnnnnnnn
 R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//1.1e-103:532:95//AC005368
 R-HEMBA1001658//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.0:197:64//AL023808
 R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.5e-100:457:93//AC005740
 R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds.//1.2e-90:496:91//AF072247
 R-HEMBA1001675
 R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds.//1.3e-101:534:94//AF038962
 R-HEMBA1001681//CIT-HSP-2345M7.TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence.//0.21:124:68//AQ056593
 R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228 P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//8.3e-06:279:63//AC004801
 R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 pro

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tein, complete cds.//1.9e-96:483:96//AB014598
 R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02.//2.3e-31:169:100//D16886
 R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence.//0.0025:200:65//B32577
 R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//6.6e-27:316:75//U12250
 R-HEMBA1001718//CIT-HSP-2171J2.TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//3.1e-41:167:87//B89781
 R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//0.53:275:61//AF018261
 R-HEMBA1001731//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE.//2.9e-48:292:84//AL023799
 R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.2e-33:290:81//AC005959
 R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21Contains Blimp-1, apoptosis specific protein similar to yeast APG5 ESTs, GSSs and retroviral sequence, complete sequence.//0.98:203:62//AL022067
 R-HEMBA1001745//Homo sapiens BAC clone RG298C08 from 7p15-p21, complete sequence.//0.00019:312:59//AC005084
 R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomicsequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.045:457:61//AC004153
 R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence.//3.8e-39:331:80//AC006121
 R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//0.0062:245:60//AC004554
 R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.1e-22:370:63//AC005740
 R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25.Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//3.0e-50:408:80//AL023575
 R-HEMBA1001800//CIT-HFP-2049N5.TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence.//9.0e-37:335:77//AQ009222
 R-HEMBA1001803//Plasmodium falciparum 3D7 chromoso

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me 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces. //0.86:536:56//AC005506
 R-nnnnnnnnnnnn//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end. //2.9e-93:553:89//M21977
 R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500. //2.8e-112:548:98//AB007969
 R-HEMBA1001809
 R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence. //2.6e-48:363:84//AC004025
 R-HEMBA1001819//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE. //1.1e-15:275:68//AJ009612
 R-HEMBA1001820//HS_3022_B1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence. //0.00054:335:59//AQ165107
 R-nnnnnnnnnnnn//Xenopus laevis intersectin mRNA, complete cds. //1.4e-19:533:63//AF032118
 R-HEMBA1001824//S.clavuligerus linear plasmid pSCL (complete sequence). //0.62:189:65//X54107
 R-HEMBA1001835//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE. //1.0:450:60//AL024507
 R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds. //1.6e-07:170:68//U50871
 R-HEMBA1001847
 R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds. //3.3e-108:553:96//AB014517
 R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q82F5A16, genomic survey sequence. //1.7e-14:245:67//AG002463
 R-HEMBA1001866//HS_2258_B2_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence. //2.8e-39:397:75//AQ221138
 R-nnnnnnnnnnnn//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence. //5.9e-56:303:94//AC005065
 R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence. //1.7e-43:281:88//AC006210
 R-HEMBA1001896
 R-HEMBA1001910
 R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence. //0.10:307:61//AC004775
 R-HEMBA1001913
 R-HEMBA1001915//HS_2037_A1_E12_MR CIT Approved Hum

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an Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence. //0.071:206:64//AQ233106
 R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence. //0.97:449:59//AC004775
 R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds. //2.0e-105:534:96//AF000145
 R-HEMBA1001939//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE. //4.6e-13:120:82//AL021707
 R-HEMBA1001940//Homo sapiens clone DJ1093I16, WORKING DRAFT SEQUENCE, 5 unordered pieces. //2.2e-36:301:81//AC005629
 R-HEMBA1001942//Human PAC clone DJ0205E24 from Xq23, complete sequence. //1.9e-10:208:68//AC003013
 R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence. //1.2e-06:393:60//AE001433
 R-HEMBA1001950//R.prowazekii genomic DNA fragment (clone A437R). //0.33:122:66//Z82646
 R-HEMBA1001960//Borrelia afzelii VS461 outer surface protein D (ospD) gene, complete cds. //0.0086:427:59//U05329
 R-HEMBA1001962//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence. //4.5e-07:176:70//AC004069
 R-HEMBA1001964//HS_2215_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence. //7.3e-25:215:74//AQ151931
 R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence. //1.7e-51:209:95//AL031178
 R-HEMBA1001979//CIT-HSP-2387I12.TF.1 CIT-HSP Homo sapiens genomic clone 2387I12, genomic survey sequence. //4.9e-06:153:71//AQ240461
 R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence. //3.1e-46:437:77//AL033521
 R-HEMBA1001991//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat. //1.1e-48:446:78//AL020997
 R-HEMBA1002003//Homo sapiens mRNA for protein phosph

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phatase 2C (beta). //5.1e-90:448:97//AJ005801
 R-HEMBA1002008//Homo sapiens DNA sequence from PAC
 95C20 on chromosome Xp11.3-11.4. Contains STSs and
 the DXS7 locus with GT and GTG repeat polymorphi
 sms, complete sequence. //3.2e-42:317:84//Z97181
 R-HEMBA1002018//HS_3006_B1_D10_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3006 Col=19 Row=H, genomic surveysequenc
 e. //1.0:63:74//AQ089717
 R-HEMBA1002022//Homo sapiens chromosome 18, clone 10
 hRPK.453_M_1, complete sequence. //0.93:339:59//AC00
 6203
 R-HEMBA1002035//Mus musculus chromosome 19, clone
 CIT282B21, complete sequence. //1.4e-11:285:67//AC0
 03694
 R-HEMBA1002039
 R-HEMBA1002049//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 117715, WORKING DRAFT S
 EQUENCE. //5.3e-52:266:84//AL022315
 R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sa
 piens genomic clone 2357L11, genomic survey sequen
 ce. //0.0013:185:66//AQ063078
 R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 tran
 scription factor (O/E-3) mRNA, complete cds. //2.7e
 -70:479:86//U92703
 R-HEMBA1002100//Homo sapiens thyroid receptor inte
 ractor (TRIP7) mRNA, 3' end of cds. //8.5e-32:206:9
 1//L40357
 R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PA
 C clone pDJ427d15, complete sequence. //4.3e-42:30 30
 2:85//AC005800
 R-HEMBA1002113//Human chromosome 12p13 sequence, c
 omplete sequence. //1.6e-64:550:80//U47924
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5,
 complete sequence. //1.2e-92:435:92//AC000378
 R-HEMBA1002125
 R-HEMBA1002139//Human nebulin mRNA, partial cds.//
 0.056:68:88//U35637
 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PA
 C clone 6-130a9 containing tryptophan hydroxylase 40
 gene, complete sequence. //2.0e-26:323:70//AC005728
 R-HEMBA1002150//Human DNA sequence from clone 742C
 19 on chromosome 22q12.3-13.1. Contains a pseudoge
 ne similar to Cytochrome C Oxidase Polypeptide VB
 and (parts of) up to four novel genes, two with ho
 mology to Phorbolin genes and one a novel Chromobo
 x protein gene. Contains ESTs, an STS, GSSs and put
 ative CpG islands, complete sequence. //1.0:371:61/
 /AL031846
 R-HEMBA1002151

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R-HEMBA1002153//Human BAC 367D17 from chromosome 1
 8, complete sequence. //2.4e-21:322:70//AC003971
 R-HEMBA1002160//Human DNA sequence from PAC 339A18
 on chromosome Xp11.2. Contains KIAA0178 gene, simi
 lar to mitosis-specific chromosome segregation pro
 tein SMC1 of S.cerevisiae, DNA binding protein sim
 ilar to URE-B1, ESTs and STS. //2.5e-38:216:84//Z970
 54
 R-HEMBA1002161//CIT-HSP-2163F10. TF CIT-HSP Homo sa
 piens genomic clone 2163F10, genomic survey sequen
 ce. //3.1e-58:284:80//B89969
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C
 11, complete sequence. //0.0079:286:57//Z80789
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Geno
 me Systems BAC library) complete sequence. //5.9e-5
 3:326:80//AC002980
 R-HEMBA1002177
 R-HEMBA1002185//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 745114, WORKING DRAFT S
 EQUENCE. //9.5e-37:356:76//AL033532
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5
 (Genome Systems Human BAC library) complete sequen
 ce. //3.4e-43:244:77//AC003684
 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKI
 NG DRAFT SEQUENCE, 2 unordered pieces. //4.3e-37:32
 3:78//AC005077
 R-HEMBA1002199//Human Cosmid g5129g124 from 7q31.
 3, complete sequence. //1.4e-89:564:87//AC002498
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Co
 smid Clone 817g In IGLC Region, complete sequence.
 //1.5e-31:313:71//AC000053
 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8
 genes for cytochromeoxidase subunit I and ATPase
 subunit 8. //0.0023:346:60//X57546
 R-HEMBA1002215//M.musculus mRNA for testin. //4.7e-
 61:414:84//X78989
 R-HEMBA1002226//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 2705, WORKING DRAFT SEQ
 UENCE. //4.6e-46:375:77//AL033529
 R-HEMBA1002229//Homo sapiens growth suppressor rel
 ated (DOC-1R) mRNA, complete cds. //4.6e-46:238:98/
 /AF089814
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC11-316M2
 4 (Roswell Park Cancer Institute Human PAC library)
 complete sequence. //4.3e-26:469:67//AC004242
 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 fr
 om 7q31, complete sequence. //5.1e-23:162:82//AC005
 016
 R-HEMBA1002257
 50 R-HEMBA1002267//Equus caballus dermatan sulfate pr

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oteoglycan II mRNA, complete cds.//4.6e-44:300:88/
 /AF038127
 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21
 -7q22, complete sequence.//1.9e-19:176:85//AC00005
 7
 R-HEMBA1002321
 R-HEMBA1002328//HS_3061_A1_D06_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3061 Col=11 Row=G, genomic surveysequenc
 e.//1.0:151:65//AQ127617
 R-HEMBA1002337//Saccharomyces cerevisiae RNA polym
 erase II holoenzyme component (SRB7) gene, complet
 e cds.//3.7e-07:328:63//U23811
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 pro
 tein, partial cds.//2.4e-128:642:96//AB018314
 R-HEMBA1002348//Human DNA sequence from clone 4090
 10 on chromosome 20q12Contains CA repeat, GSS, ST
 S, complete sequence.//3.7e-07:587:58//AL031256
 R-HEMBA1002349//Leishmania tarentolae maxicircle D
 NA fragment.//0.018:341:58//X02438
 R-HEMBA1002349//Homo sapiens chromosome-associated
 protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:
 661:93//AF092563
 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3
 -p22 anti-oncogene ofhepatocellular colorectal and
 non-small cell lung cancer , segment 11/11.//1.1e
 -70:559:79//AB020868
 R-HEMBA1002389//HS_3218_B2_E08_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3218 Col=16 Row=J, genomic surveysequenc
 e.//0.0011:122:72//AQ213602
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid
 R28784, complete sequence.//4.2e-81:232:97//AC005
 954
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 f
 rom 7q11.23-q21, complete sequence.//0.50:231:64//
 AC004848
 R-HEMBA1002430//P.falciparum complete gene map of
 plastid-like DNA (IR-B).//0.0023:604:56//X95276
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKI
 NG DRAFT SEQUENCE, 3 unordered pieces.//3.4e-23:18
 3:80//AC006026
 R-HEMBA1002458//Human DNA sequence from clone 146H
 21 on chromosome Xq22Contains cleavage stimulation
 factor, 64 KD subunit, gene similar to CYTOCHROME
 B-245 HEAVY CHAIN. pseudogene similar to hnRNP A1
 protein and ESTs, complete sequence.//7.7e-32:16
 1:83//Z83819
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, comp
 lete sequence.//2.6e-100:305:100//AC005378

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R-HEMBA1002462//Sequence 43 from patent US 570815
 7.//2.0e-10:131:77//I80068
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 f
 rom 7q21.2-q31.1, complete sequence.//6.6e-33:279:
 80//AC004841
 R-HEMBA1002486//***ALU WARNING: Human Alu-Sq subfa
 mily consensus sequence.//2.1e-50:290:92//U14573
 R-HEMBA1002495//CITBI-E1-2515J10.TR CITBI-E1 Homo
 sapiens genomic clone2515J10, genomic survey seque
 nce.//1.0:122:68//AQ261762
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORK
 ING DRAFT SEQUENCE, 15unordered pieces.//2.8e-22:2
 10:78//AC004963
 R-HEMBA1002503//Homo sapiens chromosome 17, clone
 HRPC1067M6, complete sequence.//2.7e-17:435:58//AC
 003043
 R-HEMBA1002508//Homo sapiens, clone hRPK.15_A_1, c
 omplete sequence.//3.7e-09:408:61//AC006213
 R-HEMBA1002515
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 pro
 tein, partial cds.//1.6e-104:564:93//AB007923
 R-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3197 Col=20 Row=D, genomic surveysequenc
 e.//2.8e-25:186:86//AQ188792
 R-HEMBA1002547//Mus musculus agrin gene, exon 36./
 /0.0095:93:75//M92658
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, comp
 lete sequence.//4.0e-49:308:90//AC005378
 R-HEMBA1002555//Homo sapiens full length insert cD
 NA clone YR87G10.//8.3e-65:318:99//AF085957
 R-HEMBA1002558//, complete sequence.//2.3e-38:264:
 89//AC005409
 R-HEMBA1002561//Human DNA sequence from clone 396D
 17 on chromosome 1p33-35.3 Contains EST, STS, GSS,
 complete sequence.//7.1e-44:192:80//AL008634
 R-HEMBA1002583
 R-HEMBA1002590//Homo sapiens protein associated wi
 th Myc mRNA, completecds.//4.5e-119:587:97//AF0755
 87
 R-HEMBA1002583
 R-HEMBA1002590//Homo sapiens DNA sequence from PAC
 179N16 on chromosome6p21.1-21.33. Contains the SA
 PK4 (MAPK p38delta) gene, and the alternatively sp
 liced SAPK2 gene coding for CSaids binding protein
 CSBP2 and a MAPK p38beta LIKE protein. Contains E
 STs, STSs and two predicted CpG islands, complete

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sequence.//9.4e-42:248:88//Z95152
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid
 R30385, complete sequence.//2.6e-56:302:84//AC004
 510
 R-HEMBA1002621
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 pro
 tein, complete cds.//6.7e-76:380:97//AB018351
 R-HEMBA1002628//P.falciparum complete gene map of
 plastid-like DNA (IR-A).//8.8e-05:327:60//X95275
 R-HEMBA1002629//Mus musculus clone OST16705, genom
 ic survey sequence.//4.3e-06:205:66//AF046247
 R-HEMBA1002645//***ALU WARNING: Human Alu-J subfam
 ily consensus sequence.//7.1e-39:281:84//U14567
 R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 f
 rom 7p31, complete sequence.//1.1e-104:500:95//ACO
 04839
 R-HEMBA1002659//Human DNA sequence from clone 243E
 7 on chromosome 22q12.1. Contains ESTs, STSs and G
 SSs, complete sequence.//1.2e-61:280:92//AL022323
 R-HEMBA1002661//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 225E12, WORKING DRAFT S
 EQUENCE.//3.2e-41:325:81//AL031772
 R-HEMBA1002666//Homo sapiens full length insert cD
 NA clone YY74A07.//0.00037:79:84//AF088008
 R-HEMBA1002678//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 1137F22, WORKING DRAFT
 SEQUENCE.//2.3e-107:561:94//AL034421
 R-*****//CIT-HSP-2287E8.TF CIT-HSP Homo sap
 iens genomic clone 2287E8, genomic survey sequenc
 e.//5.4e-17:137:88//B99281
 R-HEMBA1002688//Homo sapiens chromosome 5, P1 clon
 e 1354A7 (LBNL H47), complete sequence.//0.033:14
 6:70//AC004503
 R-HEMBA1002696
 R-HEMBA1002712//Homo sapiens PAC clone 166H1 from
 12q, complete sequence.//6.2e-44:302:87//AC003982
 R-HEMBA1002716//Mus musculus mRNA for ELM1, comple
 te cds.//1.1e-31:332:76//AB004873
 R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 pro
 tein, partial cds.//1.2e-35:287:81//AB014521
 R-HEMBA1002730//D.discoideum actin M6 gene, 5' fla
 nk.//0.018:233:66//M29109
 R-HEMBA1002742//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 1108H3, WORKING DRAFT S
 EQUENCE.//2.6e-13:419:62//AL033525
 R-HEMBA1002746//Mus musculus chromosome 19, clone
 CIT282B21, complete sequence.//0.019:202:65//AC003
 694
 R-HEMBA1002748//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 404K8, WORKING DRAFT SE

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QUENCE.//0.046:263:60//AL023883
 R-HEMBA1002750//Human DNA sequence from PAC 452H17
 on chromosome X contains sodium-and chloride-depe
 ndent glycine transporter 1 (GLYT-1) like, ESTs.//
 0.052:421:58//Z96810
 R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 pro
 tein, partial cds.//1.2e-104:545:95//AB011126
 R-HEMBA1002770//Plasmodium falciparum 3D7 chromoso
 me 12 PFYACB8-420 genomic sequence, WORKING DRAFT
 SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC
 005140
 R-HEMBA1002777
 R-HEMBA1002779//Human HepG2 3' region MboI cDNA, c
 lone hmd1e03m3.//9.4e-25:158:93//D17139
 R-HEMBA1002780//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone Y214H10, WORKING DRAFT
 SEQUENCE.//1.6e-42:463:75//AL022344
 R-HEMBA1002794//Plasmodium falciparum MAL3P8, comp
 lete sequence.//2.2e-05:417:59//AL034560
 R-HEMBA1002801//Meloidogyne javanica mitochondrial
 transfer RNA His, 16S ribosomal RNA (16S rRNA) gen
 es, ND3 gene, complete cds, and cytochrome b gene,
 5' end of CDS.//0.00055:444:59//L76261
 R-HEMBA1002810//Homo sapiens formin binding protei
 n 21 mRNA, complete cds.//4.4e-115:559:97//AF07118
 5
 R-HEMBA1002816//Homo sapiens clone NH0576N21, WORK
 ING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:32
 9:94//AC005043
 R-HEMBA1002826//Homo sapiens genomic DNA, chromoso
 me 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.
 //1.9e-22:262:67//AP000041
 R-HEMBA1002833//Homo sapiens chromosome 17, clone
 hRPC.117_B_12, complete sequence.//1.3e-79:396:97/
 /AC004707
 R-HEMBA1002850//Plasmodium falciparum 3D7 chromoso
 me 12 PFYAC357 genomic sequence, WORKING DRAFT SEQU
 ENCE, 7 unordered pieces.//0.013:393:61//AC005506
 R-HEMBA1002863//Homo sapiens chromosome 17, clone
 hRPK.271_K_11, complete sequence.//4.1e-73:489:85/
 /AC005562
 R-HEMBA1002876//Plasmodium falciparum DNA *** SEQU
 ENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT S
 EQUENCE.//0.21:549:55//AL034557
 R-HEMBA1002886//CIT-HSP-2013C4.TR CIT-HSP Homo sap
 iens genomic clone 2013C4, genomic survey sequenc
 e.//0.30:431:56//B53836
 R-HEMBA1002896//Homo sapiens SH3-containing adapto
 r molecule-1 mRNA, complete cds.//3.9e-106:541:95/
 /AF037261

- R-HEMBA1002921
R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7 /10.//4.6e-19:139:78//AB020875
R-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681
R-HEMBA1002935//CIT-HSP-2282P14.TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584
R-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745I14, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532
R-HEMBA1002939
R-HEMBA1002944//HS_3107_A1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952
R-HEMBA1002951//Xerolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020
R-HEMBA1002954//HS_3246_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005
R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//4.2e-38:300:83//AC005553
R-HEMBA1002970//Slime mold (D.discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579
R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128
R-nnnnnnnnnnnn//Homo Sapiens Chromosome X clone bW XD691, complete sequence.//0.00040:504:59//AC004386
R-HEMBA1002999//Rattus norvegicus lamina-associate d polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406
R-HEMBA1003033//Homo sapiens full length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026
R-HEMBA1003035//HS_2008_A2_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839
R-HEMBA1003037//347G15.TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182
R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962
R-HEMBA1003067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302
R-HEMBA1003071//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ110136
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//4.9e-69:494:84//U42975
R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome Xp11.2.Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1,ESTs and STS.//1.1e-11:331:64//Z97054
R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673
R-HEMBA1003083//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTCS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798
R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3unordered pieces.//1.2e-43:281:88//AC006039
R-HEMBA1003096//Human DNA sequence from clone J506 G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213
R-HEMBA1003098//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08; HTCS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598
R-HEMBA1003117
R-HEMBA1003129//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329

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R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-99:484:98//AC004472

R-HEMBA1003136//CIT-HSP-2281L22.TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861

R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128 M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:270:87//AC004024

R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-116:586:96//AJ005670

R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//6.4e-35:364:70//Z83822

R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta receptor.//1.9e-30:282:77//X60459

R-HEMBA1003197

R-HEMBA1003199//HS_2166_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=I, genomic survey sequence.//0.00026:271:61//AQ164162

R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUENCE, 3unordered pieces.//5.4e-44:291:83//AC005480

R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-7q22, complete sequence.//3.1e-10:293:62//AC000118

R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1unordered pieces.//1.0:118:69//AC006148

R-HEMBA1003220//HS_3092_B1_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, genomic survey sequence.//0.00014:59:91//AQ128202

R-HEMBA1003222//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z95393

R-HEMBA1003229//RPC11-16F15.TPB RPC1-11 Homo sapiens genomic clone RPC1-11-16F15, genomic survey sequence.//0.42:167:64//B83610

R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic clone 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231

R-HEMBA1003250//HS_2168_A2_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, genomic survey sequence.//1.4e-22:158:89//AQ125356

R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:268:61//U53709

R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (G

3490

enome Systems Human BAC library) complete sequence.//1.0e-32:255:84//AC002549

R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0044:212:60//AC005308

R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPC11-315 L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-34:286:74//AC002395

R-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC005840

R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//3.0e-115:551:99//AB011109

R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic clone 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073

R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:97//I25662

R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence.//0.00019:334:60//AB017061

R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//2.8e-111:545:97//AB001872

R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61//AL022153

R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.//0.00028:172:65//AC005099

R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18unordered pieces.//2.2e-44:268:90//AC005081

R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds.//2.7e-61:312:97//AF026029

R-HEMBA1003348//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.2e-38:186:83//U14567

R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequence.//0.00012:465:59//Z79600

R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, complete sequence.//3.2e-42:301:87//AC002558

R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor

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1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a carepeat polymorphism, complete sequence. //7.4e-34:375:74//AL022721
 R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LANL), complete sequence. //1.6e-46:309:88//AC004651
 R-HEMBA1003380//HS_3184_B2_E06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, genomic surveysequence. //1.0e-35:237:88//AQ189144
 R-HEMBA1003384//HS_2193_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, genomic surveysequence. //0.00029:96:76//AQ032212
 R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces. //2.6e-21:139:86//AC002993
 R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic clone 2166E19, genomic survey sequence. //0.99:144:61//B91549
 R-nnnnnnnnnnnnn
 R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence. //2.5e-112:547:98//AL031321
 R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence. //0.082:352:59//AC004879
 R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NBS1) mRNA, complete cds. //9.9e-114:544:98//AF058696
 R-HEMBA1003461
 R-HEMBA1003463
 R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence. //9.1e-106:533:96//AC005041
 R-HEMBA1003528
 R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete sequence. //3.4e-08:333:64//AC002454
 R-HEMBA1003538//Human mRNA for complement component C1r. //1.4e-23:333:68//X04701
 R-HEMBA1003545//Zebrafish mRNA for zflsl-2 (insulin gene enhancer binding protein homolog), complete cds. //0.030:144:68//D38453
 R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.0017:487:57//AC004153
 R-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE. //2.8e-99:503:96//AL031718
 R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete

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e sequence. //1.6e-114:574:97//AC005913
 R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096. //0.24:116:67//AF034416
 R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces. //3.9e-05:422:63//AC006036
 R-HEMBA1003569//Homo sapiens full length insert cDNA clone ZD82D06. //8.7e-108:545:95//AF086450
 R-HEMBA1003571//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence. //4.6e-51:570:71//AC004914
 R-HEMBA1003579//HS_3237_B2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, genomic surveysequence. //8.5e-97:495:95//AQ209302
 R-HEMBA1003581//Mouse mRNA for talin. //8.3e-12:128:82//X56123
 R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2603 (LANL), complete sequence. //2.9e-87:251:95//AC005774
 R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence. //4.5e-52:384:83//AL008715
 R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence. //4.6e-41:442:74//Z84480
 R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12, complete sequence. //1.8e-23:177:88//AC005153
 R-HEMBA1003615
 R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.039:494:57//AC005139
 R-HEMBA1003621//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces. //2.3e-26:309:75//AC004599
 R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence. //7.1e-56:545:75//AC002980
 R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete sequence. //2.8e-32:546:68//AF088219
 R-HEMBA1003637//Human BAC clone GS552A01 from 7q21

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-q22, complete sequence.//8.0e-25:457:68//AC002454
 R-HEMBA1003640//Homo sapiens chromosome X, PAC 671
 D9, complete sequence.//2.8e-40:280:86//AF031078
 R-HEMBA1003645//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQ
 UENCE.//1.7e-33:297:82//AL023693
 R-HEMBA1003646//Plasmodium falciparum MAL3P7, comp
 lete sequence.//0.44:319:59//AL034559
 R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clo
 ne CIT987SK-A-152E5, complete sequence.//6.9e-36:2 10
 42:80//AC004382
 R-HEMBA1003662//Homo sapiens chromosome 17, clone
 hRPK.332_H_18, complete sequence.//8.6e-117:588:96
 //AC005746
 R-HEMBA1003667//Sequence 8 from patent US 5420245.
 //1.8e-21:170:88//I12222
 R-HEMBA1003679//Homo sapiens BAC clone RG114B19 fr
 om 7q31.1, complete sequence.//1.6e-22:180:87//ACO
 05065
 R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06: 20
 270:61//L15313
 R-HEMBA1003684//Colias alexandra alexandra cytochr
 ome oxidase subunit I (cox1) gene, mitochondrial ge
 ne encoding mitochondrial protein, partialcds.//0.
 77:171:66//AF044872
 R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPCI5-105
 7120 (Roswell Park Cancer Institute Human PAC libr
 ary) complete sequence.//1.6e-104:523:97//AC004466
 R-HEMBA1003692//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 508I15, WORKING DRAFT S 30
 EQUENCE.//1.7e-41:414:77//AL021707
 R-HEMBA1003711//Human Chromosome 11 overlapping pa
 cs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENC
 E, 17 unordered pieces.//1.6e-29:304:77//AC000406
 R-HEMBA1003714
 R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BA
 C clone CIT987SK-A-685D8, WORKING DRAFT SEQUENCE,
 16 unordered pieces.//1.4e-63:578:77//AC005136
 R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUEN
 CE, 135 unordered pieces.//2.4e-36:350:78//AC00235 40
 3
 R-HEMBA1003725//Homo sapiens chromosome 19, cosmid
 R31973, complete sequence.//6.3e-42:250:75//AC004
 699
 R-HEMBA1003729//RPCI11-22D14.TV RPCI-11 Homo sapie
 ns genomic clone RPCI-11-22D14, genomic survey seq
 uence.//1.0:234:62//B86158
 R-HEMBA1003733//Human DNA sequence from clone 396D
 17 on chromosome 1p33-35.3 Contains EST, STS, GSS,
 complete sequence.//7.7e-80:558:83//AL008634 50

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R-HEMBA1003742//HS_3080_B2_H06_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3080 Col=12 Row=P, genomic surveysequenc
 e.//3.4e-55:331:91//AQ139179
 R-HEMBA1003758//Human DNA sequence from PAC 295C6
 on chromosome 1q24. Contains ESTs, CA repeat, STS
 and CpG island.//4.5e-59:521:75//Z97876
 R-HEMBA1003760
 R-HEMBA1003773//Mus musculus signal recognition pa
 rticle receptor beta subunit mRNA, complete cds.//
 2.6e-72:467:86//U17343
 R-HEMBA1003783//Mus musculus bromodomain-containin
 g protein BP75 mRNA, complete cds.//1.0e-77:557:81
 //AF084259
 R-HEMBA1003784
 R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 f
 rom 7p15.3-p21, complete sequence.//2.1e-49:390:72
 //AC004455
 R-HEMBA1003803
 R-HEMBA1003804//Homo sapiens chromosome 17, clone
 hCIT.175_E_5, complete sequence.//9.4e-99:359:99//A
 C004596
 R-HEMBA1003805//Human DNA sequence from clone 51J1
 2 on chromosome 6q26-27. Contains the 3' part of t
 he alternatively spliced gene for the human ortholo
 gs of mouse QKI-7 and QKI-7B (KH Domain RNA Bindin
 g proteins) and zebrafish ZKQ-1 (Quaking protein ho
 molog). Contains ESTs, STSs and GSSs, complete seq
 uence.//8.0e-113:567:96//AL031781
 R-HEMBA1003807//Bovine dinucleotide microsatellite
 HUJ1177.//5.4e-18:194:78//M96348
 R-HEMBA1003836//Human DNA from overlapping chromos
 ome 19 cosmids R31396, F25451, and R31076 containin
 g COX6B and UPKA, genomic sequence, complete seque
 nce.//3.4e-40:256:85//AC002115
 R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sa
 piens genomic clone 2380F18, genomic survey sequen
 ce.//9.7e-25:150:96//AQ196624
 R-HEMBA1003856//Human DNA sequence from clone 272E
 8 on chromosome Xp22.13-22.31. Contains a pseudoge
 ne similar to MDM2-Like P53-binding protein gene. C
 ontains STSs, GSSs and a CA repeat polymorphism, c
 omplete sequence.//4.8e-33:486:68//Z93929
 R-HEMBA1003864//, complete sequence.//4.4e-100:53
 1:94//AC005300
 R-HEMBA1003866//HS_3203_B2_C01_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3203 Col=2 Row=F, genomic survey sequenc
 e.//2.6e-05:206:64//AQ180298
 R-HEMBA1003879//Homo sapiens chromosome 10 clone C

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IT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207
 R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036
 R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576
 R-HEMBA1003893//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421
 R-HEMBA1003902//HS_3031_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549
 R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795
 R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368
 R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718
 R-HEMBA1003939
 R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904
 R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619
 R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.096:492:57//AL034560
 R-HEMBA1003958//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668
 R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahybadh4) gene, complete cds.//0.11:428:60//AF000132
 R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414
 R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//I80060
 R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPC15-927 J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804
 R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924
 R-HEMBA1003989//RPC111-52K22.TJ RPC111 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

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R-HEMBA1004000
 R-HEMBA1004011
 R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.7e-38:284:85//AC005670
 R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575
 10 R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081
 R-HEMBA1004038//Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054
 R-HEMBA1004042//Homo sapiens clone DJ0968I16, complete sequence.//0.00071:263:68//AC006016
 R-HEMBA1004045//Homo sapiens PAC clone DJ0074H20 from X, complete sequence.//8.8e-23:196:69//AC006143
 20 R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283
 R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677
 R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504
 30 R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484
 R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952
 R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//I76237
 R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.8e-11:323:63//AF091234
 40 R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918
 R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//6.0e-49:491:76//AC003665
 R-HEMBA1004133//HS_3229_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003
 50 R-HEMBA1004138//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE. //3.1e-09:277:66//AL024498
 R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence. //0.53:239:61//AL008970
 R-HEMBA1004146//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5unordered pieces. //3.0e-35:165:88//AC004820
 R-HEMBA1004150//CITBI-E1-2517I2. TR CITBI-E1 Homo sapiens genomic clone 2517I2, genomic survey sequence. //0.56:379:59//AQ277616
 R-HEMBA1004164//Human BAC clone GS200K05 from 7q21-q22, complete sequence. //4.6e-49:448:77//AC002429
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds. //2.4e-110:563:96//AF067855
 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4. //0.73:187:64//Z66569
 R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems HumanBAC library) complete sequence. //6.3e-30:293:77//AC004552
 R-HEMBA1004202//rah=ras-related homolog [mice, HT4 20 neural cell line, mRNA, 993 nt]. //3.0e-64:517:80//S72304
 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE, 15unordered pieces. //1.0e-97:303:98//AC005488
 R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds. //3.6e-116:573:97//U50748
 R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12 tRNAs and 7 genes. //5.4e-11:493:60//M37275
 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds. //6.1e-76:443:86//AF095927
 R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complete sequence. //1.1e-42:330:83//AC005763
 R-HEMBA1004241
 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE. //1.1e-45:288:85//AP000011
 R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence. //5.2e-09:516:61//AC004903
 R-HEMBA1004264
 R-HEMBA1004267//HS_2255_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=0, genomic survey sequence. //8.6e-59:318:95//AQ068854
 R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPCI5-118 50

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OD12 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //1.1e-113:576:96//AC005831
 R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence. //4.4e-110:553:96//AF091081
 R-HEMBA1004276
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds. //1.9e-106:538:97//AF022795
 R-HEMBA1004289//RPCI11-74010. TJ RPCI11 Homo sapiens genomic clone R-74010, genomic survey sequence. //2.3e-37:248:76//AQ266668
 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end. //0.0016:273:64//L13174
 R-HEMBA1004306//HS_3175_B2_F01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, genomic survey sequence. //1.6e-28:190:77//AQ169206
 R-HEMBA1004312//Human BAC clone RG119P24 from 7q31, complete sequence. //6.3e-36:267:82//AC003088
 R-HEMBA1004321//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 10155, WORKING DRAFT SEQUENCE. //4.1e-111:576:95//AJ009611
 R-HEMBA1004323//CIT-HSP-2374C8. TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence. //2.7e-42:136:91//AQ114933
 R-HEMBA1004327//CIT-HSP-2303L24. TF CIT-HSP Homo sapiens genomic clone 2303L24, genomic survey sequence. //1.0:78:67//AQ017600
 R-HEMBA1004330//Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5unordered pieces. //2.3e-119:580:98//AC004987
 R-HEMBA1004334//Pimpinella brachycarpa Phyb1 mRNA, complete cds. //3.3e-14:238:69//AF082024
 R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence. //1.8e-21:291:71//AC004638
 R-HEMBA1004341
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds. //4.1e-74:444:90//D89667
 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence. //7.0e-38:287:82//AC003002
 R-HEMBA1004356//Sequence 2 from patent US 5652144. //3.7e-108:588:92//I58611
 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.8e-14:446:63//AC005949
 R-HEMBA1004372//CIT-HSP-2005C13. TF CIT-HSP Homo sapiens genomic clone 2005C13, genomic survey sequence. //0.010:334:61//B55811

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R-HEMBA1004389//Homo sapiens full length insert cDNA clone ZE09A11.//1.5e-19:170:83//AF086540
 R-HEMBA1004394//Human (D21S198) DNA segment containing (TC)23 repeat.//1.0:50:84//X58124
 R-HEMBA1004396//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//8.2e-34:459:69//AC004057
 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//2.8e-42:314:84//AC005030
 R-HEMBA1004408
 R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//1.6e-66:449:82//Z54200
 R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-32:460:68//AJ011930
 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21unordered pieces.//3.9e-113:581:96//AC004846
 R-HEMBA1004461//HS_3244_A2_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, genomic survey sequence.//8.0e-83:397:99//AQ220876
 R-HEMBA1004479//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence.//1.7e-40:485:70//AC006012
 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//2.2e-11:513:59//AE001370
 R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-08:245:66//AC005951
 R-HEMBA1004506//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487
 R-HEMBA1004507//Caenorhabditis elegans cosmid C40C9, complete sequence.//0.56:235:64//Z70266
 R-HEMBA1004509
 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:83//I76230
 R-HEMBA1004538//HS_3189_B2_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, genomic survey sequence.//6.1e-21:140:92//AQ170330
 R-HEMBA1004554//CIT-HSP-712K9. TP CIT-HSP Homo sapiens genomic clone 712K9, genomic survey sequence.//1.7e-16:116:93//B73329
 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-14:213:71//D87457
 R-HEMBA1004573

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R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's Disease Region, chromosome 4p16.3 contains protein similar to Mouse SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.0:352:60//Z68279
 R-HEMBA1004586
 R-nnnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.0012:359:60//Z98551
 R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62//AL022071
 R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501.//1.4e-50:327:85//AB007970
 R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome Systems Human BAC Library) complete sequence.//4.4e-13:527:63//AC004805
 R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//U31866
 R-HEMBA1004632
 R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3unordered pieces.//7.7e-117:573:98//AC005534
 R-HEMBA1004638//H.sapiens mRNA for DGCR2.//3.8e-19:118:99//X84076
 R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence.//0.00013:501:58//AC005171
 R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence.//1.5e-120:571:98//AL031432
 R-HEMBA1004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241
 R-HEMBA1004672//Human DNA sequence from PAC 308I13 on chromosome 1p35-1p36.3.//3.4e-38:324:81//Z99291
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone: MP012, complete sequence.//0.86:309:57//AB006702
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T33B22, genomic survey sequence.//0.29:331:61//B97342
 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//0.051:424:58//AL034559
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.//1.7e-49:497:76//AC004638
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//1.6e-38:362:79//

- /AC005562
 R-HEMBA1004725
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26, complete sequence.//1.1e-58:489:79//AC002085
 R-HEMBA1004733
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b) POU domain proteins and an unknown gene. Contains a putative CpG island, ESTs, STS, and GSSs, complete sequence.//0.0030:362:61//AL022395
 R-HEMBA1004736//Homo sapiens clone DJ0981007, complete sequence.//1.9e-58:282:87//AC006017
 R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:81//AC004953
 R-HEMBA1004751//Human DNA sequence from PAC 507I15 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950
 R-HEMBA1004752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121
 R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498
 R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807
 R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057
 R-HEMBA1004763
 R-HEMBA1004768//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310
 R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:476:61//AE001371
 R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047
- R-HEMBA1004776
 R-HEMBA1004778//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567
 R-nnnnnnnnnnnn//HS_3192_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855
 R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728
 R-HEMBA1004806
 R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-20:333:69//AC005015
 R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545
 R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002
 R-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//7.6e-80:297:85//X53744
 R-HEMBA1004850
 R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201
 R-HEMBA1004864
 R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC11-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297
 R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.9e-49:551:73//AC004826
 R-HEMBA1004889//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943
 R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//6.6e-11:144:77//AC005972
 R-HEMBA1004909//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052
 R-HEMBA1004918//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554
 R-HEMBA1004923//Homo sapiens 47kB DNA fragment from Xq28, proximal to MTW1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

R-HEMBA1004930//Homo sapiens chromosome 11 clone C
IT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordere
d pieces.//7.7e-66:547:79//AC005848

R-HEMBA1004933//H.sapiens Humig mRNA.//0.13:233:62
//X72755

R-HEMBA1004934//CIT-HSP-2021I16.TF CIT-HSP Homo sa
piens genomic clone 2021I16, genomic survey sequen
ce.//0.66:268:62//B65345

R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sa 10
piens genomic clone 2281L12, genomic survey sequen
ce.//3.8e-20:104:82//B99849

R-HEMBA1004954//Homo sapiens chromosome 17, clone
hrPK.146_P_2, WORKINGDRAFT SEQUENCE, 4 unordered p
ieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sa
piens genomic clone 2305H22, genomic survey sequen
ce.//1.6e-84:411:99//AQ020408

R-HEMBA1004960//Human DNA sequence from PAC 358H7
on chromosome X.//3.3e-22:249:74//Z77249

R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Librar
y Oryza sativa genomic clone nbxb0003K01f, genomic
survey sequence.//0.52:171:64//AQ049982

R-HEMBA1004973//*** SEQUENCING IN PROGRESS *** EPM
1/APECED region of chromosome 21, clones A68E8, B1
27P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159
G9, B175D10, B52C10, C124G1 Note: Sequencing in th
is region has been discontinued by the Stanford Hu
man Genome Center, WORKING DRAFT SEQUENCE, 50 unor
dered pieces.//0.69:179:64//AC003656

R-HEMBA1004977//Caenorhabditis elegans cosmid F08G
2, complete sequence.//7.6e-07:492:58//Z81495

R-HEMBA1004978//Human DNA sequence from clone 522P
13 on chromosome 6p21.31-22.3. Contains a 60S Ribo
somal Protein L21 pseudogene and an HNRNP A3(Heter
ogenous Nuclear Riboprotein A3, FBRNP) pseudogene.
Contains ESTs, STSs and GSSs, complete sequence.//
0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sap
iens genomic clone 2379K5, genomic survey sequenc 40
e.//1.6e-53:331:88//AQ108614

R-HEMBA1004983//Genomic sequence from Human 17, co
mplete sequence.//0.00061:473:58//AC000389

R-HEMBA1004995//Homo sapiens chromosome 16, cosmid
clone 306E5 (LANL), complete sequence.//1.6e-90:5
27:89//AC004224

R-HEMBA1005008//Human DNA sequence from clone 461P
17 on chromosome 20q12-13.2. Contains four novel
(pseudo)genes for proteins with Kunitz/Bovinepancr
eatic trypsin inhibitor and/or WAP-type (Whey Acid 50

ic Protein) 'four-disulfide core' domains, COX6C
(Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1)
and RPL5 (60S Ribosomal Protein L5) pseudogenes, a
pseudogene similar to part of the HSPD1 (HSP60, M
itochondrial Matrix Protein P1 precursor, Heat Sho
ck Protein 60, GROEL protein, HUCHA60) gene, and t
he Major Epididymis-specific protein E4 precursor
(HE4, Epididymis Secretoryprotein E4, WAP-type (Wh
ey Acidic Protein) 'four-disulfide core' domain) g
ene. Contains ESTs, an STS, GSSs and a putative Cp
G island, complete sequence.//5.4e-65:357:83//AL031
663

R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA,
complete cds.//5.6e-107:550:96//AF041474

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 pro
tein, partial cds.//6.3e-104:542:94//AB014548

R-HEMBA1005029//Homo sapiens DNA sequence from PAC
97D16 on chromosome 6p21.3-22.2. Contains an unkn
own pseudogene, a 60S Ribosomal protein L24(L30) L
IKE pseudogene and histone genes H2BFC (H2B/c), H4
FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/
k) and a tRNA-Val pseudogene and tRNA-Thr gene. Co
ntains ESTs, STSs, GSSs and genomic marker D6S464,
complete sequence.//3.1e-67:493:83//AL009179

R-HEMBA1005035//Homo sapiens chromosome 17, clone
hCIT.175_E_5, complete sequence.//7.4e-101:537:94//
AC004596

R-HEMBA1005039//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 1018D12,
WORKING DRAFT SEQUENCE.//
9.5e-30:446:68//AL031650
R-HEMBA1005047//Mus muscu
lus mRNA for Rab24 protei
n.//1.4e-34:229:88//Z2281
9

R-HEMBA1005050//Human Chr
omosome X PAC RPC11-290C9
from the Pieter de Jong
Human PAC library; comple
te sequence.//4.0e-43:37
1:80//AC002404

R-HEMBA1005062//Homo sapi
ens chromosome 17, clone
hCIT.186_H_2, complete seq
uence.//2.3e-15:269:66//A
C004675

R-HEMBA1005066//Homo sapi
ens clone NH0001P0.9, WORK
ING DRAFT SEQUENCE, 1 unor
dered pieces.//4.0e-30:30

3505

3506

5:74//AC006030

R-HEMBA1005075

R-HEMBA1005079//Homo sapiens clone HS19.11 Alu-Ya5 sequence. //6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT. S EQUENCE. //1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds. //5.3e-110:545:96//AF080561

R-HEMBA1005113//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53C10, WORKING DRAFT SEQUENCE. //0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence. //7.1e-55:306:82//AL022336

R-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE. //6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds. //3.2e-31:310:76//U81834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island. //1.4e-33:361:79//AL021407

R-HEMBA1005159//Human DNA

sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence. //2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE. //0.0017:381:58//AL022594

R-HEMBA1005201//P. falciparum complete gene map of plastid-like DNA (IR-B). //8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA. //4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces. //1.0:209:65//AC004854

R-HEMBA1005232//Homo sapiens chromosome Y, clone 264, M, 20, complete sequence. //0.0040:439:58//AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777O23 from 7p14-p15, complete sequence. //4.2e-111:568:96//AC005154

R-HEMBA1005244//HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence. //4.9e-12:116:84//AQ127947

R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence. //3.2e-27:210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK. 318_A_15, complete s

3507

equences. //4.6e-105:437:97
//AC005837

R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system. //0.011:339:59//D86630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence. //3.4e-17:269:71//AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region chromosome 13q12-13 contains x57 mRNA, ESTs. //6.9e-20:193:73//Z75887

R-HEMBA1005296//HS_3037_B1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence. //0.26:184:64//AQ117120

R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces. //1.5e-58:445:78//AC006146

R-HEMBA1005311//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796E4, WORKING DRAFT SEQUENCE. //9.3e-42:383:78//AL022337

R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11. //0.80:179:65//AF003389

R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces. //2.4e-40:409:71//AC006030

R-HEMBA1005318//S. pombe chromosome I cosmid c2E11. //0.97:370:61//AL031181

R-HEMBA1005331//Homo sapiens chromosome 17, clone

3508

hRPK. 214_C_8, complete sequence. //1.9e-112:577:95//AC005803

R-HEMBA1005353//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 429E7, WORKING DRAFT SEQUENCE. //8.9e-80:406:97//AL031722

10 R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK. 22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces. //3.2e-50:320:84//AC005412

R-HEMBA1005367//RPCI11-85E23. TV RPCI11 Homo sapiens genomic clone R-85E23, genomic survey sequence. //0.39:148:67//AQ281915

20 R-HEMBA1005372//Homo sapiens full length insert cDNA YH93B03. //2.6e-108:557:95//AF074997

R-HEMBA1005374//Homo sapiens full length insert cDNA clone ZA95D11. //1.9e-110:531:98//AF086142

30 R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence. //6.0e-41:432:75//Z92542

R-HEMBA1005394//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE. //4.9e-107:585:93//AL031670

R-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //5.1e-118:586:97//AL034379

50

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R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds.//1.6e-06:204:68//U95958

R-HEMBA1005410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//1.2e-23:452:66//AL008722

R-HEMBA1005411//RPCI11-66N19.TK RPCI11 Homo sapiens genomic clone R-66N19, genomic survey sequence.//2.2e-38:222:79//AQ237442

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)mRNA, complete cds.//5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS.//0.86:278:60//Z97196

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment.//5.4e-46:305:87//L40391

R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//4.0e-27:469:66//AC004894

R-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//7.2e-40:410:76//AC005212

R-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1090E8, WORKING DRAFT SEQUENCE.//3.1e-40:296:85//AL033524

R-HEMBA1005475//HS_2266_B2_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence.//0.49:209:61//AQ069377

R-HEMBA1005497

R-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//4.5e-116:580:97//AC004957

R-HEMBA1005506//Arabidopsis thaliana BAC T26D22.//0.0050:442:59//AF058826

R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence.//0.020:391:59//AF003509

R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//0.44:195:63//Z96811

R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.44:470:57//L14320

R-HEMBA1005518//M.musculus mRNA for paladin gene.//6.2e-29:183:81//X99384

R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORK

3510

ING DRAFT SEQUENCE, 6unordered pieces.//7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.9e-40:482:73//Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//3.8e-84:309:99//AB020860

R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence.//8.1e-25:154:94//U84091

R-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE.//5.3e-105:534:96//AL034431

R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence.//2.8e-69:432:88//AC004743

R-HEMBA1005558

20 R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//5.9e-33:367:74//AC004087

R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence.//2.2e-67:399:91//AL020989

R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence.//1.0:156:63//AC005737

30 R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds.//9.7e-27:561:64//AB011538

R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes.//2.3e-10:404:62//X02171

R-HEMBA1005583//HS_3014_B1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence.//3.0e-81:442:94//AQ154499

40 R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//1.8e-54:490:77//Z98046

R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPF.332_H_18, complete sequence.//2.2e-28:262:79//AC005746

3511

R-HEMBA1005595//HS_2224_A2_G03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence. //3.6e-48:263:95//AQ033446

R-HEMBA1005606//Human PAC clone DJ0093103 from Xq23, complete sequence. //2.5e-08:355:63//AC003983

R-HEMBA1005609//HS_2182_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence. //2.2e-82:400:99//AQ023130

R-HEMBA1005616//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 124K22, WORKING DRAFT SEQUENCE. //0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE. //7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full length insert cDNA clone ZD53D02. //4.5e-72:398:93//AF086321

R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence. //3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence. //1.4e-13:172:75//AL022069

R-HEMBA1005634//RPCI11-13015.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-13015, genomic survey sequence. //1.0e-28:153:82//B73293

R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs. //4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE. //2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3' end. //4.2e-49:322:88//M13450

R-HEMBA1005680//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //3.0e-36:285:83//AC005924

R-HEMBA1005685//H.sapiens (MAR8) chromosome 19 DNA, 343bp. //0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds. //5.4e-46:376:84//U66406

R-HEMBA1005705//RPCI11-13014.TP RPCI-11 Homo sapiens genomic clone RPCI-11-13014, genomic survey sequence. //0.071:182:59//B76186

R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G

3512

2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat. //1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces. //2.1e-47:449:75//AC003023

R-HEMBA1005737

R-nnnnnnnnnnnnn//H.sapiens DNA for repeat unit locus D18S51 (285 bp). //0.11:174:63//X91255

R-HEMBA1005755//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence. //0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence. //5.2e-39:422:74//U71148

R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE. //0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE. //1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds. //0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence. //0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence. //3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence. //8.2e-107:551:96//AL031781

R-HEMBA1005852//F.rubripes CSS sequence, clone 163A22aA4, genomic survey sequence. //2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pDJ24m8, complete sequence. //1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPCI3-488B23 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //2.6e-20:328:67//AC006207

R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence. //2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence. //0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rR

3513

NA, and ATPase subunit 6.//0.0090:445:58//Z23072
 R-HEMBA1005931//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 54B20, WORKING DRAFT SE
 QUENCE.//1.7e-46:351:83//Z98304
 R-HEMBA1005934//Homo sapiens chromosome 17, clone
 hRPK.261_A_13, complete sequence.//0.0052:179:71//
 AC005138
 R-HEMBA1005962//Homo sapiens clone RG012D21, compl
 ete sequence.//1.1e-11:149:74//AC005045
 R-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Hum 10
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3055 Col=15 Row=I, genomic surveysequenc
 e.//5.4e-79:403:97//AQ147357
 R-HEMBA1005990//Homo sapiens I-1 receptor candidat
 e protein mRNA, complete cds.//6.9e-112:580:95//AF
 082516
 R-HEMBA1005991//Human DNA sequence from clone 58A9
 on chromosome 1q24.1-24.3. Contains STSs, GSSs, g
 enomic marker D1S210 and a ca repeat polymorphism,
 complete sequence.//2.6e-39:299:82//AL031285 20
 R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORK
 ING DRAFT SEQUENCE, 11unordered piec
 es.//1.1e-29:260:70//AC00
 4859
 R-HEMBA1006002//Rattus no
 rvegicus s-nexilin mRNA,
 complete cds.//6.3e-15:17
 4:78//AF056035
 R-HEMBA1006005//Homo sapi
 ens MLL (MLL) gene, exons 30
 1-3, and partial cds.//
 2.6e-112:574:95//AF036405
 R-HEMBA1006006//Homo sapi
 ens mRNA for KIAA0725 pro
 tein, partial cds.//7.6e-
 27:444:67//AB018268
 R-HEMBA1006035//Plasmodiu
 m falciparum 3D7 chromoso
 me 12 PFYAC336 genomicseq
 uence, WORKING DRAFT SEQU 40
 ENCE, 5 unordered pieces.
 //0.025:373:60//AC005139
 R-HEMBA1006036//Homo sapi
 ens Chromosome 16 BAC clo
 ne CIT987SK-625P11, compl
 ete sequence.//0.0056:53
 5:59//AC004125
 R-HEMBA1006042//HS_2169_A
 1_B11_MF CIT Approved Hum
 an Genomic Sperm Library 50

3514

D Homo sapiens genomic cl
 one Plate=2169 Col=21 Row
 =C, genomic surveysequenc
 e.//1.7e-73:390:95//AQ132
 995
 R-HEMBA1006081
 R-HEMBA1006090//HS_2262_A
 2_A01_T7 CIT Approved Hum
 an Genomic Sperm Library
 D Homo sapiens genomic cl
 one Plate=2262 Col=2 Row=
 A, genomic survey sequenc
 e.//2.1e-70:360:97//AQ216
 324
 R-HEMBA1006091
 R-HEMBA1006100//Homo sapi
 ens DNA sequence from PAC
 212G6 on chromosome Xp1
 1.3-p11.4. Contains synap
 sin 1, brain protein 4.1,
 properdin, tyrosinekinas
 e (ELK1) oncogene, ESTs,
 STS, GSS, complete sequen
 ce.//1.6e-36:354:77//AL00
 9172
 R-HEMBA1006108
 R-HEMBA1006121
 R-HEMBA1006124//Human DNA
 sequence from BAC 175E3
 on chromosome 22q11.2-qte
 r. Contains ESTs, STSs an
 d polymorphic CA repeat.//
 1.3e-12:327:64//Z95113
 R-HEMBA1006130//WORKING D
 RAFT SEQUENCE, 3 unordere
 d pieces.//0.60:326:62//A
 C005948
 R-HEMBA1006131//Homo sapi
 ens chromosome 19, cosmid
 F16403, complete sequenc
 e.//4.3e-52:321:80//AC005
 777
 R-HEMBA1006142//, complet
 e sequence.//1.0e-13:160:
 78//AC005500
 R-HEMBA1006155//Plasmodiu
 m falciparum 3D7 chromoso
 me 12 PFYAC69 genomicsequ
 ence, WORKING DRAFT SEQUE

3515

NCE, 4 unordered pieces. //0.0013:389:60//AC004688
 R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds. //1.4e-119:574:98//AF048693
 R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds. //4.1e-43:307:86//U28217
 R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence. //1.7e-30:300:71//AC004491
 R-HEMBA1006198//***ALU WARNING: Human Alu-J subfamily consensus sequence. //1.3e-36:284:85//U14567
 R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence. //2.1e-110:545:97//AF070557
 R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds. //0.46:365:58//AB014567
 R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence. //2.8e-41:438:71//U91323
 R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds. //1.8e-28:179:91//AF083384
 R-HEMBA1006259//RPC111-44 N14. TJ RPC111 Homo sapiens genomic clone R-44N14, genomic survey sequence. //1.5e-48:348:85//AQ203161
 R-HEMBA1006268
 R-HEMBA1006272//Human DNA sequence from clone 1198 H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE gene

3516

nes. Contains GSSs and ESTs, complete sequence. //2.8e-73:273:87//AL023753
 R-nnnnnnnnnnnnnnn//H. sapiens PAP mRNA. //1.6e-54:585:71//X76770
 R-HEMBA1006283//Sequence 7 from patent US 5776683. //9.7e-18:113:98//AR016240
 R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence. //0.97:447:59//AC004585
 R-HEMBA1006291//Homo sapiens full length insert cDNA clone ZB76B10. //2.9e-94:454:98//AF086161
 R-HEMBA1006293//Sequence 8 from patent US 5721351. //8.1e-10:111:72//I89415
 R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces. //8.6e-37:288:84//AC005412
 R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1a (PACS-1) mRNA, complete cds. //6.5e-29:132:81//AF076183
 R-HEMBA1006328//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 894K16, WORKING DRAFT SEQUENCE. //3.3e-50:340:75//AL034429
 R-HEMBA1006334
 R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds. //8.7e-22:259:72//AF087945
 R-HEMBA1006347//Human prostatic gene, complete cds. //1.8e-78:170:100//U33446
 R-HEMBA1006349//Rat brain calcium channel alpha-1

3517

subunit mRNA, completed
s. //0.00051:120:73//M5768
2

R-HEMBA1006359//CITBI-E1-
2516C16. TR CITBI-E1 Homo
sapiens genomic clone 2516
C16, genomic survey seque
nce. //4.7e-74:576:82//AQ2
77951

R-HEMBA1006364//G. gallus
gene for transforming gro
wth factor-beta 2, exons 5
-7. //2.5e-21:118:85//X590
80

R-HEMBA1006377//Homo sapiens chromosome 19, cosmid
F23149, complete sequence. //5.7e-68:367:85//AC005
239

R-HEMBA1006380//Human BAC clone RG007J15 from 7q3
1, complete sequence. //6.1e-47:300:83//AC003989

R-HEMBA1006381//Homo sapiens chromosome 5, Bac clo
ne 189 (LBNL H135), complete sequence. //1.5e-47:33
6:86//AC005914

R-HEMBA1006398//Homo sapiens chromosome 5, BAC clo
ne 203o13 (LBNL H155), complete sequence. //1.5e-67:
501:83//AC005609

R-HEMBA1006416//Homo sapiens chromosome 17, clone
347_H_5, complete sequence. //4.4e-37:319:76//AC002
119

R-HEMBA1006419//Homo sapiens chromosome 17, clone
HCIT542B22, complete sequence. //2.9e-50:502:75//AC
004253

R-HEMBA1006421//Homo sapiens chromosome 14q24.3 cl
one BAC270M14 transforming growth factor-beta 3 (T
GF-beta 3) gene, complete cds; and unknown genes. /
/4.1e-116:572:97//AF107885

R-HEMBA1006424//Human DNA sequence from clone 51J1
2 on chromosome 6q26-27. Contains the 3' part of t
he alternatively spliced gene for the human ortholo
gs of mouse QKI-7 and QKI-7B (KH Domain RNA Bindin
g proteins) and zebrafish ZKQ-1 (Quaking protein ho
molog). Contains ESTs, STSs and GSSs, complete seq
uence. //9.4e-117:578:97//AL031781

R-HEMBA1006426//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 291J10, WORKING DRAFT S
EQUENCE. //2.2e-08:353:63//Z93017

R-HEMBA1006438//HS_2008_A1_D04_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2008 Col=7 Row=G, genomic survey sequenc
e. //1.2e-29:194:91//AQ245162

R-HEMBA1006445//Homo sapiens clone RC219E16, WORKI 50

3518

NG DRAFT SEQUENCE, 3 unordered pieces. //0.011:330:
60//AC005075

R-HEMBA1006446//Plasmodium falciparum chromosome
2, section 35 of 73 of the complete sequence. //0.03
2:256:61//AE001398

R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U
115H5, U132E12, U115B9 (Lawrence Livermore human co
smid library) complete sequence. //5.6e-35:229:77//
AC002364

10 R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmi
d clone 34a5, complete sequence. //1.1e-14:354:63//A
C002052

R-HEMBA1006471

R-HEMBA1006474//p40, p24 [Borna disease virus BDV,
WT-1, Halle B1/91, horse brain, field isolate, Ge
nomic RNA, 1138 nt, segment 1 of 3]. //1.1e-14:442:
60//S67502

R-HEMBA1006483//Human chromosome 16p13.1 BAC clone
CIT987SK-551G9 complete sequence. //3.7e-37:290:82
20 //U95742

R-HEMBA1006485//H. sapiens mRNA for aminopeptidase.
//7.6e-91:517:91//Y07701

R-HEMBA1006486//Homo sapiens clone RG315H11, WORKI
NG DRAFT SEQUENCE, 5 unordered pieces. //1.1e-33:28
9:81//AC005089

R-HEMBA1006489//Human DNA sequence from clone 192P
9 on chromosome Xp11.23-11.4. Contains a pseudogen
e similar to rat Plasmolipin, ESTs and GSSs, comple
te sequence. //6.0e-07:485:60//AL020989

30 R-HEMBA1006492//Homo sapiens chromosome 17, clone
hRPK.269_G_24, complete sequence. //4.3e-112:572:95
//AC005828

R-HEMBA1006494//Homo sapiens chromosome 17, clone
HRPC987K16, complete sequence. //2.3e-10:186:67//AC
002994

R-HEMBA1006497//RPCI11-16L10. TPB RPCI-11 Homo sapi
ens genomic clone RPCI-11-16L10, genomic survey se
quence. //1.5e-10:75:100//B88015

40 R-HEMBA1006502//Human DNA sequence from clone 272E
8 on chromosome Xp22.13-22.31. Contains a pseudoge
ne similar to MDN2-Like P53-binding protein gene. C
ontains STSs, GSSs and a CA repeat polymorphism, c
omplete sequence. //3.3e-36:516:70//Z93929

R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 pro
tein, partial cds. //1.2e-115:570:96//AB014566

R-HEMBA1006521//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 54B20, WORKING DRAFT SE
QUENCE. //2.2e-20:266:71//Z98304

R-HEMBA1006530//RPCI11-52M1. TJ RPCI11 Homo sapiens
genomic clone R-52M1, genomic survey sequence. //0.

- 00015:227:64//AQ052526
 R-HEMBA1006535//HS_2234_B1_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, genomic survey sequence.//7.5e-33:191:95//AQ129525
 R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence.//0.026:497:58//AC005007
 R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complete sequence.//5.2e-41:289:86//AC004603
 R-HEMBA1006559//Mus musculus PRAJA1 (Prajai) mRNA, complete cds.//3.4e-64:551:78//U06944
 R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pDJ404m15, complete sequence.//5.7e-09:266:66//AC002554
 R-HEMBA1006566//HS_2171_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, genomic survey sequence.//0.012:306:61//AQ125421
 R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//3.8e-70:529:82//U39357
 R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete sequence.//1.0:141:65//AC006032
 R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic clone 2377M16, genomic survey sequence.//1.7e-31:271:76//AQ111875
 R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.093:270:61//AC004709
 R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete sequence.//2.7e-45:371:80//AC005031
 R-HEMBA1006612
 R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 8B22, WORKING DRAFT SEQUENCE.//2.1e-20:229:77//AL031737
 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA), Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//4.8e-40:321:83//AL023284
 R-HEMBA1006631//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//1.5e-45:477:77//AL031848
 R-HEMBA1006635//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//8.0e-40:245:91//U14572
 R-HEMBA1006639
 R-HEMBA1006643
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds.//2.5e-106:567:94//U40282
 R-HEMBA1006652//Human BAC clone RC308B22 from 7q22-q31, complete sequence.//8.7e-54:334:76//AC002089
 R-HEMBA1006653//Homo sapiens 7q telomere, complete sequence.//5.0e-36:207:89//AF027390
 10 R-HEMBA1006665//HS_3213_B2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, genomic survey sequence.//1.2e-21:235:67//AQ175625
 R-HEMBA1006674//H. sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTEL00023.seq.//2.6e-32:212:83//Z96776
 R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-10:436:60//Z98551
 R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//6.1e-06:477:59//L40608
 R-HEMBA1006695//Homo sapiens clone RC339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.8e-30:266:80//AC005096
 R-HEMBA1006696
 R-HEMBA1006708
 R-HEMBA1006709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 715N11, WORKING DRAFT SEQUENCE.//6.8e-14:139:82//AL031674
 30 R-HEMBA1006717
 R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//9.9e-18:365:66//AC005828
 R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//1.3e-37:380:75//AC003108
 R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H87), complete sequence.//2.1e-75:338:85//AC003951
 40 R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.//1.2e-112:579:95//AC005752
 R-HEMBA1006767//Plasmodium falciparum MAL3P6, complete sequence.//0.00022:528:58//Z98551
 R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.3e-46:305:87//AC005701
 R-HEMBA1006780//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-39:305:82//AL022323

3521

R-HEMBA1006789//Streptomyces coelicolor cosmid 6C 4.//0.0085:449:61//AL031317
 R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//4.1e-43:355:80//AC006120
 R-HEMBA1006796//HS_3038_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, genomic survey sequence.//0.99:158:63//AQ102483
 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33unordered pieces.//8.4e-47:481:75//AC004854
 R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_0_9, complete sequence.//3.0e-08:84:90//AC004797
 R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:496:76//Z93023
 R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//0.70:206:65//AC005668
 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPC13-521 E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-46:281:91//AC004217
 R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence.//0.61:115:70//AF056074
 R-nnnnnnnnnnnn//Mus musculus mRNA for oxysterol-binding protein, complete cds.//3.3e-102:618:87//AB017026
 R-HEMBA1006885
 4.2e-14:379:63//AC006839
 R-HEMBA1006900//CIT-HSP-2006M20.TR CIT-HSP Homo sapiens genomic clone 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395
 R-HEMBA1006921//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.1e-68:267:86//AC005154
 R-HEMBA1006926
 R-HEMBA1006929//HS_3244_A2_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, genomic survey sequence.//6.9e-21:191:83//AQ207500
 R-HEMBA1006936
 R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//2.0e-75:371:98//AJ010841

3522

R-HEMBA1006949//Homo sapiens PAC clone DJ0777C09 from 7q34-q36, complete sequence.//0.47:240:63//AC005518
 R-HEMBA1006973//HS_2009_A2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, genomic survey sequence.//9.6e-05:407:60//AQ232302
 R-HEMBA1006976//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701
 R-HEMBA1006993//Human thymopoietin (TMP0) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.9e-47:394:79//U18271
 R-HEMBA1006996//CIT-HSP-2172D17.TF CIT-HSP Homo sapiens genomic clone 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406
 R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558
 R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.6e-41:437:71//AC005277
 R-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//8.2e-73:556:80//X79088
 R-HEMBA1007045
 R-HEMBA1007051//Human DNA sequence from cosmid N69 F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006
 R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056
 R-HEMBA1007062
 R-HEMBA1007066
 R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//2.0e-66:476:85//AC006141
 R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//1.0e-38:179:82//AC005325
 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6unordered pieces.//3.2e-49:551:73//AC006015
 R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequence.//1.0:261:61//AC000385
 R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//0.043:295:62//AC004803
 R-HEMBA1007113//Homo sapiens (subclone 6_a8 from P1 H16) DNA sequence.//1.4e-52:307:87//L43392
 R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z

92547

R-HEMBA1007147//H.sapiens CpG island DNA genomic M
sel fragment, clone 65f1, reverse read cp65f1.rtl
a.//0.16:187:64//Z62246

R-HEMBA1007149//Homo sapiens chromosome 19, cosmid
F23149, complete sequence.//7.6e-108:543:96//AC00
5239

R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 f
rom 7q31, complete sequence.//0.14:323:58//AC00487
5

R-nnnnnnnnnnnn//Homo sapiens epsin 2a mRNA, comple
te cds.//5.1e-103:529:94//AF062085

R-HEMBA1007178//Homo sapiens chromosome 12p13.3 cl
one RPC111-372B4, WORKING DRAFT SEQUENCE, 129 orde
red pieces.//5.4e-106:537:96//AC005911

R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC R
PC11-122K4 (Roswell Park Cancer Institute Human PA
C Library) complete sequence.//4.1e-39:262:80//AC0
03035

R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 pro 20
tein, complete cds.//5.3e-61:332:95//D86987

R-HEMBA1007206//Homo sapiens DNA sequence from PAC
958B3 on chromosome Xp22.11-Xp22.22. Contains EST
s STS and CpG island.//1.9e-50:436:81//Z93023

R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 pro
tein, partial cds.//2.3e-96:471:97//AB018340

R-HEMBA1007251//Homo sapiens chromosome 5, PAC clo
ne 247f3 (LBNL H85), complete sequence.//0.011:34
9:62//AC004777

R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 f 30
rom 7q35-q36, complete sequence.//2.8e-10:224:70//A
C004856

R-HEMBA1007267//Homo sapiens Chr.14 PAC RPC14-794B
2 (Roswell Park Cancer Institute Human PAC Library)
complete sequence.//3.4e-53:362:86//AC005924

R-HEMBA1007273

R-HEMBA1007279//Rickettsia prowazekii strain Madri
d E, complete genome; segment 4/4.//0.042:454:57//A
J235273

R-HEMBA1007281//Rickettsia prowazekii strain Madri 40
d E, complete genome; segment 3/4.//0.99:288:60//AJ
235272

R-HEMBA1007288//Human DNA sequence from clone 422G
23 on chromosome 6q24 Contains EST, STS, GSS, CpG i
sland, complete sequence.//7.4e-107:554:95//AL0310
03

R-HEMBA1007300//Caenorhabditis elegans cosmid C48C
5.//0.22:474:59//U39994

R-HEMBA1007301

R-HEMBA1007319//Campylobacter jejuni repetitive DN 50

A, clone pINT.//4.9e-08:524:58//Y14425

R-HEMBA1007320//Homo sapiens genomic DNA, chromoso
me 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.
//3.4e-16:244:71//AP000043

R-HEMBA1007322//Homo sapiens BAC clone RC324D18 fr
om 7p15-p21, complete sequence.//3.9e-83:383:85//AC
005251

R-HEMBA1007327//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 7706, WORKING DRAFT SEQ
UENCE.//1.6e-38:533:71//Z96804

R-HEMBA1007341//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 268D13, WORKING DRAFT S
EQUENCE.//3.6e-21:394:66//AL023513

R-HEMBA1007342//Human BAC clone GS368F15 from 7q3
1, complete sequence.//1.7e-15:190:73//AC003080

R-HEMBA1007347//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone N38G6, WORKING DRAFT SE
QUENCE.//2.2e-47:455:77//Z96802

R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPC14-79
3P23 (Roswell Park Cancer Institute Human PAC Libr
ary) complete sequence.//1.1e-62:539:79//AC006208

R-HEMBA1000008//Homo sapiens chromosome 17, clone
hCIT.211_P_7, complete sequence.//1.2e-36:285:83//A
C003665

R-HEMBA1000018//Homo sapiens clone DJ0038110, WORK
ING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-51:41
6:79//AC004820

R-HEMBA1000024//Human DNA sequence from BAC 175E3
on chromosome 22q11.2-qter. Contains ESTs, STSs an
d polymorphic CA repeat.//3.9e-18:211:79//Z95113

R-HEMBA1000025//HS_3064_B2_B07_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3064 Col=14 Row=D, genomic survey sequenc
e.//5.9e-40:254:90//AQ132765

R-HEMBA1000030//Human DNA sequence from clone 108K
11 on chromosome 6p21 Contains SRP20 (SR protein fa
mily member), Ndr protein kinase gene similar to y
east suppressor protein SRP40, EST and GSS, comple
te sequence.//1.5e-32:452:70//Z85986

R-HEMBA1000036//CIT-HSP-2024L15.TF CIT-HSP Homo sa
piens genomic clone 2024L15, genomic survey sequen
ce.//9.3e-63:541:77//B66264

R-HEMBA1000037//Homo sapiens erythroblast macropha
ge protein EMP mRNA, complete cds.//7.6e-91:467:97
//AF084928

R-HEMBA1000039//Homo sapiens chromosome 17, clone
hRPK.401_0_9, complete sequence.//2.4e-44:456:68//A
C005291

R-HEMBA1000044//Human BAC clone RC016J04 from 7q2
1, complete sequence.//1.4e-54:307:80//AC002064

3525

R-HEM BB1000048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence. //3.8e-09:330:63//AC002300

R-HEM BB1000050//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence. //6.7e-12:225:65//Z94056

R-HEM BB1000054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence. //8.9e-76:557:82//AL033521

R-HEM BB1000055//Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds. //1.6e-88:350:86//M81806

R-HEM BB1000059//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces. //4.9e-12:356:65//AC006009

R-HEM BB1000083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces. //3.7e-41:311:82//AC004840

R-HEM BB1000089//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces. //3.6e-34:314:78//AC005520

R-HEM BB1000099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence. //8.8e-32:434:71//AL008715

R-HEM BB1000103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs. //2.5e-16:207:74//Z95115

R-HEM BB1000113//HS_3013_A1_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3013 Col=15 Row=C, genomic survey sequence. //0.94:211:63//AQ118730

R-HEM BB1000119//Homo sapiens ASMTL gene. //1.9e-106:531:96//Y15521

R-HEM BB1000136//Human Chromosome X, complete sequence. //0.00073:359:59//AC002407

R-HEM BB1000141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence. //6.8e-41:280:74//AF043945

R-HEM BB1000144//Homo sapiens chromosome 17, clone 50

3526

hCIT.507_E_2, complete sequence. //0.00083:206:66//AC004134

R-HEM BB1000173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces. //2.5e-82:401:90//AC004085

R-HEM BB1000175

R-HEM BB1000198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-galacturonidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence. //0.91:428:56//AL021368

R-HEM BB1000215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence. //4.4e-54:298:91//AL021397

R-HEM BB1000217

R-HEM BB1000218//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence. //5.8e-32:517:70//AC004216

R-HEM BB1000226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island. //2.5e-77:450:92//Z69706

R-HEM BB1000240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families. //4.1e-05:310:62//AF029308

R-HEM BB1000244//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE. //1.3e-43:278:85//AL034420

R-HEM BB1000250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein S10 pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //3.8e-16:484:64//AL031777

R-HEM BB1000258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HFE) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds. //4.3e-11:286:67//U91328

R-HEM BB1000264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds. //1.2e-42:406:79//AF07976

3527

R-HEM BB1000266//RPCI11-76C20.TV RPCI11 Homo sapiens genomic clone R-76C20, genomic survey sequence.//1.0:232:59//AQ265533

R-HEM BB1000272//HS_3032_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702

R-HEM BB1000274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053

R-HEM BB1000284//Homo sapiens full length insert cDNA clone YY88A05.//6.9e-112:572:96//AF088018

R-HEM BB1000307//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence.//5.7e-96:523:93//AC005244

R-HEM BB1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

R-HEM BB1000317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

R-HEM BB1000318//Human DNA sequence from PAC 292H14 on chromosome Xp21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710

R-HEM BB1000335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179

R-HEM BB1000336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147

R-HEM BB1000337//CIT-HSP-2329010.TF CIT-HSP Homo sapiens genomic clone 2329010, genomic survey sequence.//1.2e-31:192:92//AQ035976

R-HEM BB1000338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//1.9e-39:477:71//AC004605

R-HEM BB1000339//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681

R-HEM BB1000341//Homo sapiens 12q24 PAC RPCI3-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350

R-HEM BB1000343//Homo sapiens chromosome 16, cosmid clone 367E12 (LANL), complete sequence.//3.6e-41:457:72//AC004644

R-HEM BB1000354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751

1.

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R-HEM BB1000369//Homo sapiens chromosome 4 clone B3 66024 map 4q25, complete sequence.//9.0e-25:179:79//AC004067

R-HEM BB1000374//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199

R-HEM BB1000376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675

10 R-HEM BB1000391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080

R-HEM BB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838

R-HEM BB1000402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052

20 R-HEM BB1000404//HS_2246_A2_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251

R-HEM BB1000420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.2e-29:358:72//AC000053

R-HEM BB1000434//Homo sapiens chromosome 4 clone B7 1M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069

30 R-HEM BB1000438//HS_2239_B2_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700

R-HEM BB1000441//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207

R-HEM BB1000449//Homo sapiens clone DJ0898018, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920

R-HEM BB1000455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007

40 R-HEM BB1000472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104

R-HEM BB1000480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849

R-HEM BB1000487

50 R-HEM BB1000490//Human DNA sequence *** SEQUENCING

3529

IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE. //1.5e-34:281:81//AL034423

R-HEM BB1000491//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island. //8.5e-37:483:72//Z93023

R-HEM BB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUCI, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a carepeat polymorphism, complete sequence. //7.6e-14:217:71//AL022721

R-HEM BB1000510//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE. //7.1e-44:221:80//AL033397

R-HEM BB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence. //3.5e-51:280:90//AC002477

R-HEM BB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence. //1.7e-53:304:82//AC004079

R-HEM BB1000530//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence. //4.2e-74:428:92//AC006236

R-HEM BB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence. //5.6e-13:112:80//U91321

R-HEM BB1000554//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE. //5.1e-14:239:63//Z83824

R-HEM BB1000556//Homo sapiens envoplakin (EVPL) mRNA, complete cds. //0.031:275:60//U53786

R-HEM BB1000564//Homo sapiens chromosome 5, BAC clone 189 (LBNL H135), complete sequence. //3.1e-17:227:76//AC005914

R-HEM BB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer. //0.078:161:63//D84405

R-HEM BB1000575//Homo sapiens chromosome 17, clone hRPC.859_0_20, complete sequence. //7.2e-52:260:80//AC003695

R-HEM BB1000586//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X. //2.0e-33:305:79//Z70280

R-HEM BB1000589//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence. //1.3e-14:409:65//AC005208

R-HEM BB1000591//Homo sapiens Xp22 bins 45-47 BAC G 50

3530

SHB-665N22 (Genome Systems Human BAC Library) complete sequence. //6.2e-39:493:71//AC005184

R-HEM BB1000592//Homo sapiens 12p13.3 PAC RPCI5-118OD12 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //1.6e-08:254:64//AC005831

R-HEM BB1000598//Homo sapiens chromosome 11 pac pDJ159o1, complete sequence. //3.3e-38:407:76//AC000381

10 R-HEM BB1000623//CIT-HSP-2374P17. TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence. //1.3e-41:212:100//AQ109717

R-HEM BB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence. //5.2e-31:319:78//AL022724

R-HEM BB1000631//Sequence 28 from patent US 5708157. //6.8e-20:208:80//I80058

20 R-HEM BB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces. //7.4e-47:457:75//AC004176

R-HEM BB1000637//Human BAC clone RG094B21 from 7q21-q22, complete sequence. //2.9e-45:263:87//AC003085

R-HEM BB1000638//Genomic sequence from Human 6, complete sequence. //9.1e-34:375:73//AC002112

R-HEM BB1000643//HS_2242_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=14 Row=C, genomic survey sequence. //0.010:239:60//AQ065993

30 R-HEM BB1000649//Homo sapiens RBP56/hTAFII168 gene, exon 7. //8.3e-63:306:100//AB010061

R-HEM BB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMPR (GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with apolymorphic C A repeat. //3.3e-14:450:64//AL009031

40 R-HEM BB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MXA21, complete sequence. //0.98:251:63//AB005247

R-HEM BB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chromosome X. //6.8e-58:296:85//Z83313

R-HEM BB1000673//CITBI-E1-2506F20. TR CITBI-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence. //0.98:71:76//AQ264731

R-HEM BB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence. //2.6e-11:153:7

3531

7//AL031584

R-nnnnnnnnnnn//Homo sapiens neuroanl mRNA, complete cds.//2.0e-50:287:93//AF040723

R-HEM BB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943

R-HEM BB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380

R-HEM BB1000709//RPCI11-79A8.TV RPCI11 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374

R-HEM BB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence.//0.00018:386:60//AB017066

R-HEM BB1000726//Homo sapiens PAC clone DJ1185107 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990

R-HEM BB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875

R-HEM BB1000749//Homo sapiens clone RC140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069

R-HEM BB1000763//Plasmid Col Ib-P9 (from E.coli K12) colicin Ib promoterregion and 5' coding region.//1.0:115:63//K02071

R-HEM BB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205

R-HEM BB1000781//Homo sapiens Xp22 PACs RPCI1-263P4 and RPCI1-164K3 complete sequence.//0.00054:154:67//AC003046

R-HEM BB1000789//RPCI11-2114.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-2114, genomic survey sequence.//3.0e-09:299:64//B63628

R-HEM BB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362C6, complete sequence.//4.5e-46:185:85//U95740

R-HEM BB1000794//HS_3253_A1_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291

R-HEM BB1000807

R-HEM BB1000810//Human BAC clone RC114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542

R-HEM BB1000821

R-HEM BB1000822//CITBI-E1-2517E13.TF CITBI-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944

3532

R-HEM BB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043

R-HEM BB1000827//Homo sapiens clone DJ0981007, complete sequence.//6.8e-43:319:84//AC006017

R-HEM BB1000831//HS_3247_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850

10 R-HEM BB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with abeta-galacturonidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368

20 R-HEM BB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283

R-HEM BB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086

R-HEM BB1000852//HS_3075_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816

30 R-HEM BB1000870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523

R-HEM BB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474

R-HEM BB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//AC005621

R-HEM BB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061

R-HEM BB1000888//CIT-HSP-2282A13.TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ000826

R-HEM BB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995

R-HEM BB1000893//Homo sapiens BAC clone RC363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492

R-HEM BB1000908//RPCI11-13P12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13P12, genomic survey sequence.//0.98:183:61//B76199

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R-HEM BB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence. //1.7e-28:302:76//AC000024

R-HEM BB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems HumanBAC library) complete sequence. //4.1e-34:314:76//AC003037

R-HEM BB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-224D6 complete sequence. //6.3e-09:536:59//U95739

R-HEM BB1000917//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE. //1.6e-47:234:86//Z93015

R-HEM BB1000927

R-HEM BB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence. //0.090:115:69//B99228

R-HEM BB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence. //5.7e-89:544:90//AC003098

R-HEM BB1000973//Arabidopsis thaliana chromosome II BAC F219 genomic sequence, complete sequence. //0.038:377:58//AC005560

R-HEM BB1000975//Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence. //1.0e-05:342:62//AC006234

R-HEM BB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence. //1.1e-18:231:74//AQ239443

R-HEM BB1000985//HS_3184_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence. //6.3e-52:286:95//AQ150008

R-HEM BB1000991

R-HEM BB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence. //1.4e-42:343:81//AC002368

R-HEM BB1001004

R-HEM BB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence. //3.1e-57:317:94//AQ262056

R-HEM BB1001011//HS_3017_B1_G03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence. //7.3e-34:237:86//AQ101944

R-HEM BB1001014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE. //2.4e-49:417:80//AL031662

R-HEM BB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence. //7.6e-41:303:76//AC002549

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R-HEM BB1001024//Homo sapiens (subclone 2_g5 from P1 H16) DNA sequence. //7.4e-48:341:85//L48475

R-HEM BB1001037//Homo sapiens 22q11 BAC Clone 489d1 In MDR Region, complete sequence. //2.0e-50:416:82//AC005527

R-HEM BB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence. //8.4e-22:288:71//AC004699

R-HEM BB1001051//H. sapiens mRNA for FAN protein. //7.1e-18:114:98//X96586

R-HEM BB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5unordered pieces. //6.1e-94:520:93//AC006014

R-HEM BB1001058//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence. //1.1e-56:242:82//AC004187

R-HEM BB1001060//Human Tigger1 transposable element, complete consensus sequence. //4.2e-66:323:81//U49973

R-HEM BB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING DRAFT SEQUENCE. //4.0e-114:556:98//AL034375

R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds. //2.8e-105:512:97//AF034803

R-HEM BB1001096//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs. //2.4e-13:225:69//Z76735

R-HEM BB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //2.4e-35:295:80//AL022577

R-HEM BB1001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462023, WORKING DRAFT SEQUENCE. //7.9e-46:380:80//AL031431

R-HEM BB1001114//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (CTR2-2), 5'UTR. ESTs, STS. //1.1e-38:306:84//Z99570

R-HEM BB1001117//RPCI11-3518.TK RPCI-11 Homo sapiens genomic clone RPCI-11-3518, genomic survey sequence. //1.5e-08:67:100//AQ047113

R-HEM BB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence. //9.0e-26:481:67//AC003071

R-HEM BB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete s

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equence. //0.045:127:69//Z99495
 R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds. //5.0e-23:285:73//M25077
 R-HEM BB1001137//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 4-09, complete sequence. //2.5e-07:334:62//AL010222
 R-HEM BB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence. //2.5e-46:412:79//AC002564
 R-HEM BB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA. //1.8e-11:148:77//U51904
 R-HEM BB1001153//RPCI11-10L7.TP RPCI-11 Homo sapiens genomic clone RPCI-11-10L7, genomic survey sequence. //2.3e-34:213:82//B71766
 R-HEM BB1001169//Homo sapiens chromosome 17, clone HCIT39C8, complete sequence. //0.040:465:56//AC003070
 R-nnnnnnnnnnnn//Sequence 1 from patent US 5618695. //2.8e-15:176:80//I40055
 R-HEM BB1001177
 R-HEM BB1001182//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 4-52, complete sequence. //1.9e-05:174:70//AL010226
 R-HEM BB1001199
 R-HEM BB1001208
 R-HEM BB1001209//RPCI11-41E13.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41E13, genomic survey sequence. //1.1e-95:473:97//AQ029098
 R-HEM BB1001210//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence. //6.2e-08:412:61//AC005199
 R-HEM BB1001218//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence. //1.0e-46:498:74//B75158
 R-HEM BB1001221//RPCI11-62024.TJ RPCI11 Homo sapiens genomic clone R-62024, genomic survey sequence. //3.2e-09:215:68//AQ200950
 R-HEM BB1001234
 R-HEM BB1001242
 R-HEM BB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4unordered pieces. //1.4e-33:361:72//AC005377
 R-HEM BB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence. //3.8e-105:517:98//AF042089
 R-HEM BB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome. //0.96:203:61//U67461
 R-HEM BB1001267//Human DNA sequence from clone 1409

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on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence. //2.8e-39:320:80//Z98046
 R-HEM BB1001271//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence. //3.9e-47:494:75//AC005544
 R-HEM BB1001282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE. //0.0011:97:79//AL031428
 R-HEM BB1001288
 R-HEM BB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence. //2.0e-31:301:78//AC005601
 R-HEM BB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence. //0.053:283:60//AC003083
 R-HEM BB1001302
 R-HEM BB1001304//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE. //6.3e-15:396:64//AL033397
 R-HEM BB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8SpN6, genomic survey sequence. //3.4e-42:293:86//AC013777
 R-HEM BB1001315//Human NFE genomic fragment. //7.5e-30:243:78//M98511
 R-HEM BB1001317//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence. //2.3e-39:301:82//AC004585
 R-HEM BB1001326//HS_3054_A1_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence. //0.90:117:63//AQ106096
 R-HEM BB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c. //0.037:103:77//D63850
 R-HEM BB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems HumanBAC library) complete sequence. //9.1e-19:229:77//AC003037
 R-HEM BB1001337
 R-HEM BB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region. //2.9e-45:551:72//U85056
 R-HEM BB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds. //2.7e-59:292:99//AF097441
 R-HEM BB1001348//Homo sapiens clone DJ0691F11, WORK

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ING DRAFT SEQUENCE, 11unordered pieces.//9.1e-41:3
26:82//AC004859
R-HEM BB1001356//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 424J12, WORKING DRAFT S
EQUENCE.//1.8e-11:213:67//Z82207
R-HEM BB1001364//HS_3050_A2_F05_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3050 Col=10 Row=K, genomic surveysequenc
e.//1.8e-21:158:91//AQ133940
R-HEM BB1001366//Homo sapiens chromosome 10 clone C 10
IT987SK-1188I5 map 10p11.2-10p12.1, complete seque
nce.//4.1e-37:419:73//AC005876
R-HEM BB1001367//Human Chromosome 16 BAC clone CIT9
87SK-A-234F9, complete sequence.//9.5e-15:201:75//U
91326
R-HEM BB1001369//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 477J10, WORKING DRAFT S
EQUENCE.//1.8e-28:224:83//AL021686
R-HEM BB1001380//HS_2267_B1_F11_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl 20
one Plate=2267 Col=21 Row=L, genomic surveysequenc
e.//4.0e-14:100:95//AQ084896
R-HEM BB1001384//Mus musculus COP9 complex subunit
4 (COPS4) mRNA, complete cds.//9.6e-55:312:81//AF0
71314
R-HEM BB1001387//Homo sapiens chromosome 9, P1 clon
e 8660 (LBNL H105), complete sequence.//1.0:166:63
//AC003953
R-HEM BB1001394//Homo sapiens chromosome 17, clone
hRPK.215_E_13, complete sequence.//1.4e-55:494:76/
/AC005549
R-HEM BB1001410//Homo sapiens PAC clone DJ1102B04 f
rom 7q11.23-7q21, complete sequence.//0.011:208:63
//AC006204
R-HEM BB1001424//Homo sapiens, WORKING DRAFT SEQUEN
CE, 76 unordered pieces.//1.5e-22:325:69//AC002370
R-HEM BB1001426//Homo sapiens 12q24 PAC RPCI3-424M6
(Roswell Park Cancer Institute Human PAC library)
complete sequence.//1.3e-46:328:84//AC002350
R-HEM BB1001429//*** SEQUENCING IN PROGRESS *** Hom 40
o sapiens chromosome 4, BAC clone C0481P14; HTGS p
hase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.
//6.6e-105:550:95//AC006160
R-HEM BB1001436
R-HEM BB1001443//HS_2228_A1_B05_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2228 Col=9 Row=C, genomic survey sequenc
e.//0.37:173:62//AQ066934
R-HEM BB1001449//Homo sapiens clone DJ1129E22, WORK
ING DRAFT SEQUENCE, 7unordered pieces.//2.7e-23:33 50

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9:69//AC005522
R-HEM BB1001454//Homo sapiens chromosome 5, P1 clon
e 1307e8 (LBNL H60), complete sequence.//1.1e-39:2
99:84//AC005355
R-HEM BB1001458//Plasmodium falciparum chromosome
2, section 67 of 73 of the complete sequence.//6.0e
-05:486:59//AE001430
R-HEM BB1001463//Homo sapiens PAC clone DJ0777023 f
rom 7p14-p15, complete sequence.//1.2e-50:317:89//A
C005154
R-HEM BB1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sa
piens genomic clone 2370C10, genomic survey sequen
ce.//0.20:95:71//AQ107941
R-HEM BB1001482//Mus musculus clone OST20235, genom
ic survey sequence.//4.3e-09:192:70//AF046762
R-HEM BB1001500//Human DNA sequence from PAC 465G10
on chromosome X contains Menkes Disease (ATP7A) p
utative Cu++-transporting P-type ATPase exons 2 to
21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801
R-HEM BB1001521//Mus musculus clone OST1209, genom
ic survey sequence.//7.5e-30:332:75//AF046642
R-HEM BB1001527//Homo sapiens clone DJ241P17, WORKI
NG DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:48
3:76//AC005000
R-HEM BB1001531//Human BAC clone 7E17 from 12q, com
plete sequence.//1.3e-08:159:71//AC002070
R-HEM BB1001535//Human DNA sequence from cosmid E12
7C11 on chromosome 22q11.2-qter contains STS.//4.0
e-30:286:79//Z74581
R-HEM BB1001536//Homo sapiens cosmid clone LUCA16 f
rom 3p21.3, complete sequence.//1.6e-39:342:80//U7
3169
R-HEM BB1001537//Genomic sequence from Human 9q34,
complete sequence.//3.7e-41:361:77//AC000394
R-HEM BB1001555//Homo sapiens Chromosome 16 BAC clo
ne CIT987SK-A-485G10, complete sequence.//0.34:212:
61//AC003049
R-HEM BB1001562//Homo sapiens Chromosome 16 BAC clo
ne CIT987SK-A-328A3, complete sequence.//8.0e-40:2
67:88//AC002301
R-HEM BB1001564//Homo sapiens clone DJ0414A15, WORK
ING DRAFT SEQUENCE, 9unordered pieces.//5.1e-30:28
6:76//AC005225
R-HEM BB1001565//Homo sapiens clone DJ0607J02, WORK
ING DRAFT SEQUENCE, 12unordered pieces.//2.5e-15:1
94:75//AC004840
R-HEM BB1001585//Human DNA sequence from clone 790B
6 on chromosome 20p11.22-12.2. Contains STSs and G
SSs, complete sequence.//2.6e-33:234:79//AL031677
R-HEM BB1001586//Homo sapiens clone NH0479C13, WORK

- ING DRAFT SEQUENCE, 12unordered pieces.//2.7e-30:371:74//AC005236
- R-HEM BB1001588//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106
- R-HEM BB1001603//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 4-59, complete sequence.//0.034:302:59//AL010235
- R-HEM BB1001618//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.1e-31:503:68//Z93023
- R-HEM BB1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368
- R-HEM BB1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062
- R-HEM BB1001635//Homo Sapiens Chromosome X clone bW XD90, complete sequence.//1.5e-23:407:69//AC004075
- R-HEM BB1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368
- R-HEM BB1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, CSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506
- R-HEM BB1001653//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344
- R-HEM BB1001665//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572
- R-HEM BB1001668
- R-HEM BB1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//1.8e-115:573:97//AB014546
- R-HEM BB1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//I86429
- R-HEM BB1001685//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//2.6e-43:311:83//AC005411
- R-HEM BB1001695
- R-HEM BB1001704//CIT-HSP-2324C15. TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704
- R-HEM BB1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5unordered pieces.//9.1e-34:296:80//AC004851
- R-HEM BB1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020
- R-HEM BB1001717//CIT-HSP-2378C19. TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992
- R-HEM BB1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBNL H94), complete sequence.//1.8e-10:80:90//AC005613
- R-HEM BB1001736//CIT-HSP-2369K6. TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221
- R-HEM BB1001747//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10C9, LA1733 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671
- R-HEM BB1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.4e-60:242:92//AC005829
- R-HEM BB1001753//RPC111-59J22. TK RPC111 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ200046
- R-HEM BB1001756//Homo sapiens BAC clone RG293F17 from 7p15-p21, complete sequence.//3.1e-18:395:67//AC004130
- R-HEM BB1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050
- R-HEM BB1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IE beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157
- R-HEM BB1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6 -ATPase 9 genes.//0.00073:189:65//X02170
- R-HEM BB1001797//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140
- R-HEM BB1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391
- R-HEM BB1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882
- R-HEM BB1001816//Homo sapiens chromosome 21 PAC LLN LP704C1150Q13.//8.4e-21:164:76//AJ006996
- R-HEM BB1001831//Homo sapiens PAM C00H-terminal int

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erector protein 1 (PCIP1) mRNA, complete cds. //1.7 e-104:498:98//AF056209

R-HEM BB1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence. //9.2e-44:388:71//AC005328

R-HEM BB1001839

R-HEM BB1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence. //0.00093:488:60//AB005241

R-HEM BB1001863//Human poly(ADP-ribose) polymerase 10 gene, 5' end. //1.2e-16:458:65//M60436

R-HEM BB1001867//Human DNA sequence from cosmid U25 D11, between markers DXS366 and DXS87 on chromosome X. //5.0e-31:399:74//Z68327

R-HEM BB1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence. //0.26:303:59//AB020754

R-HEM BB1001869//Homo sapiens chromosome 17, clone hCIT529110, complete sequence. //7.0e-37:285:85//AC002553

R-HEM BB1001872//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y44F5, WORKING DRAFT SEQUENCE. //0.093:367:58//AL009027

R-HEM BB1001874

R-HEM BB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmid sequence. //0.037:406:60//AE001272

R-HEM BB1001880//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence. //1.3e-49:461:77//AC005922

R-HEM BB1001899//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y116A8, WORKING DRAFT SEQUENCE. //0.56:295:60//Z98858

R-HEM BB1001905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE. //1.9e-28:181:75//AL022345

R-HEM BB1001906

R-HEM BB1001908//Genomic sequence from Human 17, complete sequence. //2.9e-36:274:76//AC001231

R-HEM BB1001910//Homo sapiens chromosome 17, clone hCIT39C8, complete sequence. //3.5e-41:408:76//AC003070

R-HEM BB1001911//Homo sapiens *** SEQUENCING IN PROGRESS *** , WORKING DRAFT SEQUENCE. //6.1e-64:310:89//AJ011929

R-HEM BB1001915//Mouse mRNA for arylhydrocarbon receptor, complete cds. //2.0e-20:220:78//D38417

R-HEM BB1001921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE. //1.9e-47:410:80//AL034422

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R-HEM BB1001922//Homo sapiens chromosome 17, clone hCIT421K24, complete sequence. //6.2e-32:378:74//AC004099

R-HEM BB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces. //8.2e-41:304:84//AC000406

R-HEM BB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11. //8.3e-12:202:69//AB020867

R-HEM BB1001944//P. falciparum gene for beta subunit RNA polymerase. //0.00090:264:62//X75544

R-HEM BB1001945//Swietenia humilis DNA for simple tandem repeat (242bp). //0.056:224:62//AJ000408

R-HEM BB1001947//RPC111-60L13.TJ RPC111 Homo sapiens genomic clone R-60L13, genomic survey sequence. //7.4e-23:146:94//AQ202335

R-HEM BB1001950//Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GS S, complete sequence. //0.57:115:68//Z83846

R-HEM BB1001952//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces. //5.6e-36:283:84//AC004676

R-HEM BB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces. //8.9e-60:334:82//AC005037

R-HEM BB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //1.9e-56:518:77//AC005077

R-HEM BB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence. //3.2e-19:157:86//AC005736

R-HEM BB1001967//Homo sapiens DNA for amyloid precursor protein, completed cds. //5.7e-68:314:89//D87675

R-HEM BB1001973//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC E7.1 /

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cosmid 40M1, WORKING DRAFT SEQUENCE. //1.4e-37:484:70//AJ009617
 R-HEMBB1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE. //2.1e-28:286:75//AL034417
 R-HEMBB1001988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE. //6.9e-29:203:88//AL034420
 R-HEMBB1001990//Homo sapiens full length insert cDNA clone ZC33G03. //7.8e-95:456:99//AF086192
 R-HEMBB1001996
 R-HEMBB1001997//Homo sapiens clone RG050N15, WORKING DRAFT SEQUENCE, 26 unordered pieces. //6.4e-26:162:83//AC005055
 R-HEMBB1002002//Human DNA sequence from PAC 2A2 on chromosome X contains ESTs. //8.2e-83:362:93//Z84816
 R-HEMBB1002005//Homo sapiens chromosome 3p clone RPCI5-1034C16, WORKING DRAFT SEQUENCE, 45 unordered pieces. //8.5e-36:291:83//AC005903
 R-HEMBB1002009//Homo sapiens clone DJ0828F13, complete sequence. //5.6e-08:307:65//AC004904
 R-HEMBB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence. //1.9e-05:375:62//B36336
 R-HEMBB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic clone 2313E13, genomic survey sequence. //0.34:241:62//AQ028389
 R-HEMBB1002043//Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence. //7.4e-35:297:82//AC005612

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R-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //5.8e-96:582:90//AC005740
 R-HEMBB1002045//Homo sapiens chromosome 19, cosmid F22676, complete sequence. //4.7e-63:575:77//AC005778
 R-HEMBB1002049//Human Chromosome X clone bWXD187, complete sequence. //1.9e-21:384:64//AC004383
 R-HEMBB1002050//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence. //2.5e-37:368:76//AC005553
 R-HEMBB1002068//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL H170), complete sequence. //0.30:167:65//AC004782
 R-HEMBB1002069//Homo sapiens chromosome 19, cosmid R33516, complete sequence. //2.3e-73:449:84//AC004799
 R-HEMBB1002092//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence. //3.8e-45:307:87//AC005828
 R-HEMBB1002094//Homo sapiens chromosome 19, cosmid R30538, complete sequence. //3.1e-47:457:76//AC005943
 R-HEMBB1002115//HS_2223_B1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, genomic survey sequence. //3.0e-58:295:98//AQ152279
 R-HEMBB1002139//***ALU WARNING: Human Alu-Sq subfamily consensus sequence. //6.6e-49:283:93//U14573
 R-HEMBB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces. //1.1e-45:451:76//AC006006
 R-HEMBB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16 map 10q25, complete sequence. //1.3e-57:359:81//AC005881
 R-HEMBB1002189//Human Chromosome 11 pac pDJ392a17, complete sequence. //4.5e-43:420:77//AC000385
 R-HEMBB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces. //8.2e-33:340:64//AC004913
 R-HEMBB1002193//Sequence 5 from patent US 5709858. //3.2e-23:154:92//I80846
 R-HEMBB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence. //2.6e-52:415:81//AF015148
 R-HEMBB1002218//, complete sequence. //3.4e-17:178:82//AC005300
 R-HEMBB1002232//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces. //1.6e-55:292:88//AC004599

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R-HEM BB1002247//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//2.9e-13:227:70//AC005829

R-HEM BB1002249//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL031733

R-HEM BB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.3e-104:593:91//AC002415

R-HEM BB1002255//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930

R-HEM BB1002266//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//1.3e-09:371:63//AL010216R-HEM BB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, complete

sequence.//1.3e-39:247:86//AC004534

R-HEM BB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//4.1e-84:549:86//U73642

R-HEM BB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.5e-10:164:71//AC004129

R-HEM BB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, complete sequence.//0.39:365:59//AC005028

R-HEM BB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genomic survey sequence.//0.96:180:58//B39313

R-HEM BB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.9e-17:258:73//AC004849

R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//6.9e-96:479:97//AJ010841

R-HEM BB1002358//Human Xp22 BAC CT-285I15 (from Cal Tech/Research Genetics), PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-53:309:83//AC002366

R-HEM BB1002359//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.9e-27:350:74//AC005038

R-HEM BB1002364//Homo sapiens Xp22 PAC RPCI1-108M6 (Roswell Park Cancer Center PAC library) complete sequence.//8.6e-53:302:79//AC003036

R-HEM BB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapping to chromosome 11, band p13.//3.2e-38:199:100//X04094

R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial c 50

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ds.//3.2e-07:120:78//AF072467

R-HEM BB1002383//Human DNA sequence from cosmid U19H10 on chromosome X. Contains ESTs and CA repeat.//0.98:351:58//AL021182

R-HEM BB1002387//HS-1052-B2-G10-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence.//2.0e-07:276:67//B41091

R-HEM BB1002415//Homo sapiens chromosome 17, clone hRPK.209_D_14, complete sequence.//1.4e-25:202:79//AC005730

R-HEM BB1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence.//3.6e-60:401:87//AC004799

R-HEM BB1002442//Homo sapiens clone UWGC:r9a from 6p21, complete sequence.//3.1e-51:358:81//AC006046

R-HEM BB1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//1.4e-115:557:98//AL034349

20 R-HEM BB1002457//Human DNA sequence from clone 364I22 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//6.3e-37:338:80//AL031012

R-HEM BB1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//9.7e-09:314:64//AE000659

R-HEM BB1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSAII project).//0.42:110:74//AL021635

R-HEM BB1002489//Salvelinus fontinalis microsatellite sequence SF0-12.//6.6e-06:167:71//U50302

R-HEM BB1002492//RPCI11-74F21.TK RPCI11 Homo sapiens genomic clone R-74F21, genomic survey sequence.//3.1e-14:410:63//AQ238960

R-HEM BB1002495//HS_3220_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence.//1.3e-24:137:100//AQ180762

40 R-HEM BB1002502//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//9.6e-81:538:86//AC006120

R-HEM BB1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.0061:482:57//AL031313

R-HEM BB1002510//HS_2179_A1_F03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence

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e. //6.9e-35:423:72//AQ298309
 R-HEM BB1002520//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 27K12, WORKING DRAFT SE
 QUENCE. //2.0e-62:201:85//AL033397
 R-HEM BB1002522//Homo sapiens chromosome 5, Pac clo
 ne 61c2 (LBNL H139), complete sequence. //0.99:323:
 58//AC004225
 R-HEM BB1002531
 R-HEM BB1002534//Homo sapiens genomic DNA, chromoso
 me 21q22.2 (Down Syndrome region), segment 2/15, W 10
 ORKING DRAFT SEQUENCE. //1.0e-61:380:79//AP000009
 R-HEM BB1002545//RPCI11-2F3.TVB RPCI-11 Homo sapien
 s genomic clone RPCI-11-2F3, genomic survey sequen
 ce. //3.5e-12:414:63//B63283
 R-HEM BB1002550
 R-HEM BB1002556//*** SEQUENCING IN PROGRESS *** Hom
 o sapiens chromosome 4, BAC clone C0481P14; HTGS p
 hase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.
 //2.6e-62:299:85//AC006160
 R-HEM BB1002579//Human DNA sequence *** SEQUENCING 20
 IN PROGRESS *** from clone 1141E15, WORKING DRAFT
 SEQUENCE. //1.7e-42:286:88//AL034422
 R-HEM BB1002582//Homo sapiens clone DJ1119N05, comp
 lete sequence. //3.0e-14:426:60//AC004968
 R-HEM BB1002590//Homo sapiens clone RG132J19, compl
 ete sequence. //1.1e-30:392:74//AC005163
 R-HEM BB1002596//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 508115, WORKING DRAFT S
 EQUENCE. //8.5e-44:335:83//AL021707
 R-HEM BB1002600//Homo sapiens 12p13.3 PAC RPCI5-106 30
 3M23 (Roswell Park Cancer Institute Human PAC Libr
 ary) complete sequence. //2.0e-105:470:96//AC005865
 R-HEM BB1002601//Homo sapiens chromosome 17, clone
 HRPC837J1, complete sequence. //1.3e-44:445:77//ACO
 04223
 R-HEM BB1002603//Homo sapiens clone UWCC:y23c049 fr
 om 6p21, complete sequence. //7.0e-40:321:82//AC006
 162
 R-HEM BB1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sap
 iens genomic clone 2347D7, genomic survey sequenc 40
 e. //1.1e-44:234:98//AQ060197
 R-HEM BB1002610//Human Chromosome 16 BAC clone CIT9
 87SK-A-363E6, complete sequence. //7.0e-22:455:65//U
 91321
 R-HEM BB1002613//Homo sapiens 12p13.3 BAC RPCI11-47
 6M19 (Roswell Park Cancer Institute Human BAC Libr
 ary) complete sequence. //3.0e-72:302:85//AC005908
 R-HEM BB1002614//Homo sapiens 12q13.1 PAC RPCI1-228
 P16 (Roswell Park Cancer Institute Human PAC Libra
 ry) complete sequence. //3.8e-10:512:60//AC004801 50

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R-HEM BB1002617//Homo sapiens clone DJ1021I20, WORK
 ING DRAFT SEQUENCE, 6 unordered pieces. //6.8e-24:48
 6:63//AC005520
 R-HEM BB1002623//Homo sapiens PAC clone DJ1059M17 f
 rom 7q21-q31.1, complete sequence. //2.4e-41:326:83
 //AC004953
 R-HEM BB1002635//Homo sapiens chromosome 12p13.3 cl
 one RPCI11-189M20, WORKING DRAFT SEQUENCE, 39 unor
 dered pieces. //2.6e-42:360:80//AC005910
 R-HEM BB1002664//Homo sapiens chromosome 21q22.3 PA
 C 171F15, complete sequence. //9.1e-51:335:87//AF04
 2090
 R-HEM BB1002677//Plasmodium falciparum strain Dd2 h
 eat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02
 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9),
 CG1 (cg1), CG6 (cg6), chloroquine resistance candi
 date protein (cg2), and CG7 (cg7) genes, complete
 cds. //0.0011:399:59//AF030694
 R-HEM BB1002683//Homo sapiens chromosome 21q22.3 PA
 C 171F15, complete sequence. //4.1e-55:515:76//AF04
 2090
 R-HEM BB1002684//Human BAC clone RG066D11 from 7q2
 2, complete sequence. //1.7e-18:504:62//AC002430
 R-HEM BB1002686//Homo sapiens full length insert cD
 NA clone ZC65D06. //7.0e-85:413:99//AF086217
 R-HEM BB1002692//Homo sapiens 12p13.3 BAC RPCI11-31
 9E16 (Roswell Park Cancer Institute Human BAC Libr
 ary) complete sequence. //9.8e-69:505:82//AC006206
 R-HEM BB1002697//Plasmodium falciparum 3D7 chromoso
 me 12 PFYAC812 genomic sequence, WORKING DRAFT SEQU
 ENCE, 8 unordered pieces. //0.26:390:58//AC004153
 R-HEM BB1002699//Human NFE genomic fragment. //8.0e-
 32:226:79//M98511
 R-HEM BB1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sa
 piens genomic clone 344K23, genomic survey sequenc
 e. //8.6e-43:351:80//B59764
 R-HEM BB1002705//Plasmodium yoelii rhoptry protein,
 complete cds. //0.0064:454:59//L27838
 R-HEM BB1002712//Human DNA sequence from clone 505B
 13 on chromosome 1p36.2-36.3 Contains CA repeat an
 d GSSs, complete sequence. //9.6e-09:187:67//Z98052
 R-MAMMA1000009//Homo sapiens clone NH0469M07, WORK
 ING DRAFT SEQUENCE, 7 unordered pieces. //4.1e-21:20
 1:80//AC005037
 R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PA
 C clone P169K17, complete sequence. //4.2e-48:306:8
 2//AF015720
 R-MAMMA1000020//Human DNA sequence from clone 551E
 13 on chromosome Xp11.2-11.3 Contains farnesyl pyr
 ophosphate synthetase pseudogene, VT4 protein pseu

- dogene, EST, GSS, complete sequence.//1.4e-41:306:86//AL022163
- R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin 1 (DPI) gene, ESTs, STSs and GSSs, complete sequence.//6.1e-36:281:83//AL031058
- R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c In DGCRRegion, complete sequence.//1.3e-67:321:88//AC000090
- R-MAMMA1000045//Homo sapiens chromosome 4 clone B2 20G8 map 4q21, complete sequence.//6.7e-86:559:86//AC004054
- R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bcamicr01.//0.79:63:77//AF025889
- R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in an intron of the HSET gene coding for a Kinesin related protein, the PHF1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence.//1.6e-53:397:83//AL021366
- R-MAMMA1000069//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.0e-37:295:83//AC005057
- R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//7.1e-45:296:88//AC005867
- R-MAMMA1000085
- R-MAMMA1000092//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//8.2e-34:539:69//AL034410
- R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//3.4e-39:297:85//AC003976
- R-MAMMA1000117//Homo sapiens p47-phox (NCF1) pseudogene, clone P38, exon5.//2.6e-07:162:67//U69641
- R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.1e-13:141:80//AC004882
- R-MAMMA1000133
- R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.7e-18:171:80//AC005
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- R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-49:366:75//AC005000
- R-MAMMA1000143//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC D9.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615
- R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken P52 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//2.1e-68:562:78//AL022476
- R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.3e-06:408:58//AC005089
- R-MAMMA1000171//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381
- R-MAMMA1000173
- R-MAMMA1000175//H. sapiens CpG island DNA genomic Msel fragment, clone 186c5, reverse read cpg186c5.rtlb.//0.072:90:72//Z57594
- R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems HumanBAC library) complete sequence.//1.5e-44:445:75//AC004552
- R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//1.9e-23:135:85//AF038667
- R-MAMMA1000221//HS_3242_B2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, genomic survey sequence.//0.031:167:67//AQ220385
- R-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL031728
- R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, Tapetochoroidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//6.2e-07:445:59//AL022401
- R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complete sequence.//1.6e-25:390:69//AC005266
- R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninein and the K

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IAA0609 gene for a protein similar to *C. elegans* K09C8.4. Contains ESTs, GSSs and a gggt repeat polymorphism, complete sequence. //1.1e-37:327:80//AL008715

R-MAMMA1000257//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE. //1.3e-22:281:74//AL034549

R-MAMMA1000264//*** SEQUENCING IN PROGRESS *** EPM1/APECED region of chromosome 21, clones A68E8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159 G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces. //1.7e-29:337:67//AC003656

R-MAMMA1000266//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE. //7.7e-37:339:80//AL031670

R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence. //1.2e-40:283:86//AF001549

R-MAMMA1000277//CIT-HSP-516K6.TP CIT-HSP Homo sapiens genomic clone 516K6, genomic survey sequence. //3.0e-29:265:80//B49900

R-MAMMA1000278//Sequence 25 from patent US 5708157. //2.6e-39:282:82//I80056

R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence. //1.6e-52:295:84//AC004494

R-MAMMA1000284//CITBI-E1-2522B20.TF CITBI-E1 Homo sapiens genomic clone 2522B20, genomic survey sequence. //1.8e-11:288:61//AQ280722

R-MAMMA1000287

R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence. //4.1e-16:169:77//AC005553

R-MAMMA1000307//RPC111-89L1.TV RPC111 Homo sapiens genomic clone R-89L1, genomic survey sequence. //1.3e-86:429:97//AQ284795

R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds. //0.00020:384:60//AF029779

R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequence. //0.0026:310:60//AF003518

R-MAMMA1000313//Human cosmid Xq28_IA649, complete sequence. //1.5e-26:317:67//U82694

R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUENCE, 5 unordered pieces. //3.1e-39:277:86//AC004947

R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence. //3.2e-44:180:89//AF015147

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R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence. //0.97:293:64//AE001388

R-MAMMA1000348//Homo sapiens BAC129, complete sequence. //4.4e-27:365:72//U85195

R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252 (D97)), complete sequence. //0.73:332:61//AC002493

10 R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence. //4.6e-80:279:89//AC005189

R-MAMMA1000361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 753D4, WORKING DRAFT SEQUENCE. //7.8e-18:346:63//AL031676

R-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE. //5.3e-40:299:83//AL022344

20 R-MAMMA1000385//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE. //1.0e-28:225:84//AL031658

R-MAMMA1000388//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clone 2321D3, genomic survey sequence. //4.7e-60:298:99//AQ038102

R-MAMMA1000395

R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence. //1.4e-84:276:88//AC004692

R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence. //6.7e-35:360:76//AC002394

R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence. //3.1e-69:327:79//AC004662

R-MAMMA1000414//Homo sapiens DNA sequence from PAC164L12 on chromosome Xq13.1-Xq21.2. Contains GSS (BAC end sequence), STS. //3.6e-41:180:87//AL009028

R-MAMMA1000416//Homo sapiens clone DJ1136C02, WORKING DRAFT SEQUENCE, 4 unordered pieces. //3.1e-59:478:77//AC005377

40 R-MAMMA1000421//Human coxVIb gene, last exon and flanking sequence. //5.3e-53:294:82//X58139

R-MAMMA1000422//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 8B22, WORKING DRAFT SEQUENCE. //1.0:252:59//AL031737

R-MAMMA1000423//Homo sapiens clone DA0065C23, complete sequence. //2.0e-50:491:76//AC004816

50 R-MAMMA1000424//Human DNA sequence from PAC 507115 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat. //3.5e-40:340:80//Z98950

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R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:79//AF062484

R-MAMMA1000431//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE, 5unordered pieces.//2.0e-58:564:77//AC004821

R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//3.0e-43:328:83//AC002067

R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequence.//0.95:209:65//U82672

R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.//0.99:182:61//AB019236

R-MAMMA1000468

R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9N34, genomic survey sequence.//1.0e-38:142:88//AG010148

R-MAMMA1000478//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//1.3e-37:286:83//Z93015

R-MAMMA1000483//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//4.3e-34:158:86//B54637

R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//4.2e-98:569:90//AC006130

R-MAMMA1000500//Human BRCA1, Rho7 and vatl genes, complete cds, and ipf35 gene, partial cds.//1.2e-41:334:79//L78833

R-MAMMA1000501//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153C14, WORKING DRAFT SEQUENCE.//1.4e-38:250:84//AL031118

R-MAMMA1000516//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//1.3e-43:318:83//Z82207

R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequence.//4.4e-13:202:73//AL031289

R-MAMMA1000559//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE.//2.2e-30:245:83//Z93015

R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01_183_B_7 map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:80//U82205

R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, complete cds.//9.2e-19:216:76//U18419

R-MAMMA1000576

R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//5.4e-53:297:85//AC005666

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R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUENCE, 4unordered pieces.//1.2e-35:450:71//AC006018

R-MAMMA1000594//Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid5L5, WORKING DRAFT SEQUENCE.//4.3e-26:293:75//AJ009613

R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clone 2341F4, genomic survey sequence.//0.83:110:70//AQ057131

10 R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4unordered pieces.//2.6e-50:290:86//AC004956

R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic clone 2334J18, genomic survey sequence.//0.76:132:65//AQ038364

R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, partial sequence.//6.8e-06:431:59//U06970

R-MAMMA1000621//Human NBR2 mRNA, complete cds.//5.3e-27:258:80//U88573

R-MAMMA1000623

R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complete sequence.//3.3e-07:325:63//AC005498

R-MAMMA1000643//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39B17, WORKING DRAFT SEQUENCE.//1.4e-06:236:68//AL023656

R-MAMMA1000664//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0326F06; HTGS phase 1, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-40:338:81//AC004555

R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//1.2e-46:327:86//AL021578

R-MAMMA1000670

R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence.//2.2e-29:328:76//AL031785

R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds.//0.21:247:63//AF054623

R-MAMMA1000696//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.7e-46:464:71//AC004387

R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.4e-09:244:66//AC005075

50 R-MAMMA1000713//Homo sapiens clone DJ0425I02, WORK

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ING DRAFT SEQUENCE, 5 unordered pieces. //3.7e-51:439:74//AC005478

R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, complete sequence. //2.8e-29:288:75//AC004694

R-MAMMA1000718//Human Xp22 BAC CT-285I15 (from Cal Tech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence. //3.0e-37:231:91//AC002366

R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence. //1.4e-35:299:81//AC005781

R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence. //3.9e-59:409:79//AL022163

R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //9.4e-29:560:66//AC005077

R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces. //2.4e-14:309:68//AC004832

R-MAMMA1000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE. //4.1e-29:377:71//AL008722

R-MAMMA1000734//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE. //2.0e-108:420:99//AL024507

R-MAMMA1000738//Human V beta T-cell receptor (TCRB V) gene locus. //6.6e-41:347:82//U03115

R-MAMMA1000744//T2708-T7 TAMU Arabidopsis thaliana genomic clone T2708, genomic survey sequence. //0.095:367:60//B20150

R-MAMMA1000746//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005; HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces. //7.4e-95:569:87//AC004661

R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence. //1.3e-48:295:84//AC003071

R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence. //5.7e-45:347:82//Z82178

R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence. //1.1e-32:292:80//U73169

R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pi

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eces. //2.5e-50:467:79//AC005412

R-MAMMA1000776//Human BAC clone GS552A01 from 7q21-q22, complete sequence. //1.0e-63:429:79//AC002454
R-MAMMA1000778//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3. //3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence. //0.0021:119:74//AL031120

10 R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3. //6.3e-08:269:64//AJ229042

R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence. //1.1e-36:261:80//AC005339

R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic clone 2387J3, genomic survey sequence. //0.68:156:65//AQ240807

R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726_0_12, WORKING DRAFT SEQUENCE, 6 unordered pieces. //4.6e-50:335:86//AC005517

R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence. //1.3e-40:322:77//U91323

R-MAMMA1000842//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE. //4.1e-44:471:74//Z97985

R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.85:394:60//AC004815

30 R-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE. //0.54:303:63//AL031744

R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete sequence. //1.7e-10:115:83//AF030876

R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete sequence. //5.0e-44:352:83//AC004263

R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complete sequence. //1.8e-10:149:74//AC004611

R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #16. //8.1e-05:205:66//AF009075

R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9 (Lawrence Livermore human cosmid library) complete sequence. //2.9e-49:421:80//AC002364

R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence. //9.1e-41:302:83//AC002301

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R-MAMMA1000867//Human BRCA1, Rho7 and vatI genes, complete cds, and ipf35 gene, partial cds.//1.9e-17:500:61//L78833

R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LANL), complete sequence.//1.2e-17:211:74//AC004653

R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC library) complete sequence.//4.7e-09:160:65//AC003658

R-MAMMA1000877//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.2e-34:354:75//Z93023

R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.4e-41:411:74//AC002425

R-MAMMA1000883

R-MAMMA1000897

R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence.//1.3e-73:304:91//AC004506

R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F14150, genomic sequence, complete sequence.//8.4e-23:194:83//AC003110

R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ41616, complete sequence.//1.5e-09:170:71//AC003024

R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//8.3e-13:323:67//AC005247

R-MAMMA1000921//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//6.8e-28:333:72//AL034379

R-MAMMA1000931//HS_3227_B1_B03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=D, genomic survey sequence.//1.4e-55:443:79//AQ191777

R-MAMMA1000940//Homo sapiens clone RC013F03, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:340:84//AC005046

R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete sequence.//1.8e-53:330:84//AC002347

R-MAMMA1000942//Human Chromosome X clone bWXd187, complete sequence.//1.2e-39:391:74//AC004383

R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.6e-75:566:81//AC002477

R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence.//0.013:285:59//AL034559

R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.2e-45:28

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8:90//AC005096

R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-108:561:96//AC006001

R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.9e-41:287:87//AC004263

R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M06 from 7q11, complete sequence.//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074

R-MAMMA1001035//RPCI-1-46C8Sp6 RPCI-1 Homo sapiens genomic clone RPCI-1-46C8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

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R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20. TF CIT-HSP Homo sa

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piens genomic clone 2371K20, genomic survey sequence.//7.2e-65:346:95//AQ111326

R-MAMMA1001073

R-MAMMA1001074//Homo sapiens BAC clone NH0400010 from Y, complete sequence.//8.6e-33:457:69//AC006040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence.//1.6e-45:344:84//AC005609

R-MAMMA1001082//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//I15499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-51:267:82//AC005951

R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (Intestinal protein OCI-5) (GTR2-2), 5' UTR. ESTs, STS.//6.9e-22:178:85//Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPC1169K15, complete sequence.//3.0e-19:141:81//AC003963

R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345

R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684

R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.//9.5e-49:512:74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-88D1 -complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289

R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA MMDDB (f1

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0080) and MMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWDX173, WORKING DRAFT SEQUENCE, 2 ordered pieces.//3.7e-29:351:74//AC004387

R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662

R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//8.9e-61:567:78//AC005412

R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBNL H44), complete sequence.//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HS P BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708

R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862

R-MAMMA1001249//H. sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221

R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115

R-MAMMA1001259

R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds.//6.3e-20:226:75//AB014561

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTS, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

R-MAMMA1001274//H. sapiens DNA for trapped exon (ID

3561

HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457
 R-MAMMA1001280//Homo sapiens full length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976
 R-MAMMA1001292//Human DNA sequence from clone 1170 K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-14:582:96//AL022314
 R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730
 R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.5e-38:306:83//AC005703
 R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838
 R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398
 R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614
 R-MAMMA1001330//Human BAC clone RC066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430
 R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 20q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93016
 R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041
 R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685
 R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815

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R-MAMMA1001388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508I15, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707
 R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044
 R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805
 10 R-MAMMA1001411//T15F1-T7.1 TAMU Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957
 R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//2.8e-09:377:63//AC005179
 R-MAMMA1001435//S.pombe chromosome I cosmid c26H5. 20 //1.0:356:59//Z99126
 R-MAMMA1001442//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//3.4e-17:259:72//AC004047
 R-MAMMA1001446//Homo sapiens BAC clone RC139P11 from 7q11-q21, complete sequence.//2.9e-17:231:71//AC004491
 R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:73 30 //AL024493
 R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequence.//3.0e-23:141:96//B04295
 R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.4e-09:309:64//L31783
 R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108_L_11, complete sequence.//5.1e-30:286:79 40 //AC005206
 R-MAMMA1001501
 R-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL031714
 R-MAMMA1001510
 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBNL H194), complete sequence.//1.5e-09:136:75//AC005352
 R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:300:84//AC002418 50

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R-MAMMA1001551//Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat. //1.1e-57:282:89//AL020997

R-MAMMA1001575

R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds. //7.6e-60:530:78//M61764

R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds. //1.3e-29:161:86//U78027

R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence. //2.1e-18:390:66//AC004216

R-MAMMA1001604//Human DNA sequence from clone 1042 K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence. //1.0:227:62//AL022238

R-MAMMA1001606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE. //1.3e-17:219:69//AL031985

R-MAMMA1001620//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE. //2.1e-51:298:84//AL031650

R-MAMMA1001627//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE. //7.8e-45:328:85//Z86090

R-MAMMA1001630//, complete sequence. //2.5e-08:170:72//AC005399

R-MAMMA1001633//Homo sapiens chromosome 10 clone C1T987SK-1057L21 map 10q25, complete sequence. //2.2e-21:241:70//AC005386

R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence. //1.1e-32:346:74//Z84466

R-MAMMA1001649

R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence. //9.4e-68:267:89//AC004811

R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands. //1.7e-49:322:88//Z82216

R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence. //2.4e-114:575:96//AC005614

R-MAMMA1001679//CIT-HSP-2335N4. TF CIT-HSP Homo sapiens genomic clone 2335N4, genomic survey sequence. //2.4e-82:400:99//AQ037393

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R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces. //5.7e-47:533:72//AC004166

R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HS P-444n24, complete sequence. //6.6e-12:194:72//AC005261

R-MAMMA1001692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE. //9.6e-44:414:77//AL022345

R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21, complete sequence. //3.1e-31:436:70//AF110324

R-MAMMA1001715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 73E16, WORKING DRAFT SEQUENCE. //8.8e-76:524:84//Z95330

R-MAMMA1001730

R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta tubulin (clone B9T), partial. //2.7e-13:382:63//X60786

R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE. //3.9e-47:318:87//AP000050

R-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence. //4.0e-108:566:95//AC006017

R-MAMMA1001744

R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence. //3.5e-113:564:97//AF070718

R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complete sequence. //3.6e-30:312:75//AC005625

R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds. //4.7e-34:320:77//AF041338

R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence. //4.7e-10:244:67//AC003688

R-MAMMA1001760//RPC11-38L16. TV RPC1-11 Homo sapiens genomic clone RPC1-11-38L16, genomic survey sequence. //1.3e-10:236:64//AQ029432

R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.74:361:60//AC005140

R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPC.147_L_13, complete sequence. //1.6e-42:416:76//AC005332

R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence. //1.4e-13:129:83//AC004686

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R-MAMMA1001771//M. musculus mRNA for semaphorin B. /1.1e-34:530:69//X85991
 R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFTSEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360
 R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8 complete sequence.//3.0e-49:282:86//U91319
 R-MAMMA1001788
 R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6unordered pieces.//9.8e-43:530:71//AC004913
 R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//1.8e-43:324:79//AC004020
 R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of 73 ofthe complete sequence.//0.65:183:63//AE001432
 R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-10:417:62//AC005018
 R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324H7 (Genome Systems Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859
 R-MAMMA1001818
 R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.2e-45:340:82//AC004086
 R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUENCE, 8unordered pieces.//1.9e-53:291:85//AC004966
 R-MAMMA1001836//HS_3164_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, genomic survey sequence.//6.5e-08:79:89//AQ185484
 R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-55:309:85//AC003682
 R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, complete sequence.//1.6e-16:125:90//AC006144
 R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099
 R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.//1.7e-38:308:82//AC002425
 R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X inactivation transcript (XIST) gene, complete sequence.//6.5e-50:283:86//U80460
 R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone

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pDJ398g19, WORKING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143
 R-nnnnnnnnnnnnn//Plasmodium falciparum chromosome 2, section 54 of 73 ofthe complete sequence.//1.4e-11:495:63//AE001417
 R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117
 R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKN1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase andreceptor genes and ESTs, STSs and CpG islands.//6.9e-44:391:78//Z85996R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosome 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097
 R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-670B5 -complete genomic sequence, complete sequence.//1.7e-43:283:86//AC002303
 R-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL031720
 R-nnnnnnnnnnnnn//Saccharomyces cerevisiae chromosome IV cosmid 9481.//2.9e-14:505:60//U28373
 R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008
 R-MAMMA1001956//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380
 R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149
 R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128
 R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071
 R-MAMMA1001992//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581
 R-MAMMA1002009//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109C6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879
 R-MAMMA1002011
 R-MAMMA1002032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284
 R-MAMMA1002033//Homo sapiens chromosome 5, Pac clo

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ne 162o17 (LBNL H147), complete sequence. //2.5e-17:170:81//AC003954
 R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence. //8.7e-79:296:85//AC004865
 R-MAMMA1002042//Human chromosome 16 BAC clone CIT9 87SK-A-962B4, complete sequence. //8.8e-46:386:80//U91318
 R-MAMMA1002047//Human chromosome 16 BAC clone CIT9 87SK-A-962B4, complete sequence. //1.9e-32:326:75//U91318
 R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506_H_21, complete sequence. //6.6e-48:367:82//AC005962
 R-MAMMA1002058//Homo sapiens clone RG038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.25:139:69//AC005052
 R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces. //2.2e-45:406:78//AC004676
 R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence. //2.3e-22:357:64//AC005291
 R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence. //2.5e-38:304:82//AC004263
 R-MAMMA1002084//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9, WORKING DRAFT SEQUENCE. //8.9e-41:319:83//AL031602
 R-MAMMA1002093//CIT-HSP-2060J9.TF CIT-HSP Homo sapiens genomic clone 2060J9, genomic survey sequence. //9.7e-17:129:88//B69983
 R-MAMMA1002108
 R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence. //0.94:168:64//Z73495
 R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence. //4.8e-40:313:83//AC005670
 R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence. //2.0e-70:461:83//AC004953
 R-MAMMA1002140//Human DNA sequence from PAC 465C10 on chromosome X contains Menkes Disease (ATP7A) putative Cu⁺⁺-transporting P-type ATPase exons 2 to 21, PCAM-B, ESTs. //1.1e-32:477:73//Z94801
 R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1. //6.6e-06:130:73//AF027357
 R-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE. //6.0e-19:242:73//AL031447

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R-MAMMA1002153//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0281M17; HTCS phase 1, WORKING DRAFT SEQUENCE, 3 unordered pieces. //2.1e-51:291:75//AC006052
 R-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 608E8, WORKING DRAFT SEQUENCE. //1.2e-53:461:79//AL022343
 R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence. //5.1e-37:305:82//AC004997
 R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence. //8.1e-34:296:81//AL034418
 R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celsr1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylate)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence. //7.9e-39:332:82//AL031588
 R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence. //4.4e-12:189:72//AC005871
 R-MAMMA1002198//Homo sapiens clone DJ0800C07, complete sequence. //1.1e-48:338:81//AC004890
 R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence. //1.2e-23:269:74//AC005821
 R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE, 5 unordered pieces. //3.2e-12:243:68//AC005158
 R-MAMMA1002219//Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence. //3.3e-45:295:88//AC004802
 R-MAMMA1002230//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //7.3e-41:385:78//AL034379
 R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit(eIF-2B gamma) mRNA, complete cds. //7.3e-45:363:79//U38253
 R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence. //2.8e-119:582:98//AC005666
 R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9C (LANL), complete sequence. //4.7e-42:319:

- 84//AC005600
 R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-33:571:67//AC006120
 R-MAMMA1002268//Mus musculus sphingosine kinase (S PHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749
 R-MAMMA1002269//345I17.TV CIT978SKA1 Homo sapiens genomic clone A-345I17, genomic survey sequence.//4.7e-05:153:69//B15590
 R-MAMMA1002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987
 R-MAMMA1002292//Hordeum vulgare lipoygenase 2 (Lo xC) mRNA, complete cds.//0.074:178:61//L37358
 R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568
 R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-35:281:82//AC004231
 R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375
 R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from 7q11.23, complete sequence.//1.8e-17:296:70//AC005074
 R-MAMMA1002299//HS_3116_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526
 R-MAMMA1002308
 R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979
 R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869
 R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:323:87//AL031054
 R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756
 R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042
 R-MAMMA1002329//M.musculus mRNA for semaphorin B.//50
 2.0e-12:210:73//X85991
 R-MAMMA1002332//Homo sapiens PAC clone DJ1139I01 from Xq23, complete sequence.//3.4e-46:393:71//AC004973
 R-MAMMA1002333//HS_3245_A1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759
 R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549
 R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPCI3-305120 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088
 R-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100
 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228
 R-MAMMA1002353//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996
 R-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241
 R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//8.3e-28:187:91//AC004662
 R-MAMMA1002359//Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//Z68869
 R-MAMMA1002360//HS_2163_B2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213
 R-MAMMA1002361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520
 R-MAMMA1002362//H.sapiens PEX gene.//1.8e-40:243:86//Y10196
 R-MAMMA1002380//RPCI11-73J4.TJ RPCI11 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168
 R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPCI11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801
 R-MAMMA1002385
 R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430
 R-MAMMA1002411//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE. //9.4e-22:496:65//AL031668

R-MAMMA1002413//Homo sapiens 12q24.2 PAC RPCI1-157 K6 (Roswell Park Cancer Institute Human PAC library) complete sequence. //2.3e-15:153:77//AC005146
R-MAMMA1002417//Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat. //1.8e-23:508:62//AL020997
R-MAMMA1002427//Human Chromosome 16 BAC clone CIT9 87SK-A-363E6, complete sequence. //2.5e-37:288:84//U91321

R-MAMMA1002428//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE. //6.0e-05:130:75//AL034423

R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS. //4.8e-18:205:78//AL022396

R-MAMMA1002446//CIT-HSP-2021L14. TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence. //4.6e-41:387:72//B65379

R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence. //1.2e-67:491:82//AC005512

R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence. //1.4e-28:188:85//AC003982

R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205. //6.3e-09:280:61//U10556

R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs. //1.5e-25:310:74//Z83822

R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //1.2e-98:533:93//AC005077

R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds. //2.7e-114:560:97//AF055460

R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3. //2.1e-46:329:84//Z69375

R-MAMMA1002498//Rat mRNA. //0.0068:223:64//M59859

R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.012:460:60//AC005139

R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds. //1.2e-101:529:95//AF065214

R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds. //6.6e-50:471:77//AF041427

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R-MAMMA1002554//Homo sapiens chromosome 4 clone B2 27H22 map 4q25, complete sequence. //5.7e-38:279:84//AC004056

R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence. //9.6e-13:237:67//AC005878

R-MAMMA1002566//CITBI-E1-2509P21. TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence. //9.7e-14:216:73//AQ261427

10 R-MAMMA1002571//CITBI-E1-2516L21. TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence. //4.6e-25:142:99//AQ279542

R-MAMMA1002573//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 811H13, WORKING DRAFT SEQUENCE. //1.1e-30:250:82//AL023805

R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end. //1.0:196:61//M58580

R-MAMMA1002590//H. sapiens CpG island DNA genomic Msel fragment, clone 8d5, forward read cpg8d5.flg. //1.0:114:64//Z63758

R-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE. //9.0e-96:459:98//AL034548

R-MAMMA1002598//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE. //0.79:362:58//AL031847

R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPF.214_C_8, complete sequence. //1.3e-46:333:80//AC005803

30 R-MAMMA1002612//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 269M15, WORKING DRAFT SEQUENCE. //7.4e-41:283:86//AL021395

R-MAMMA1002617//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE. //1.7e-20:308:71//AL031594

R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence. //1.2e-31:230:76//AC005067

R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPC IP704E14135Q2. //9.0e-113:551:98//AJ010598

40 R-MAMMA1002622//Homo sapiens chromosome 4 clone B2 07D4 map 4q25, complete sequence. //2.8e-43:324:83//AC004050

R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence. //2.7e-80:344:84//AC004687

R-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING DRAFT SEQUENCE. //2.6e-34:391:72//AL031727

50 R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmids R32543, , and F15613 containing

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ining ZNF gene family member, genomic sequence, complete sequence. //5.5e-58:346:81//AC003006
 R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces. //1.1e-52:285:92//AC004895
 R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds. //2.1e-13:359:64//AF055666
 R-MAMMA1002646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING DRAFT SEQUENCE. //2.5e-24:285:68//AL023585
 R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11. //0.64:237:61//X03424
 R-MAMMA1002655//Homo sapiens minisatellite ceb1 repeat region. //0.18:152:65//AF048727
 R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence. //2.5e-46:370:82//AC004870
 R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs. //7.4e-55:298:92//Z92844
 R-MAMMA1002671//RPC11-45M10.TK RPC11 Homo sapiens genomic clone R-45M10, genomic survey sequence. //0.99:151:66//AQ194411
 R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and CSSs, complete sequence. //3.1e-38:410:76//AL022162
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds. //1.4e-107:544:96//D86987
 R-MAMMA1002685//HS_2052_A1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=0, genomic survey sequence. //1.2e-23:255:75//AQ231087
 R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence. //1.1e-38:299:83//AC004673
 R-MAMMA1002699//Mus musculus intersectin-EH binding protein Ibp1 mRNA, partial cds. //3.3e-05:61:93//AF057285
 R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds. //3.5e-39:317:81//AB011399
 R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPC15-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence. //0.26:365:62//AC005293
 R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13. //2.5e-31:304:77//AJ006995
 R-MAMMA1002721//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SE

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QUENCE. //2.3e-40:279:87//Z83826
 R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces. //0.45:183:64//AC004710
 R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence. //1.1e-42:410:74//AC002037
 R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence. //1.6e-19:473:63//U96629
 R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence. //2.2e-108:544:97//AC005856
 R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //5.9e-106:551:95//AC006055
 R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces. //1.7e-34:305:79//AC005020
 R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence. //0.00014:130:74//U95626
 R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete sequence. //8.7e-10:118:81//AC005781
 R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence. //1.2e-31:290:78//AC006128
 R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X. //0.94:260:62//Z82975
 R-MAMMA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE. //2.6e-21:529:62//AL031667
 R-MAMMA1002782//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE. //2.8e-30:234:72//AL022320
 R-MAMMA1002796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE. //1.0:155:66//AL021394
 R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence. //5.0e-42:443:75//Z95331
 R-MAMMA1002820//345M16.TVB CIT978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence. //1.3e-14:95:87//B17487
 R-MAMMA1002830//Human PAC clone DJ515N1 from 22q1

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1.2-q22, complete sequence.//4.1e-20:223:74//AC002073

R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPC I4-617A9 (Roswell ParkCancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295

R-MAMMA1002835

R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic Ro RNA.//4.4e-14:108:92//V00585

R-MAMMA1002842//CIT-HSP-2017022. TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141

R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007

R-MAMMA1002844

R-MAMMA1002858//H. sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067

R-MAMMA1002868//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2unordered pieces.//9.6e-39:288:81//AC004906

R-MAMMA1002871//Homo sapiens BAC clone NH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:57//AC006044

R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome System s Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296

R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//5.1e-41:264:87//U18271

R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence.//4.7e-32:216:90//AL022069

R-MAMMA1002887

R-MAMMA1002890

3.4e-49:376:81//AG006257

R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 f

rom 7q11, complete sequence.//6.0e-60:344:79//AC004881

R-MAMMA1002895//RPC111-90K13. TV RPC111 Homo sapiens genomic clone R-90K13, genomic survey sequence.//2.1e-34:300:77//AQ283502

R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070

R-MAMMA1002909//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798

R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//AC006019

R-MAMMA1002938//C. pasteurianum gap gene.//1.0:343:59//X72219

R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//6.3e-88:556:87//AC006120

R-MAMMA1002947

0.48:156:69//AC005469

R-MAMMA1002964//Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997

R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200

R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt].//0.97:305:62//S81737

R-MAMMA1002973//Human DNA sequence from cosmid V21OE9, between markers DXS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280

R-MAMMA1002982

1.0e-27:110:85//AC005524

R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14,

3577

complete sequence.//1.4e-28:527:66//AC004460
 R-MAMMA1003003//Homo sapiens chromosome 10 clone C
 RI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUE
 NCE, 1 ordered pieces.//7.9e-48:418:78//AC006109
 R-MAMMA1003004//, complete sequence.//2.0e-12:442:
 61//AC005406
 R-MAMMA1003007//Homo sapiens chromosome 10 clone C
 RI-JC2059 map 10q24.1-10q24.2, WORKING DRAFT SEQUE
 NCE, 1 ordered pieces.//1.7e-48:293:91//AC006109
 R-MAMMA1003011//A-306G8.TP CIT978SK Homo sapiens g
 enomic clone A-306G8, genomic survey sequence.//0.4
 5:168:64//B18092
 R-MAMMA1003015//Homo sapiens chromosome 5p, BAC cl
 one 50g21 (LBNL H154), complete sequence.//2.9e-44:
 399:77//AC005740
 R-MAMMA1003019//RPCI11-9J9.TV RPCI-11 Homo sapiens
 genomic clone RPCI-11-9J9, genomic survey sequenc
 e.//2.7e-14:294:68//B71583
 R-MAMMA1003026//HS_2166_B2_C12_MF CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2166 Col=24 Row=F, genomic surveysequenc
 e.//0.021:189:64//AQ125639
 R-MAMMA1003031//Homo sapiens chromosome 5, BAC clo
 ne 319C17 (LBNL H159), complete sequence.//1.8e-98:
 525:95//AC005214
 R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5
 (Lawrence Livermore LL12NC01 or LL12NC02 human co
 smid libraries) complete sequence.//6.7e-06:297:63
 //AC004550
 R-MAMMA1003039//RPCI11-56J17.TJ RPCI11 Homo sapien
 s genomic clone R-56J17, genomic survey sequence./
 /0.21:375:59//AQ081889
 R-MAMMA1003040//Human DNA sequence from cosmid L10
 8f12, Huntington's Disease Region, chromosome 4p1
 6.3.//2.7e-29:298:67//Z49235
 R-MAMMA1003044//Homo sapiens chromosome 19, cosmid
 R30676, complete sequence.//2.9e-14:113:91//AC004
 560
 R-MAMMA1003047
 R-MAMMA1003049
 R-MAMMA1003055//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 377F16, WORKING DRAFT S
 EQUENCE.//2.3e-45:317:86//Z93783
 R-MAMMA1003056//Homo sapiens chromosome 19, cosmid
 R34275, complete sequence.//1.0:229:63//AC005305
 R-MAMMA1003057//M.domesticus MD6 mRNA.//6.2e-42:32
 6:82//X54352
 R-MAMMA1003066//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 473B4, WORKING DRAFT SE
 QUENCE.//3.1e-49:299:87//Z83826

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R-MAMMA1003089//Homo sapiens BAC clone RG298G08 fr
 om 7p15-p21, complete sequence.//2.7e-30:520:67//AC
 005084
 R-MAMMA1003099//RPCI11-8N9.TP RPCI-11 Homo sapiens
 genomic clone RPCI-11-8N9, genomic survey sequenc
 e.//4.2e-44:338:82//B71494
 R-MAMMA1003104//Mus musculus rostral cerebellar ma
 lformation protein (rcm) mRNA, complete cds.//3.4e
 -48:423:79//U72634
 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 cl
 one RPCI11-433J6, WORKING DRAFT SEQUENCE, 100 unor
 dered pieces.//4.8e-114:567:97//AC006087
 R-MAMMA1003127//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 250D10, WORKING DRAFT S
 EQUENCE.//1.4e-34:283:83//Z99716
 R-MAMMA1003135//P.knowlesi Mbn-cutting sites in la
 mbda KBS50.//0.010:243:62//M38776
 R-MAMMA1003140//Homo sapiens chromosome 17, clone
 HCIT87C17, complete sequence.//6.7e-34:288:81//ACO
 03663
 R-MAMMA1003146//Saccharomyces douglasii mitochondr
 ial cytochrome c oxidase subunit I (COXI) gene, co
 mplete cds.//4.8e-08:438:59//M97514
 R-nnnnnnnnnnnnn//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 598F2, WORKING DRAFT SE
 QUENCE.//1.7e-63:149:94//AL021579
 R-MAMMA1003166//HS_3128_A1_B01_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3128 Col=1 Row=C, genomic survey sequenc
 e.//3.0e-17:261:70//AQ140766
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequ
 ence.//2.6e-111:593:94//AF070640
 R-NT2RM4000024
 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 f
 rom 7p21, complete sequence.//0.026:476:56//AC0049
 93
 R-NT2RM4000030//Mus musculus musculus sex determin
 ing protein (Sry) gene, complete cds.//0.00044:37
 8:59//U70653
 R-NT2RM4000046//M.mulatta MHC DR beta 6 gene encod
 ing major histocompatibility complex.//0.27:130:64
 //Z26239
 R-NT2RM4000061
 R-NT2RM4000085//Homo sapiens clone 24700 unknown m
 RNA, partial cds.//7.2e-112:550:97//AF070639
 R-NT2RM4000086//RPCI11-6J23.TV RPCI-11 Homo sapien
 s genomic clone RPCI-11-6J23, genomic survey sequen
 ce.//7.2e-18:277:71//B49463
 R-NT2RM4000104//F.rubripes GSS sequence, clone 063
 K10aG5, genomic surveysequence.//3.6e-08:287:61//Z

88817

R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence. //9.4e-08: 336:65//AC005199

R-NT2RM4000155

R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence. //3.4e-23: 335:72//AC005856

R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds. //1.6e-87: 551:87//D12646

R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence. //5.9e-14: 122:88//L22154

R-NT2RM4000191

R-NT2RM4000197//HS_3241_A2_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=10 Row=0, genomic survey sequence. //2.8e-86: 430:97//AQ206812

R-NT2RM4000199//Mus musculus Yp BAC GSHB-368G7 (Genome Systems Mouse BACLibrary) complete sequence. //0.0047: 193:63//AC006056

R-NT2RM4000200

R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LANL), complete sequence. //2.1e-40: 334:76//AC004035

R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds. //5.2e-102: 546:94//AB018255

R-NT2RM4000215

R-nnnnnnnnnnnn//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence. //2.1e-55: 303:86//AC005383

R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7. //1.2e-07: 198:67//AF003735

R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence. //1.7e-49: 322:88//AC006116

R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 72F8 In DCCR Region, complete sequence. //0.97: 184:66//AC000085

R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence. //6.2e-66: 552:78//AC000055

R-NT2RM4000290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 394I7, WORKING DRAFT SEQUENCE. //1.4e-05: 229:65//AL023585

R-NT2RM4000324

R-NT2RM4000327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE. //3.3e-42: 443:75//Z97199

R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces. //6.4e-64: 450

33:84//AC004826

R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds. //7.7e-11: 210:69//D13630

R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8. //0.084: 257:60//U50066

R-NT2RM4000356

R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds. //8.7e-112: 577:95//AB014542

R-NT2RM4000368

1.6e-48: 348:85//AG006257

R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds. //4.4e-35: 141:87//D42148

R-NT2RM4000395//RPCI11-8N9.TP RPCI-11 Homo sapiens genomic clone RPCI-11-8N9, genomic survey sequence. //1.4e-25: 207:75//B71494

R-NT2RM4000414//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE. //7.1e-17: 492:64//AL031985

R-NT2RM4000421//RPCI11-66B1.TK RPCI11 Homo sapiens genomic clone R-66B1, genomic survey sequence. //1.8e-40: 311:82//AQ241167

R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces. //2.5e-47: 316:87//AC005867

R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Stra6) mRNA, complete cds. //1.6e-17: 133:78//AF062476

R-NT2RM4000457

R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial. //4.6e-113: 559:96//AJ010952

R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone: RES4-22C. //0.00015: 170:67//AB000461

R-NT2RM4000496

R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds. //0.21: 290:58//M80829

R-NT2RM4000514//CIT-HSP-2169K4. TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey sequence. //1.5e-20: 150:89//B95717

R-nnnnnnnnnnnn//HS-1024-B2-G01-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 803 Col=2 Row=N, genomic survey sequence. //6.3e-10: 74:98//B34556

R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12. //0.15: 406:61//AF078790

R-NT2RM4000531

R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of the complete sequence. //1.0: 119:66//AE001391

R-NT2RM4000534//paramecium species 4.51er mt dna d

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imer: replication init. region, clone 2.//9.8e-05:
326:60//K00909
R-NT2RM4000585//HS_3252_A2_G08_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3252 Col=16 Row=M, genomic surveysequenc
e.//1.9e-69:376:93//AQ219890
R-NT2RM4000590//CIT-HSP-539024.TV CIT-HSP Homo sap
iens genomic clone 539024, genomic survey sequenc
e.//1.7e-38:226:93//B50657
R-NT2RM4000595//Human Chromosome X clone bWXD342, 10
complete sequence.//1.0:239:61//AC004072
R-NT2RM4000603//RPC111-49P13.TK RPC111 Homo sapien
s genomic clone R-49P13, genomic survey sequence.//
/0.77:139:64//AQ051950
R-nnnnnnnnnnnnn
R-NT2RM4000616//HS_3107_A2_B03_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3107 Col=6 Row=C, genomic survey sequenc
e.//1.3e-54:272:99//AQ210034
R-NT2RM4000674
R-NT2RM4000689//Mus musculus pericentrin mRNA, com
plete cds.//3.5e-70:551:80//U05823
R-NT2RM4000698
R-nnnnnnnnnnnnn
R-NT2RM4000712//Homo sapiens clone NH0512E16, comp
lete sequence.//0.54:294:58//AC005039
R-NT2RM4000717//Plasmodium falciparum MAL3P8, comp
lete sequence.//0.050:387:58//AL034560
R-NT2RM4000733//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 423B22, WORKING DRAFT S 30
EQUENCE.//1.0e-107:566:95//AL034379
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 pro
tein, partial cds.//1.1e-103:536:95//AB018303
R-NT2RM4000741//CIT-HSP-2294N4.TR CIT-HSP Homo sap
iens genomic clone 2294N4, genomic survey sequenc
e.//5.2e-41:244:93//AQ006361
R-NT2RM4000751//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 537K23, WORKING DRAFT S
EQUENCE.//2.7e-28:416:67//AL034405
R-NT2RM4000764//Human HepG2 3' region HboI cDNA, c 40
lone hmd3g01m3.//2.1e-33:199:96//D17217
R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Geno
me Systems BAC library) complete sequence.//0.0006
0:241:62//AC002980
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 pro
tein, complete cds.//2.9e-104:546:94//AB007920
R-NT2RM4000787//Homo sapiens, clone hRPK.3_A_1, co
mplete sequence.//5.3e-32:321:77//AC006198
R-NT2RM4000790//Homo sapiens chromosome 19, cosmid
R27216, complete sequence.//1.9e-111:552:97//AC00 50

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5306
R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosm
id Clone cos39, complete sequence.//0.74:364:57//U
58675
R-NT2RM4000796//Homo sapiens full length insert cD
NA clone ZD62D10.//2.7e-105:510:98//AF086348
R-NT2RM4000798//Human polymorphic epithelial mucin
core protein mRNA, 3' end.//7.7e-27:158:96//M21868
R-NT2RM4000813
R-NT2RM4000820//, complete sequence.//2.0e-104:43
2:97//AC005406
R-NT2RM4000833//Arabidopsis thaliana genomic DNA,
chromosome 5, P1 clone: MXI22, complete sequence./
/2.0e-07:166:68//AB012248
R-NT2RM4000848//Rabies virus matrix (M) protein mR
NA, complete cds.//0.073:70:84//M22013
R-NT2RM4000852//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC1122 genomic sequence, WORKING DRAFT SE
QUENCE, 3 unordered pieces.//1.0:237:62//AC004709
20 R-NT2RM4000855
R-nnnnnnnnnnnnn//HS_3189_B2_B08_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3189 Col=16 Row=D, genomic surveysequenc
e.//2.1e-06:114:73//AQ300597
R-NT2RM4000895//Pan troglodytes HS19.8-similar loc
us and Y Alu element, genomic survey sequence.//3.8
e-46:207:91//AF077058
R-NT2RM4000950//Human BAC clone RC341D10 from 7p15
-p21, complete sequence.//1.0:336:60//AC002530
30 R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2,
U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U15
3E6, L35485, and R7-163A8 containing iduronate 2-s
ulfatase gene and pseudogene, complete sequence.//
7.1e-09:259:64//AF011889
R-NT2RM4000979
R-NT2RM4000996//HS_3164_A1_E02_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=3164 Col=3 Row=I, genomic survey sequenc
e.//2.0e-82:443:94//AQ141622
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 pro
tein, partial cds.//1.2e-112:545:97//AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 pro
tein, partial cds.//7.9e-113:556:97//AB014539
R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 gen
es.//1.2e-10:120:82//AJ224639
R-NT2RM4001047//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 163G9, WORKING DRAFT SE
QUENCE.//1.0:158:67//AL008733
R-NT2RM4001054//CIT-HSP-2292N8.TR CIT-HSP Homo sap
iens genomic clone 2292N8, genomic survey sequenc

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e. //5.8e-19:118:97//AQ004096
 R-nnnnnnnnnnnn//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2. //1.0e-05:271:64//M10296
 R-NT2RM4001092//CITBI-E1-2524J20. TR CITBI-E1 Homo sapiens genomic clone2524J20, genomic survey sequence. //1.0:186:63//AQ277294
 R-NT2RM4001116
 R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence. //3.6e-79:468:90//AC004593
 R-NT2RM4001151//HS_2270_B1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence. //5.5e-62:312:98//AQ163739
 R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces. //1.4e-107:536:97//AC005841
 R-NT2RM4001160//HS_3015_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence. //7.1e-35:201:95//AQ118712
 R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1. //0.019:177:63//X57201
 R-NT2RM4001191//HS_3002_A1_F05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence. //3.9e-33:230:75//AQ088791
 R-NT2RM4001200//Homo sapiens full length insert cDNA clone YL35H03. //7.5e-69:335:99//AF085857
 R-NT2RM4001203
 R-NT2RM4001204
 R-NT2RM4001217
 R-NT2RM4001256
 R-NT2RM4001258
 R-NT2RM4001309
 R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPC11-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence. //0.00055:183:63//AC004551
 R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117_K_16, complete sequence. //4.5e-21:212:79//AC004757
 R-NT2RM4001320//CIT-HSP-2303E22. TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence. //3.8e-30:86:89//AQ021084
 R-NT2RM4001340
 0.0027:493:60//AC005133
 R-NT2RM4001344
 R-NT2RM4001347//CITBI-E1-2506I20. TR CITBI-E1 Homo sapiens genomic clone2506I20, genomic survey sequence 50

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nce. //6.5e-16:101:99//AQ262797
 R-NT2RM4001371//CITBI-E1-2503G21. TR CITBI-E1 Homo sapiens genomic clone2503G21, genomic survey sequence. //0.063:140:65//AQ265776
 R-NT2RM4001382//HS_3044_A1_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence. //0.96:103:66//AQ098668
 R-NT2RM4001384//R.norvegicus mRNA for dendrin. //8.5e-07:120:75//Y09000
 R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment. //2.3e-15:199:75//M25920
 R-NT2RM4001411//Rattus norvegicus FceRI gamma-chain interacting proteinSH2-B (SH2-B) mRNA, complete cds. //1.7e-55:235:83//U57391
 R-NT2RM4001412
 R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence. //1.7e-80:489:89//U69730
 20 R-NT2RM4001437//RPC111-56D2. TJ RPC111 Homo sapiens genomic clone R-56D2, genomic survey sequence. //3.8e-43:250:93//AQ081969
 R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-312I4 (Genome Systems Human BAC Library) complete sequence. //0.0034:224:63//AC005926
 R-NT2RM4001454//Homo Sapiens Chromosome X clone bW XD90, complete sequence. //2.4e-33:360:68//AC004075
 R-NT2RM4001455//HS_3229_B1_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence. //1.0:183:61//AQ191289
 R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces. //2.2e-51:451:79//AC005282
 R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds. //2.2e-102:547:93//AB014585
 R-NT2RM4001519//HS_2208_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence. //0.25:214:63//AQ091836
 R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase. //3.6e-13:246:70//Z29336
 R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence. //0.055:320:58//AL008970
 R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces. //3.9e-26:329:72//AC005910
 R-NT2RM4001566//Human trophinin mRNA, complete cds. //6.3e-38:296:86//U04811
 R-NT2RM4001569//Human DNA sequence from clone 461P

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17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovinepancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C Oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence. //2.0e-35:213:89//AL031663

R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds. //5.4e-60:558:77//AF071317

R-nnnnnnnnnnnn//M.musculus mRNA of enhancer-trap-1 locus 1. //4.8e-86:565:85//X69942

R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds. //0.083:283:61//U31120

R-NT2RM4001597//HS_2059_A1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence. //4.4e-09:105:83//AQ245136

R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds. //6.7e-111:565:95//AB018334

R-NT2RM4001611//Homarus americanus ryanodine receptor (RyR) mRNA, partial cds. //1.0:364:61//AF051936

R-NT2RM4001629//RPC111-54G14.TJ RPC111 Homo sapiens genomic clone R-54G14, genomic survey sequence. //0.0018:347:61//AQ083173

R-NT2RM4001650

R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein. //0.75:212:62//AL022575

R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence. //2.6e-26:461:65//AC004685

R-NT2RM4001682//Human DNA sequence from clone 30W3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaeal bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence. //1.5e-107:544:96//AL031775

R-NT2RM4001710//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE. //1.8e-110:580:95//AL031447

R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //3.1e-10:543:59//AC004153

R-nnnnnnnnnnnn//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence. //8.7e-111:577:94//AL034430

10 R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF92 locus. //0.017:93:73//M80527

R-NT2RM4001741//Mouse mRNA for talin. //2.4e-34:273:83//X56123

R-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE. //1.7e-112:567:96//AL031709

R-NT2RM4001754//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence. //1.4e-64:475:83//AC002483

20 R-NT2RM4001758//R. norvegicus mRNA for serine/threonine kinase MARK1. //1.9e-18:202:78//Z83868

R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds. //2.0e-22:236:80//AB018270

R-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence. //4.4e-106:551:95//AC006017

R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence. //0.76:279:60//B27099

R-NT2RM4001813

30 R-NT2RM4001823

R-NT2RM4001828//HS_3073_A2_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence. //1.6e-46:255:96//AQ121030

R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence. //9.4e-06:141:69//U78024

R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA. //1.5e-06:175:65//AF019184

R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //5.0e-07:332:61//AC005077

R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence. //4.8e-30:235:85//AF046633

R-nnnnnnnnnnnn//HS_3244_B1_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence. //3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC. //5.0e-119:592:97//Y17711

50 R-NT2RM4001876//Megastigmus wachtlia dinucleotide m

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icrosatellite, clone MWA47CT.//0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS_2016_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic surveysequence.//0.0066:264:59//AQ226877

R-NT2RM4001922//HS_2228_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic surveysequence.//2.5e-35:205:96//AQ065498

R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34_M_24, complete sequence.//0.26:325:63//AC004562

R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//2.9e-85:421:98//AC005207

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162

R-NT2RM4001953//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044

R-nnnnnnnnnnnn//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330

R-NT2RM4001979//Homo sapiens full length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241

R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

R-NT2RM4001987

R-NT2RM4002013

R-NT2RM4002018

R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H195), complete sequence.//3.6e-42:277:89//AC005353

R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204

R-NT2RM4002054

R-NT2RM4002062//Human microsomal epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659

R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267

R-nnnnnnnnnnnn//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742

R-NT2RM4002067//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832

R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758

R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0031:403:57//AC005504

10 R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383

R-nnnnnnnnnnnn//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646

R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000

R-NT2RM4002140

R-NT2RM4002145//Homo sapiens full length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247

R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562

R-NT2RM4002161//Homo sapiens laforin (EPN2A) mRNA, partial cds.//4.5e-110:560:96//AF084535

R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPC.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002189

R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960

R-NT2RM4002205//Spiroplasma virus (SpV1-R8A2 B) complete genome.//3.5e-05:432:56//X51344

R-NT2RM4002213

R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448

R-NT2RM4002251

R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//AC004837

R-NT2RM4002266//H.sapiens CpG island DNA genomic Msel fragment, clone 179f11, forward read cpg179f11.ft1a.//0.72:97:69//Z57487

R-NT2RM4002278//Homo sapiens clone RC140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069

R-NT2RM4002281//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531

R-NT2RM4002287

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R-NT2RM4002294//Homo Sapiens Chromosome X clone bW XD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676

R-NT2RM4002301//HS_2028_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262

R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPIISG20 and other exonucleases). Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a carepeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822

R-nnnnnnnnnnnn//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317

R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709

R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549

R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417

R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316

R-NT2RM4002390

R-NT2RM4002409//RPCI11-45M10.TK RPCI11 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-NT2RM4002438

R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008

R-NT2RM4002452

R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 321D4 (LANL), complete sequence.//0.99:171:64//AC004034

R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CRepeat.//0.96:94:71//Z92545

R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255

R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 pro

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tein, complete cds.//7.0e-31:172:98//AB014591

R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882

R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711

R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//3.9e-11:334:63//AC002368

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R-NT2RM4002532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985

R-NT2RM4002534

R-NT2RM4002567//Homo sapiens chromosome 7 clone UWGC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271

R-NT2RM4002571

R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579

R-NT2RM4002623//Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862

R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422

R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205

R-NT2RP2000008//RPCI11-41G16.TP RPCI-11 Homo sapiens genomic clone RPCI-11-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090

R-NT2RP2000027//Homo sapiens chromosome 17, clone HClT305D20, complete sequence.//6.0e-05:307:62//AC004098

R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290

R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749

R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163

R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758

R-NT2RP2000067//Rat mRNA for growth potentiating f

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- actor, complete cds.//6.0e-10:137:79//D42148
R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.1e-76:381:98//AC005754
R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372
R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97//AF050079
R-NT2RP2000079//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549
R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338
R-NT2RP2000091//Homo sapiens clone RG015P03, complete sequence.//9.3e-21:226:76//AC005048
R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873
R-NT2RP2000098//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015
R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973
R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//1.8e-74:386:95//AB018356
R-NT2RP2000120//CITBI-E1-2503M8. TR CITBI-E1 Homo sapiens genomic clone 2503M8, genomic survey sequence.//5.1e-05:87:77//AQ263909
R-nnnnnnnnnnnnn
R-nnnnnnnnnnnnn//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827
R-NT2RP2000147
R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626
R-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924
R-NT2RP2000161//CIT-HSP-2045P7. TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728
R-NT2RP2000175
R-NT2RP2000183
R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//4.3e-39:306:83//AC005325
R-NT2RP2000205//Human DNA sequence from clone 302L 50
24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155
R-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-152E5, complete sequence.//7.3e-55:306:94//AC004382
R-NT2RP2000232
R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAG) mRNA, complete cds.//7.6e-13:144:75//U88401
10 R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066
R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//U58726R-NT2RP2000257//Homo sapiens PAC clone DJ0808C16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894
R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077
20 R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24(L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3F1K (H3.1/k) and a tRNA-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179
R-NT2RP2000274//CIT-HSP-237901. TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409
30 R-NT2RP2000288
R-NT2RP2000289
R-NT2RP2000297//Homo sapiens full length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165
R-NT2RP2000298
R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310
R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-113:580:96//AL022398
R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039
R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunit 1 (1-3); and cytochrome b subunit 1 (1-3) complete sequence.//1.1e-10:100:100//AF010310

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nits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits). //4.9e-08:494:58//L04272

R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds. //3.4e-46:262:94//U83981

R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces. //3.0e-07:334:61//AC002993

R-NT2RP2000414//Mouse DNA sequence *** SEQUENCING IN PROGRESS *** from clone BAC394, WORKING DRAFT SEQUENCE. //7.0e-08:98:83//AJ004828

R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence. //0.99:150:62//AC005324

R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds. //4.6e-19:142:90//AF102265

R-NT2RP2000438//RPC111-62I13.TK RPC111 Homo sapiens genomic clone R-62I13, genomic survey sequence. //3.1e-06:103:79//AQ199572

R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. //2.0e-22:276:73//AC004691

R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence. //5.5e-27:205:87//B53940

R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence. //6.0e-12:119:84//AC001234

R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1. //0.48:201:64//D10170

R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence. //3.6e-07:472:59//AF033929

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R-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE. //2.3e-61:317:97//AL022318

R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds. //6.6e-29:167:97//AB005543

R-NT2RP2000617

R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds. //2.5e-64:335:96//AB014514

R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contain

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s polymorphic CA repeat. //1.8e-28:383:70//Z92545

R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZBP pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //0.0093:110:70//AL021997

R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds. //0.73:301:60//U89796

R-NT2RP2000668

R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE. //2.8e-11:256:66//AP000015

R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.036:176:69//AC002346

R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence. //2.7e-110:555:96//AC004540

R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence. //2.6e-18:319:68//AL023775

R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence. //1.0:189:60//B50590

R-NT2RP2000764

R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence. //1.7e-24:215:81//AC004002

R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence. //9.5e-32:176:97//B99575

R-nnnnnnnnnnnnn//paramecium species 5,87 mt dna dimer: replication init. region. //0.0077:418:57//K00916

R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence. //0.61:52:73//AL011013

R-NT2RP2000819

R-NT2RP2000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 43408, WORKING DRAFT SEQUENCE. //0.00012:181:70//AL033504

R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from renin-expressing kidney tumor cell line, partial sequence. //3.7e-27:388:72//U13370

R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence. //0.0022:200:68//

AC005703

R-NT2RP2000863

R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412

R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 antioncogene of flat epithelium cancer, segment 7/10.//0.0028:221:62//AB020875

R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266

R-NT2RP2000938//Homo sapiens full length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336

R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298

R-NT2RP2000965

R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence.//4.5e-87:440:97//AL021393

R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//5.4e-93:484:95//AC005277

R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372

R-NT2RP2001036//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732

R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140

R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029

R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973

R-NT2RP2001094//Mycoplasma mycoides mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mtlD) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140

R-NT2RP2001119

R-NT2RP2001127//Homo sapiens HRIHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348

R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCC1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. Contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394

R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//I01838

R-NT2RP2001168

R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB007949

R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680

R-NT2RP2001196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134

R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//8.5e-15:278:68//AL022153

R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 23

56P23, genomic survey sequence.//8.0e-108:547:96//AQ081110

R-NT2RP2001245//Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713

R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353

R-NT2RP2001277//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870

R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709

R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//0.59:218:62//AC006041

R-NT2RP2001312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520

R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212

R-NT2RP2001328//HS_2213_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey sequence

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e. //1.7e-22:200:83//AQ136874
 R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence. //0.81:509:56//AL034560
 R-NT2RP2001378//H.sapiens DNA sequence. //0.94:147:63//Z22404
 R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds. //3.2e-09:75:97//AF091433
 R-NT2RP2001392//Myxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds. //0.079:178:62//L19301
 R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat. //3.4e-60:351:90//Z93242
 R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds. //5.4e-55:320:83//D17294
 R-NT2RP2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108D11, WORKING DRAFT SEQUENCE. //1.0e-44:246:85//AL034419
 R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence. //3.7e-05:417:61//AL031273
 R-NT2RP2001427//Human Chromosome 11 Cosmid cSRL34e5, complete sequence. //0.94:287:59//U73643
 R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence. //5.2e-31:299:77//AF046702
 R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-subtype, complete cds. //7.8e-75:548:83//D17447
 R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPC11-228 P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //1.0e-06:452:59//AC004801
 R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21unordered pieces. //5.1e-08:218:67//AC004846
 R-NT2RP2001450
 R-NT2RP2001467//Human BAC clone RG343P13 from 7q31, complete sequence. //3.8e-31:254:83//AC002465
 R-NT2RP2001506//C.barati p-47, ntnh, bonT genes. //1.2e-06:415:60//Y12091
 R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence. //0.11:155:63//AL034559
 R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1. //2.1e-104:545:95//Y14494
 R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence. //7.0e-16:283:68//AC004596
 R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containingXRCC3 DNA repair gene, genomic

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c sequence, complete sequence. //7.7e-16:108:96//AF037222
 R-NT2RP2001560//CIT978SK-A-56H4. TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence. //0.052:112:66//B73597
 R-NT2RP2001569//CIT-HSP-2335F8. TF CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey sequence. //6.0e-78:383:98//AQ042029
 R-NT2RP2001576//Homo sapiens sulfonylurea receptor (SUR2) gene, exon 37. //0.33:135:66//AF061322
 R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer. //2.7e-07:240:63//L15407
 R-NT2RP2001597//HS_3016_B2_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey sequence. //5.3e-45:310:87//AQ118854
 R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence. //0.015:445:58//AC006079
 R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence. //3.5e-16:413:63//AF009326
 R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, complete cds. //0.11:190:63//AF034626
 R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence. //3.0e-26:157:81//AC004125
 R-NT2RP2001677//Homo sapiens chromosome 9, P1 clone 11659, complete sequence. //3.0e-58:305:96//AC004472
 R-NT2RP2001678//Human BAC clone RG222A16 from 7q31, complete sequence. //0.95:107:66//AC002385
 R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternatively spliced erythroid ankyrins (Ank1) gene, putative exon 41 and partial cds. //8.8e-05:211:63//U76758
 R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence. //4.7e-68:352:97//AC004079
 R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence. //7.7e-05:346:59//B40914
 R-NT2RP2001740//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence. //1.1e-16:162:82//AQ175104
 R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds. //2.0e-33:312:77//D16583

- R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT
-HSP-292g8 (BC262482), complete sequence. //2.3e-10
0:435:97//AC004783
- R-NT2RP2001813//Human leukocyte common antigen T20
0 (CD45, LCA) gene, exon 9. //0.031:261:60//M23468
- R-NT2RP2001861
- R-NT2RP2001869//Sequence 5 from patent US 5595900.
//4.2e-21:194:77//I34189
- R-NT2RP2001876
- R-NT2RP2001883//Human DNA sequence from clone 612B 10
18 on chromosome 1q24-25.3 Contains exon from gene
similar to 40S ribosomal protein, first coding ex
on of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Islan
d, complete sequence. //5.0e-111:485:97//AL031864
- R-NT2RP2001900
- R-NT2RP2001907//Human proto-oncogene tyrosine-prot
ein kinase (ABL) gene, exon 1a and exons 2-10, com
plete cds. //5.4e-42:382:77//U07563
- R-NT2RP2001926//HS_3180_B2_F02_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl 20
one Plate=3180 Col=4 Row=L, genomic survey sequenc
e. //2.8e-25:138:80//AQ185415
- R-NT2RP2001936//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC1383 genomic sequence, WORKING DRAFT SE
QUENCE, 3 unordered pieces. //1.0:320:60//AC005504
- R-NT2RP2001943//Dictyostelium discoideum PkgA (pkg
A) gene, partial cds. //1.4e-08:378:59//AF020280
- R-NT2RP2001946//Homo sapiens clone NH0140K04, comp
lete sequence. //3.6e-85:409:100//AC005033
- R-NT2RP2001947//Human mRNA for KIAA0390 gene, comp 30
lete cds. //0.85:140:64//AB002388
- R-NT2RP2001969
- R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sap
iens genomic clone 2281C3, genomic survey sequenc
e. //2.0e-60:307:98//B99575
- R-NT2RP2001985//Arabidopsis thaliana DNA chromosom
e 4, BAC clone F1N20 (ESSAII project). //0.031:282:
61//AL022140
- R-NT2RP2002025
- R-NT2RP2002032//CITBI-E1-2502C19.TF CITBI-E1 Homo 40
sapiens genomic clone 2502C19, genomic survey seque
nce. //1.2e-52:285:95//AQ264715
- R-NT2RP2002033//Human (lambda) DNA for immunoglobi
n light chain. //1.1e-08:389:61//D88270
- R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPCI11-31
9E16 (Roswell Park Cancer Institute Human BAC Libr
ary) complete sequence. //1.1e-49:264:97//AC006206
- R-NT2RP2002046//Human BAC clone GS119P05 from 7q2
1, complete sequence. //0.0023:429:61//AC004011
- R-NT2RP2002047//P. falciparum PK1 gene. //0.00015:23 50
9:62//X83707
- R-NT2RP2002058//HS_2183_A1_G01_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2183 Col=1 Row=M, genomic survey sequenc
e. //1.2e-21:185:84//AQ022560
- R-NT2RP2002066//G.gallus microsatellite DNA (LEI02
22 (=T15ivD04)). //0.18:102:70//Z83792
- R-NT2RP2002070//P. falciparum major merozoite surfa
ce antigen (PMMSA) mRNA, complete cds, isolate FC2
7. //0.95:192:61//M19143
- R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequ
ence. //3.8e-25:182:86//AF052183
- R-NT2RP2002079//Human DNA sequence from clone 431P
23 on chromosome 6q27. Contains the first coding ex
on of the MLLT4 gene for myeloid/lymphoid or mixed
-lineage leukemia (trithorax (Drosophila) homolo
g); translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1
fusion partner), and a Serine Palmitoyltransferas
e 2 (EC 2.3.1.50, Long Chain Base Biosynthesis pro
tein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, S
Tss, GSSs, and a putative CpG island, complete seq
uence. //1.7e-10:97:90//AL009178
- R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-as
sociated protein. //4.6e-59:376:89//AJ007509
- R-NT2RP2002105
- R-NT2RP2002124//RPCI11-75J16.TJ RPCI11 Homo sapien
s genomic clone R-75J16, genomic survey sequence. /
/0.58:191:64//AQ266779
- R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB
-484017 (Genome Systems Human BAC Library) complet
e sequence. //0.0065:294:61//AC005913
- R-NT2RP2002154
- R-NT2RP2002172//RPCI11-90C20.TJ RPCI11 Homo sapien
s genomic clone R-90C20, genomic survey sequence. /
/0.049:160:65//AQ282591
- R-NT2RP2002185//CIT-HSP-2341I15.TF CIT-HSP Homo sa
piens genomic clone 2341I15, genomic survey sequen
ce. //6.0e-36:230:90//AQ053355
- R-NT2RP2002192//HS_2222_B1_F08_MF CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2222 Col=15 Row=L, genomic survey sequenc
e. //1.9e-15:249:71//AQ178491
- R-NT2RP2002193//Rattus norvegicus potassium channe
l regulatory protein KChAP mRNA, complete cds. //4.
7e-35:438:73//AF032872
- R-NT2RP2002208//Hansenula wingei mitochondrial DN
A, complete sequence. //0.00057:468:57//D31785
- R-NT2RP2002219//HS_2058_A1_C09_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2058 Col=17 Row=E, genomic survey sequenc

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e. //3.4e-55:512:77//AQ234380
 R-NT2RP2002231//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-31, complete sequence. //1.5e-06:398:61//Z98557
 R-nnnnnnnnnnnn//Sequence 11 from patent US 562481 8. //3.3e-91:553:87//141141
 R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds. //3.0e-14:132:84//AF005418
 R-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE. //1.6e-96:548:91//AL033527
 R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence. //5.1e-06:391:60//AC004605
 R-NT2RP2002292//Genomic sequence from Human 13, complete sequence. //0.91:159:64//AC001226
 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds. //1.3e-101:527:94//AF069532
 R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence. //0.00052:389:59//AE001408
 R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds. //2.3e-112:567:95//AF093668
 R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA. //1.5e-22:323:73//L23204
 R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds. //3.7e-102:600:89//AF038958
 R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.039:399:59//AC005308
 R-NT2RP2002408//HS_2212_A1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=I, genomic survey sequence. //9.6e-35:231:88//AQ184632
 R-NT2RP2002426//Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an AC02 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence. //2.8e-39:308:82//AL021877
 R-NT2RP2002439//Leishmania tarentolae mitochondria 1 electron transport chain component mRNA. //0.022:102:71//M74225
 R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudoge

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ne, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence. //0.00099:354:59//Z99289
 R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE. //0.0015:219:67//AP000013
 R-NT2RP2002475
 R-nnnnnnnnnnnn//Homo sapiens mRNA for ABC transporter 7 protein, complete cds. //3.1e-113:605:92//AB005289
 R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence. //0.32:210:64//Z98047
 R-NT2RP2002503//Homo sapiens, clone hRPK.15_A_1, complete sequence. //4.0e-86:429:98//AC006213
 R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds. //2.7e-105:583:91//AB018334
 R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes. //0.14:406:58//AJ223323
 R-NT2RP2002537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE. //2.8e-16:188:78//AL023583
 R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA. //4.7e-108:571:93//AF009314
 R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence. //1.1e-103:422:95//AC005316
 R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds. //1.8e-36:526:67//M27878
 R-NT2RP2002595
 R-NT2RP2002606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE. //7.2e-10:211:71//AL033529
 R-NT2RP2002609
 R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence. //2.9e-05:566:60//Z98551
 R-NT2RP2002621//Human DNA sequence from PAC 341I10 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs. //1.1e-38:348:78//Z97352
 R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence. //1.2e-35:414:66//AF074030
 R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence. //1.3e-77:403:95//AC005384

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R-NT2RP2002701
 R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778
 R-NT2RP2002710//P. falciparum serine rich protein (SERP 1) gene.//0.84:135:67//J03983
 R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815
 R-NT2RP2002736//Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence.// 10 0.44:267:60//AC004138
 R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence.//0.0016:474:60//AC004674
 R-NT2RP2002741//HS_3051_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic surveysequence.//1.1e-38:217:86//AQ106283
 R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPCI1-315 L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395
 R-NT2RP2002752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494
 R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//6.8e-100:496:97//AC004882
 R-NT2RP2002769//paramecium species 5,311 mt dna dimer: replication init.region.//7.4e-10:404:60//X00917
 R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:341:94//AF070537
 R-NT2RP2002800//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence.//4.9e-60:321:95//AQ029850
 R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078
 R-NT2RP2002857//HS_3026_B2_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic surveysequence.//8.9e-06:242:62//AQ128697
 R-NT2RP2002862//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//1.5e-44:270:85//AQ052700
 R-NT2RP2002880//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318
 R-NT2RP2002891

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R-NT2RP2002925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395
 R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556
 R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140
 R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//1.0:275:61//AC005701
 R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483
 R-NT2RP2002979//RPCI11-20F13.TPK RPCI-11 Homo sapiens genomic clone RPCI-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132
 R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140
 R-NT2RP2002986//Human DNA sequence from clone 1147016 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542
 R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence.//1.3e-51:283:88//AC005968
 30 R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21.//4.3e-11:430:63//AL021307
 R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887
 R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 antl-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870
 R-NT2RP2003073
 40 R-NT2RP2003099//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914
 R-NT2RP2003108
 R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378
 R-NT2RP2003121//HS_2238_A1_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=I, genomic surveysequence.//0.00055:324:61//AQ293058
 50 R-NT2RP2003125

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- R-NT2RP2003129
- R-NT2RP2003137//Human BAC clone RC084D04 from 7q31, complete sequence.//1.1e-46:521:74//AC003084
- R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879
- R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581
- R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPK.1018_N_14, complete sequence.//2.2e-71:467:86 //AC005823
- R-NT2RP2003177
- R-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597
- R-NT2RP2003206//P. falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877
- R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551
- R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence.//1.0:311:60//AB016888
- R-NT2RP2003243//CIT-HSP-2368D12. TR CIT-HSP Homo sapiens genomic clone 2368D12, genomic survey sequence.//0.39:112:66//AQ077738
- R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cellline NCD5) mRNA, complete cds.//1.3e-38:273:83//L38481
- R-NT2RP2003272//Homo sapiens clone UWGC:y17c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187
- R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525
- R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPC15-118 OD12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.2e-12:221:70//AC005831
- R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261
- R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0e-39:418:74//AC005079
- R-NT2RP2003295//HS_2053_B1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251
- R-NT2RP2003297//Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332
- R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960
- R-NT2RP2003329//C. reinhardtii psbB 5' flanking region.//0.79:161:59//X59731
- R-NT2RP2003339//RPC111-57H15.TK RPC111 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039
- R-NT2RP2003347//RPC111-15B19.TV RPC111 Homo sapiens genomic clone RPC111-15B19, genomic survey sequence.//6.4e-31:218:89//B76357
- R-NT2RP2003367//Human Chromosome 16 BAC clone CIT9 87SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321
- R-NT2RP2003391//HS_2255_B2_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937
- R-NT2RP2003393//RPC111-44K6.TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence.//3.9e-31:290:79//AQ202481
- R-NT2RP2003394//Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I.//5.1e-14:579:61//X14910
- R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, partial cds.//0.32:174:66//U81429R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536
- R-NT2RP2003445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.4e-99:585:89//AL023808
- R-NT2RP2003446
- R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559
- R-NT2RP2003480//Homo sapiens full length insert cDNA clone ZE09A11.//4.7e-111:540:98//AF086540
- R-NT2RP2003499
- R-NT2RP2003506
- R-NT2RP2003511
- R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460
- R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2)mRNA, complete cds.//1.5e-60:518:79//M12783
- R-NT2RP2003522//HS_2182_A1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304
- R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE, 31 unordered

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red pieces. //1.5e-37:328:80//AC005841
 R-NT2RP2003543//HS_3028_A2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=24 Row=E, genomic surveysequence. //2.0e-39:203:100//AQ094957
 R-NT2RP2003559//Homo sapiens full length insert cDNA clone ZD65E09. //2.3e-59:325:95//AF088055
 R-NT2RP2003564
 R-NT2RP2003581
 R-NT2RP2003596//HS_2163_B1_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=21 Row=H, genomic surveysequence. //0.0011:212:67//AQ125143
 R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds. //5.4e-102:501:97//U97067
 R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.0012:363:61//AC005507
 R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase. //5.1e-37:561:68//AJ006215
 R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs. //0.0053:395:58//Z76735
 R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence. //8.0e-10:205:67//AC002385
 R-NT2RP2003691//HS_3252_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=22 Row=A, genomic survey sequence. //5.3e-05:332:60//AQ219783
 R-NT2RP2003702//CIT-HSP-2333P5.TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey sequence. //3.9e-43:431:75//AQ035000
 R-NT2RP2003704
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds. //2.6e-45:265:93//AB011097
 R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X *. //0.64:169:67//Z84470
 R-NT2RP2003714//Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3. //4.6e-11:152:73//Z95704
 R-ntnnnnnnnnnn//H.sapiens mRNA for PIBF1 protein, complete. //0.94:443:59//Y09631
 R-NT2RP2003737//Homo sapiens clone DJ1022I14, WORKING DRAFT SEQUENCE, 14unordered pieces. //2.2e-109:547:96//AC004951
 R-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence. //4.1e-109:545:97//AC004626

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R-NT2RP2003760//B. taurus mRNA for gamma-COP. //6.3e-28:400:69//X70019
 R-NT2RP2003764//Mouse preprosomatostatin gene. //0.90:285:62//X51468
 R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete cds. //0.96:446:58//D87956
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds. //1.8e-104:531:96//AF047437
 R-NT2RP2003777
 R-NT2RP2003781//HS_3109_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence. //1.3e-60:346:92//AQ186749
 R-NT2RP2003793
 R-NT2RP2003840
 R-NT2RP2003857//HS_2205_A2_H12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=0, genomic surveysequence. //8.1e-22:127:99//AQ151299
 R-NT2RP2003859//RPCI11-37G8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-37G8, genomic survey sequence. //8.3e-60:320:95//AQ029850
 R-NT2RP2003871//HS_3210_A1_C08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic surveysequence. //8.6e-09:322:61//AQ175028
 R-NT2RP2003885//RPCI11-7M10.TP RPCI-11 Homo sapiens genomic clone RPCI-11-7M10, genomic survey sequence. //4.7e-67:380:92//B72214
 R-NT2RP2003912//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE. //1.2e-33:379:75//AL023693
 R-NT2RP2003952
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds. //2.3e-114:568:97//AB014458
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds. //1.1e-107:540:97//AB007916
 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds. //7.7e-114:568:96//AB018347
 R-NT2RP2003984
 R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces. //6.6e-99:551:92//AC000382
 R-NT2RP2003988
 R-NT2RP2004014
 R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence. //4.9e-114:568:97//AC00

- R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library
Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389
R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555
R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308
R-NT2RP2004098//H.sapiens CpG island DNA genomic map fragment, clone 133h3, reverse read cpg133h3.rta.//7.9e-25:140:100//Z64530
R-NT2RP2004124
R-NT2RP2004142//CIT-HSP-2316F21. TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964
R-NT2RP2004152//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776
R-NT2RP2004165//Anthracidaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021
R-NT2RP2004170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064
R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047
R-NT2RP2004187//RPC111-59E12.TK RPC111 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120
R-NT2RP2004194
R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601
R-NT2RP2004207//Homo sapiens BAC clone GS421I03 from Xq25-q26, complete sequence.//0.19:175:64//AC005023
R-NT2RP2004226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808
R-NT2RP2004232//M.musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524
R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.1e-101:530:93//AF039687
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R-NT2RP2004242
R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:236:65//AL023280
R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603
R-NT2RP2004300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913
R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416
R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662
R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229
R-NT2RP2004347//RPC111-90N11.TJ RPC111 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548
R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010
R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433
R-NT2RP2004366//F.rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528
R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC111-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065
R-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969
R-NT2RP2004392//Ceratomyxa sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993
R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from 7q21, complete sequence.//6.4e-111:572:96//AC005164
R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//

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O.13:253:64//AC006085
 R-NT2RP2004400//HS_3238_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=0, genomic survey sequence.//5.1e-23:162:89//AQ211412
 R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//2.6e-09:458:60//M97514
 R-NT2RP2004425//Human DNA sequence from clone 1052 M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718
 R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3' UTR.//5.3e-99:600:90//AF030091
 R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591
 R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547
 R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890
 R-NT2RP2004538//Homo sapiens BAC clone RC318C11 from 7p14-p15, complete sequence.//1.7e-47:322:87//AC005091
 R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184
 R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766
 R-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768
 R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.0079:223:63//AQ108976
 R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//5.3e-10:493:62//AC004605
 R-NT2RP2004600//Homo sapiens full length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522
 R-NT2RP2004602//Homo sapiens full length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033
 R-NT2RP2004614
 R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:587:96//AJ006291

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R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.8e-105:520:96//AB007929
 R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-22:197:79//U63721
 R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661
 R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525
 R-NT2RP2004709//Homo sapiens full length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259
 R-NT2RP2004710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447
 R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947
 R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505
 R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1p36.2-1p36.3.//2.0e-81:568:84//Z97988
 R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.0e-08:365:62//L04272
 R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-111:541:98//AC005216
 R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953
 R-NT2RP2004802
 R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179
 R-NT2RP2004841//Human BAC clone RG308B22 from 7q22-q31, complete sequence.//4.0e-46:447:72//AC002089
 R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence.//0.19:189:66//AL034556
 R-NT2RP2004897//Human Chromosome X clone bWXD187, complete sequence.//1.1e-08:330:61//AC004383
 R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey sequence.//0.99:129:65//AQ110571
 R-nnnnnnnnnnnnn//Plasmodium falciparum MAL3P6, complete sequence.//0.014:402:61//Z98551
 R-NT2RP2004961//RPC111-45P2.TK RPC111 Homo sapiens genomic clone R-45P2, genomic survey sequence.//9.

- 3e-90:453:97//AQ202282
R-NT2RP2004962//*Caenorhabditis elegans* DNA *** SEQUENCING IN PROGRESS *** from clone Y40H4, WORKING DRAFT SEQUENCE. //0.017:291:61//AL022573
R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces. //4.6e-52:496:77//AC005077
R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence. //0.088:322:63//AC005614
R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence. //0.025:339:61//AC003071
R-NT2RP2004985//T31H24TF TAMU *Arabidopsis thaliana* genomic clone T31H24, genomic survey sequence. //0.40:111:70//B78148
R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces. //0.23:157:68//AC005682
R-NT2RP2005000
R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds. //3.0e-111:577:95//AB014515
R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence. //2.4e-21:246:77//AC004673
R-nnnnnnnnnnnn//Homo sapiens SEC63 (SEC63) mRNA, complete cds. //9.5e-115:568:97//AF100141
R-NT2RP2005018//HS_3108_B1_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence. //1.9e-31:222:89//AQ104050
R-NT2RP2005020//*Rattus norvegicus* cationic amino acid transporter-1 (CAT-1) mRNA, complete cds. //6.6e-41:566:73//U70476
R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A2, genomic survey sequence. //4.1e-31:357:75//B49897
R-NT2RP2005037
R-NT2RP2005038//Sequence 5 from patent US 5552281. //2.2e-32:178:98//I25644
R-NT2RP2005108//*Mus musculus* orphan nuclear hormone receptor (CAR) gene, complete sequence. //3.7e-23:475:67//AF009326
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds. //8.4e-104:518:97//AB014564
R-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myo-regulated dead box protein). //1.4e-67:464:85//X98743
R-NT2RP2005139
R-NT2RP2005140//*Leishmania mexicana amazonensis* kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence. //7.9e-08:460:60//U00101
R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPC111-372B4, WORKING DRAFT SEQUENCE, 129 ordered pieces. //2.5e-103:519:96//AC005911
R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces. //0.068:100:75//AC004971
R-NT2RP2005159//CITBI-E1-2506A8.TF CITBI-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence. //0.90:113:71//AQ262104
R-NT2RP2005162//Homo sapiens chromosome 17, clone HCIT307A16, complete sequence. //5.0e-14:183:75//AC003041
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein. //7.5e-100:513:95//AJ007509
R-NT2RP2005204
R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence. //7.2e-119:583:97//AC005189
R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial. //8.4e-62:312:98//AJ010952
R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuroneurin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs. //5.7e-09:328:62//Z99297R-NT2RP2005270//*Plasmodium falciparum* MAL3P8, complete sequence. //2.3e-05:355:61//AL034560
R-NT2RP2005276//Genomic sequence for *Arabidopsis thaliana* BAC F17F8, complete sequence. //0.0014:541:58//AC000107
R-NT2RP2005287//*Cavia porcellus* zinc finger protein (zfoc1) mRNA, complete cds. //4.4e-69:459:86//L26335
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds. //7.4e-124:594:98//AF060219
R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein. //1.5e-110:545:96//AJ007590
R-NT2RP2005293//*Leishmania mexicana amazonensis* kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence. //1.1e-12:554:61//U00101
R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence. //9.5e-15:218:77//AL022069

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R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence. //2.0e-72:478:88//L06804

R-NT2RP2005336//***ALU WARNING: Human Alu-J subfamily consensus sequence. //7.3e-33:139:82//U14567

R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS. //0.094:451:60//Z97629

R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein. //1.3e-11:89:96//AJ010841

R-NT2RP2005360//Homo sapiens clone RG023115, WORKING DRAFT SEQUENCE, 1 unordered pieces. //0.046:266:60//AC005049

R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence. //6.0e-41:226:86//AC005695

R-NT2RP2005407

R-NT2RP2005436//Polistes annularis (clone pan117AA T) tandem repeat region. //0.039:169:63//L10835

R-NT2RP2005441//CIT-HSP-2338P5.TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence. //3.0e-38:263:88//AQ055548

R-NT2RP2005453//CIT-HSP-2367N1.TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence. //0.67:409:59//AQ079845

R-NT2RP2005457//Homo sapiens partial XPGC gene, exon 2. //2.0e-42:315:82//X71342

R-NT2RP2005464//CIT-HSP-2359C16.TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence. //1.0:251:60//AQ075816

R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 44D1-44D2, P1 clone DS08616, complete sequence. //0.25:288:62//AC005457

R-NT2RP2005472//Chlorarachnion CCMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clp protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNAHEL) genes, complete cds. //1.0:356:59//U58510

R-NT2RP2005476//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P3, WORKING DRAFT SEQUENCE. //0.00092:421:60//AL031746

R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces. //6.2e-71:187:100//AC006030

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R-NT2RP2005491//paramecium species 5,311 mt dna dimer: replication init. region. //1.6e-10:403:62//K00917

R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces. //1.3e-25:208:82//AC005051

R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence. //1.5e-22:196:84//AL022722

R-NT2RP2005498

R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence. //1.7e-29:252:76//AC005828

R-NT2RP2005509//CIT-HSP-2060J6.TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence. //3.1e-53:402:84//B69979

R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds. //9.9e-109:570:94//AF092563

R-NT2RP2005525//Human clone Jka2 mRNA induced upon T-cell activation, 3' end. //5.1e-32:175:98//U38432

R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence. //0.94:288:61//AC004911

R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP). //2.7e-106:560:94//AJ012449

R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds. //5.3e-114:583:96//AB007963

R-NT2RP2005549//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE. //0.91:287:58//AJ011929

R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPCI5-927 J10 (Roswell Park Cancer Institute Human PAC library) complete sequence. //3.6e-05:222:66//AC004804

R-NT2RP2005557//Homo sapiens PAC clone DJ1200123 from 7p15, complete sequence. //8.2e-22:236:76//AC004996

R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces. //7.2e-45:286:85//AC006146

R-NT2RP2005600//Human polymorphic microsatellite DNA. //0.043:304:58//M99148

50 R-NT2RP2005605//Human Cosmid g1572c190, complete s

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equence.//2.4e-17:163:77//AC000126
 R-NT2RP2005620
 R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei genomic clone 11B7, genomic survey sequence.//0.010:308:58//B13538
 R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996
 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Scca2) gene, complete cds.//0.030:370:60//AF063937
 R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398
 R-NT2RP2005651
 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908
 R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814
 R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei genomic clone 11B7, genomic survey sequence.//0.037:283:58//B13538
 R-NT2RP2005690//Homo sapiens clone DJ0425I02, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478
 R-NT2RP2005694//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-106, complete sequence.//0.0026:414:57//AL010210
 R-NT2RP2005701
 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342
 R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277
 R-NT2RP2005722//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985
 R-NT2RP2005723
 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842
 R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384
 R-NT2RP2005748//RPC111-64K11.TK RPC111 Homo sapiens genomic clone R-64K11, genomic survey sequence.//0.00039:215:66//AQ239313

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R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516
 R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098
 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672
 R-NT2RP2005773//HS_2168_B1_G12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414
 R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310
 R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623
 R-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423
 R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPK.147_L_13, complete sequence.//6.3e-16:481:63//AC005332
 R-NT2RP2005812//Caenorhabditis elegans cosmid F15B10.//0.81:147:63//AF036696
 R-NT2RP2005815
 R-NT2RP2005835
 R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873
 R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047
 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308
 R-NT2RP2005859//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-83, complete sequence.//0.0097:363:59//AL010152
 R-NT2RP2005868//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971
 R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//L11316
 R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661
 R-NT2RP2005908

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R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds. //1.2e-40:285:80//U63840
 R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connectivetissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence. //0.0011:480:58//Z99289
 R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence. //8.9e-21:136:78//AC004616
 R-NT2RP2006023//HS_2176_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence. //2.5e-66:369:95//AQ023148
 R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence. //0.0029:408:58//AE001369
 R-NT2RP2006043//Polistes annularis (clone pan117AA T) tandem repeat region. //0.032:195:62//L10835
 R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.11:263:61//AC005140
 R-NT2RP2006069
 R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.00044:333:61//AC004709
 R-NT2RP2006098//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-77, complete sequence. //4.1e-09:393:62//AL010151
 R-NT2RP2006100//HS_2020_A2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=0, genomic survey sequence. //8.3e-53:304:92//AQ228761
 R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds. //1.5e-16:199:79//M85300
 R-NT2RP2006141
 R-NT2RP2006166//Human Chromosome 16 BAC clone CIT9 87SK-A-589H1, complete sequence. //8.2e-48:329:76//AC002045
 R-NT2RP2006184//RPCI11-6016.TP RPCI-11 Homo sapiens genomic clone RPCI-11-6016, genomic survey sequence. //0.52:273:61//B49539
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds. //1.9e-108:553:95//AB014554

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R-NT2RP2006196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-57, complete sequence. //4.2e-05:420:59//AL008981
 R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPCI1-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces. //2.1e-100:409:96//AC006057
 R-NT2RP2006219//H. sapiens mRNA for DGCR6 protein. //3.8e-93:532:90//X96484R-NT2RP2006237//P. falciparum PK1 gene. //2.9e-08:481:59//X83707
 10 R-NT2RP2006238//Human chromosome 16 BAC clone CIT9 87SK-A-962B4, complete sequence. //3.5e-79:405:89//U91318
 R-NT2RP2006258//Human PAC clone DJ0899B21 from 7p15-p21, complete sequence. //2.2e-08:283:63//AC004008
 R-NT2RP2006261//H. sapiens mRNA for serine/threonine protein kinase EMK. //6.2e-13:234:68//X97630
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds. //2.0e-108:542:97//AF035262
 20 R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence. //1.2e-27:215:65//B17768
 R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds. //1.7e-48:298:90//U72761
 R-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE. //2.8e-104:524:96//AL033531
 R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence. //3.9e-33:298:78//AC004893
 30 R-NT2RP2006334
 R-NT2RP2006365//RPCI11-72I15.TK RPCI11 Homo sapiens genomic clone R-72I15, genomic survey sequence. //2.6e-35:217:92//AQ267043
 R-NT2RP2006393//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces. //8.0e-40:317:81//AC004046
 R-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE. //3.2e-42:184:86//AL022345
 R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence. //0.00021:188:68//AF010568
 R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence. //0.30:265:60//AE001423
 R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence. //2.5e-104:532:96//AF052098
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein. //6.6e-108:524:97//AJ006266

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R-NT2RP2006467//Sequence 50 from patent US 569114 7. //8.3e-22: 235: 74//176222
 R-NT2RP2006472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE. //5.4e-12: 407: 62//AL034386
 R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR. //0.44: 111: 65//M25216
 R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence. //0.19: 392: 58//AE001370
 R-NT2RP2006565//Sus scrofa SCAMP1 gene, exon 9. //1.5e-13: 292: 68//AJ223742
 R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence. //0.0024: 409: 58//AC004660
 R-ntnnnnnnnnnn//Human BRCA2 region, mRNA sequence CG005. //3.3e-16: 334: 64//U50532
 R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds. //1.6e-19: 448: 64//U22015
 R-NT2RP3000002//Human DNA sequence from cosmid N104C7 on chromosome 22, complete sequence. //4.4e-14: 501: 63//Z82246
 R-NT2RP30000031//Homo sapiens mRNA for histone deacetylase-like protein (JW21). //5.9e-115: 560: 97//AJ011972
 R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces. //3.9e-57: 402: 83//AC005995
 R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence. //1.0: 158: 66//AC005697
 R-NT2RP3000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE. //2.7e-32: 411: 69//AL033522
 R-NT2RP3000055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1000N6, WORKING DRAFT SEQUENCE. //7.9e-17: 309: 69//AL034378
 R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds. //2.9e-07: 516: 60//D88192
 R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence. //1.7e-27: 186: 90//AC005630
 R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds. //0.0051: 289: 59//U23155
 R-NT2RP3000109//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=C, genomic survey sequence. //2.5e-62: 304: 100//AQ137776

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R-NT2RP3000134//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE. //0.027: 414: 57//AL031746
 R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds. //3.8e-115: 578: 96//AB011164
 R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence. //1.3e-67: 354: 95//AC005746
 R-NT2RP3000186
 10 R-NT2RP3000197//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeat*. //2.5e-31: 295: 78//Z82899
 R-NT2RP3000207//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence. //0.016: 305: 61//AC004514
 R-NT2RP3000220//RPC11-6307. TJ RPC11 Homo sapiens genomic clone R-6307, genomic survey sequence. //0.25: 118: 66//AQ201832
 R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195. //3.2e-11: 440: 59//X15063
 R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pd1. //0.81: 114: 64//U19530
 R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1-27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence. //4.8e-73: 362: 86//AL023279
 30 R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence. //0.025: 131: 66//AC005726
 R-NT2RP3000252
 R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence. //0.67: 119: 66//B34879
 R-NT2RP3000267
 R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds. //1.2e-23: 424: 69//D29766
 R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence. //0.55: 414: 59//AL008970
 R-NT2RP3000320//HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence. //4.1e-32: 214: 89//AQ134064
 R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds. //1.5e-22: 265: 75//U78090
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50

R-NT2RP3000527//HS_3228_A1_H07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=0, genomic surveysequence.//4.5e-30:184:93//AQ209131

R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:68//AQ248538

R-NT2RP3000542//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126B4, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316

R-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.1e-107:548:95//AC006012

R-NT2RP3000562//HS_2041_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic surveysequence.//9.6e-55:279:98//AQ230207

R-NT2RP3000578//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-105, complete sequence.//0.00060:356:58//AL010212

R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKINGDRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666

R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377

R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077

R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomicsequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.022:491:56//AC005505

R-nnnnnnnnnnnnn//HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic surveysequence.//2.6e-21:161:88//AQ101452

R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560

R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128

R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414

R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262

R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115

R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85

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//U73379
 R-NT2RP3000644//Homo sapiens DNA from chromosome 1
 9p13.2 cosmids R31240, R30272 and R28549 containing
 the EKLF, GCDH, CRTG, and RAD23A genes, genomic s
 equence.//1.0e-43:408:77//AD000092
 R-NT2RP3000661//F.rubripes GSS sequence, clone 148
 D22bB9, genomic surveysequence.//2.7e-17:234:69//A
 L005927
 R-NT2RP3000665//Human chromosome 11 46b2 cosmid, c
 omplete sequence.//2.1e-42:526:72//U73645
 R-NT2RP3000685//HS_3007_A2_F02_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3007 Col=4 Row=K, genomic survey sequenc
 e.//1.6e-101:506:97//AQ118425
 R-NT2RP3000690//Plasmodium falciparum MAL3P6, comp
 lete sequence.//1.3e-13:411:61//Z98551
 R-NT2RP3000736
 R-NT2RP3000742//Rattus norvegicus phospholipase C
 delta-4 mRNA, completecds.//0.0071:231:65//U16655
 R-NT2RP3000753//Homo sapiens DNA sequence from BAC 20
 55C20 on chromosome 6. Contains a Spinal Muscular
 Atrophy (SMA3) LIKE gene overlapping with abeta-g
 lucuronidase LIKE pseudogene. Contains a membrane
 protein LIKE pseudogene, a Glyceraldehyde 3-phosph
 ate dehydrogenase (GAPDH) LIKE pseudogene, five pr
 edicted tRNA genes. Contains ESTs, GSSs (BAC end s
 equences) and a CA repeat polymorphism, complete se
 quence.//0.88:366:56//AL021368
 R-NT2RP3000759//HS_2055_A2_D09_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=2055 Col=18 Row=G, genomic surveysequenc
 e.//0.45:251:60//AQ234828
 R-NT2RP3000815//Homo sapiens chromosome 17, clone
 hRPK.209_J_20, complete sequence.//2.0e-20:293:72/
 /AC005822
 R-NT2RP3000825//Plasmodium falciparum MAL3P6, comp
 lete sequence.//0.0044:325:62//Z98551
 R-NT2RP3000826//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 117715, WORKING DRAFT S
 EQUENCE.//5.3e-25:375:72//AL022315
 R-NT2RP3000836//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone Y214H10, WORKING DRAFT
 SEQUENCE.//1.3e-19:181:81//AL022344
 R-NT2RP3000841//Homo sapiens, clone hRPK.1_A_1, co
 mplete sequence.//0.20:226:61//AC006196
 R-NT2RP3000845//Homo sapiens chromosome 19, cosmid
 R33632, complete sequence.//6.8e-91:512:92//AC005
 781
 R-NT2RP3000847//***ALU WARNING: Human Alu-Sp subfa
 mily consensus sequence.//7.9e-38:179:86//U14572

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R-NT2RP3000850//Homo sapiens BAC clone GS166A23 fr
 om 7p21, complete sequence.//4.4e-48:505:76//AC005
 014
 R-NT2RP3000852//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 97P20, WORKING DRAFT SE
 QUENCE.//2.9e-82:311:98//AL031297
 R-NT2RP3000859
 R-NT2RP3000865//Human DNA sequence from clone 23K2
 0 on chromosome Xq25-26.2 Contains EST, STS, GSS,
 complete sequence.//1.2e-15:482:63//AL022153R-NT2R
 P3000868//Fruitfly strain g20 mitochondrial DNA, A
 +T-rich region, partial sequence.//0.00045:260:59//
 AB003097
 R-NT2RP3000869//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 330012, WORKING DRAFT S
 EQUENCE.//0.0058:172:64//AL031731
 R-NT2RP3000875//H.sapiens /Hepatitis B virus fusio
 n mRNA for mevalonatekinase.//1.4e-99:531:93//X75
 311
 R-NT2RP3000901
 R-NT2RP3000904//Genomic sequence for Arabidopsis t
 haliana BAC T7N9, complete sequence.//0.32:261:57/
 /AC000348
 R-NT2RP3000917//Plasmodium falciparum MAL3P7, comp
 lete sequence.//0.00092:456:58//AL034559
 R-NT2RP3000919
 R-NT2RP3000968//H.sapiens mRNA for ribosomal prote
 in S15a.//4.5e-24:375:71//X84407
 R-NT2RP3000980//Homo sapiens chromosome 17, clone
 hRPK.855_D_21, complete sequence.//0.36:186:62//AC
 006079
 R-NT2RP3000994//Plasmodium falciparum 3D7 chromoso
 me 12 PFYACB8-420 genomic sequence, WORKING DRAFT
 SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC
 005140
 R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gen
 e, mitochondrial gene encoding mitochondrial prote
 in, 3' processing site, partial sequence.//1.1e-0
 7:330:64//U32857
 R-NT2RP3001007//Plasmodium falciparum DNA *** SEQU
 ENCING IN PROGRESS ***from contig 4-82, complete s
 equence.//0.045:286:61//AL010255
 R-NT2RP3001055//Human DNA sequence from PAC 27K14
 on chromosome Xp11.3-Xp11.4. Contains monoamine ox
 idase B (MAOB), ESTs and polymorphic CA repeats.//
 2.3e-56:348:91//Z95125
 R-NT2RP3001057//H.sapiens HZF4 mRNA for zinc finge
 r protein.//8.2e-84:531:86//X78927
 R-NT2RP3001081//Plasmodium falciparum DNA *** SEQU
 ENCING IN PROGRESS ***from MAL1P3, WORKING DRAFT S

3627

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EQUENCE. //1.1e-08:537:60//AL031746

R-NT2RP3001084

R-NT2RP3001096

R-NT2RP3001107

R-nnnnnnnnnnn//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence. //7.4e-62:272:73//AC005316

R-NT2RP3001111

R-NT2RP3001113

R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence. //7.2e-112:550:97//AC005189

R-NT2RP3001116//CIT-HSP-2282K23. TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence. //0.00013:160:69//AQ002011

R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence. //5.9e-99:497:96//AL031864

R-NT2RP3001120

R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence. //0.035:266:56//AL034559

R-NT2RP3001133

R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds. //8.1e-114:549:97//AB018305

R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence. //0.69:198:63//AC004448

R-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //2.4e-108:542:97//AL034379

R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein. //2.9e-116:563:98//AJ006266

R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.44:227:62//AC004688

R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence. //0.0023:381:61//AE000785

R-NT2RP3001216//RPCI11-18C15.TPC RPCI-11 Homo sapiens genomic clone RPCI-11-18C15, genomic survey sequence. //7.0e-29:167:97//B88077

R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces. //0.020:211:63//AC005827

R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat po

lymorphism, complete sequence. //2.7e-08:390:62//AL021326

R-NT2RP3001236//RPCI11-25C17.TKBR RPCI-11 Homo sapiens genomic clone RPCI-11-25C17, genomic survey sequence. //9.5e-41:217:88//AQ014003

R-NT2RP3001239//Human microtubule-associated protein 1B (MAP1B) gene, complete cds. //2.9e-21:438:63//L06237

R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS. //0.00026:439:59//AL021398

R-NT2RP3001253//HS_3002_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=0, genomic survey sequence. //0.98:190:63//AQ251982

R-NT2RP3001260

R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces. //0.012:509:57//AC004936

20 R-NT2RP3001272//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence. //2.2e-22:134:87//AC005589

R-NT2RP3001274//Sequence 11 from Patent W09517522. //0.0058:133:66//A45341

R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS. //4.4e-55:558:76//Z96811

R-NT2RP3001307//HS_2058_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence. //7.2e-33:260:86//AQ305868

R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence. //0.27:210:65//AC004848

R-NT2RP3001325

R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial). //1.0:184:64//M86367

R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds. //1.2e-112:566:96//AB007920

40 R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds. //3.2e-86:450:95//AF083105

R-NT2RP3001355

R-NT2RP3001374//HS_2184_A2_G04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey sequence. //3.7e-10:101:84//AQ024647

R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence. //7.4e-07:279:63//AE001397

50 R-NT2RP3001384//Homo sapiens chromosome 19, cosmid

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R33907, complete sequence.//4.4e-75:382:97//AC005785
 R-NT2RP3001392//HS_3078_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587
 R-NT2RP3001396//RPC111-63N18.TJ RPC111 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544
 R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046
 R-NT2RP3001399
 R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160
 R-NT2RP3001420//Human BAC clone GS165I04 from 7q21, complete sequence.//3.7e-29:412:74//AC002379
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158
 R-NT2RP3001427//Caenorhabditis elegans cosmid K11D5.//0.39:174:64//U53152
 R-NNNNNNNNNN//Human nuclear pore complex-associated protein TPR (tpr)mRNA, complete cds.//1.4e-94:533:91//U69668
 R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029
 R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903
 R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630
 R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2unordered pieces.//4.0e-47:295:86//AC004906
 R-NT2RP3001457
 R-NT2RP3001459
 R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b gRNA-mRNA chimera, clone:24.//0.33:150:66//D13030
 R-NT2RP3001490//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208
 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.1e-110:549:97//AF064801
 R-NT2RP3001527//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT

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SEQUENCE.//5.3e-32:310:78//AL034549
 R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420
 R-NT2RP3001538
 R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292
 R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688
 R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337
 R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//0.066:360:60//AC005410
 R-NT2RP3001607//CIT-HSP-2010M8.TR CIT-HSP Homo sapiens genomic clone 2010M8, genomic survey sequence.//0.041:194:67//B53490
 R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase. (EC 2.3.1.37). 6-phosphofructose-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//0.69:151:64//Z83821
 R-NT2RP3001621//Human DNA sequence from clone 24018 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VN0-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.//1.4e-46:354:83//AL021808
 R-NT2RP3001629//H.sapiens simple DNA sequence region clone wgl10.//0.99:137:63//X76572
 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds.//8.5e-108:541:96//AF099149
 R-NT2RP3001642
 R-NT2RP3001646//HS_3218_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence.//2.6e-32:215:91//AQ303003
 R-NT2RP3001671//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-88, complete sequence.//0.018:262:61//AL010157
 R-NT2RP3001672
 R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2.//2.1e-48:413:77//AF039905
 R-NT2RP3001678//RPC111-50C17.TK RPC111 Homo sapiens genomic clone R-50C17, genomic survey sequence.//0.15:232:62//AQ116359
 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3

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-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//7.8e-104:549:95//AB020860

R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//6.6e-41:291:86//AC006019

R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//3.1e-07:433:59//AE001415

R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence.//6.0e-06:237:64//AF053523

R-NT2RP3001712//CITBI-E1-2516N9.TF CITBI-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence.//1.5e-95:456:99//AQ279562

R-NT2RP3001716//Homo sapiens chromosome Y, clone 264,M,20, complete sequence.//0.0012:346:58//AC004617

R-NT2RP3001724//Human HepG2 3' region MboI cDNA, clone hmd6a06m3.//1.3e-27:163:95//D17273

R-NT2RP3001730//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//7.6e-43:409:76//Z98200

R-NT2RP3001739

R-NT2RP3001752//Human clone 23774 mRNA sequence.//1.9e-08:104:84//U79279

R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence.//8.8e-06:102:78//AQ113378

R-NT2RP3001764

R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican).//0.99:166:66//X54232

R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds.//1.3e-111:549:97//AB007928

R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//1.6e-32:266:83//U13262

R-NT2RP3001799//H.sapiens mRNA for OX40 homologue.//8.5e-44:374:79//X75962

R-NT2RP3001819

R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7.//0.0042:231:63//U40410

R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//1.0:404:59//AF030694

R-NT2RP3001855

R-NT2RP3001896//CIT978SK-A-636F10.TV CIT978SK Homo

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sapiens genomic clone A-636F10, genomic survey sequence.//0.0012:68:82//AQ116409

R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.//0.37:266:65//AC005950

R-NT2RP3001915//Human BAC clone RC367017 from 7p15-p21, complete sequence.//0.018:144:66//AC002486

R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds.//2.4e-10:77:100//M77142

R-NT2RP3001929

R-NT2RP3001931//Homo sapiens full length insert cDNA clone YU73B11.//1.0e-110:562:96//AF087969

R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome Xq13.1-Xq13.3.//0.38:386:56//Z95328

R-NT2RP3001943//Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.//0.87:298:61//AC004500

20 R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence.//0.0095:76:78//U03836

R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC11-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//7.0e-109:552:96//AC005844

R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.15:111:68//Z81029

R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds.//0.016:286:60//AF065987

30 R-NT2RP3002004//H.sapiens mRNA for FAST kinase.//5.1e-41:335:82//X86779

R-NT2RP3002007

R-NT2RP3002014//Human DNA sequence from clone 228A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence.//6.6e-41:297:86//AL022322

R-NT2RP3002033

R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds.//0.77:320:60//M80537

40 R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence.//0.82:362:57//Z98877

R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence.//0.010:185:63//Z87006

R-NT2RP3002057

R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-17:164:81//AC004002

R-nnnnnnnnnnnnn

R-NT2RP3002081//HS_3082_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence

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e. //4.2e-25:344:73//AQ122260
 R-NT2RP3002097//Homo sapiens Xp22-150. BAC GSHB-309 P15 (Genome Systems Human BAC Library) complete sequence. //2.6e-23:212:80//AC006210
 R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence. //0.43:168:64//AC004746
 R-NT2RP3002108//CIT-HSP-2346P16. TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence. //3.5e-08:110:78//AQ059071
 R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds. //0.11:534:55//U80077
 R-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE. //4.1e-108:551:96//AL031710
 R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulatory Protein, complete cds. //6.8e-62:347:80//AB003503
 R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA 20 A, partial cds. //0.77:281:63//U46857
 R-NT2RP3002165
 R-NT2RP3002166//D.sargus satellite DNA (clone PSE 3). //0.81:124:62//Z48711
 R-NT2RP3002173
 R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence. //1.3e-35:305:81//B36980
 R-NT2RP3002244//Caenorhabditis elegans cosmid R11E 30 3. //0.0024:393:61//AF100669
 R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 22q12-qter contains ESTs. //0.30:217:63//Z82189
 R-NT2RP3002255
 R-NT2RP3002273//Homo sapiens BAC clone 393I22 from 8q21, complete sequence. //0.84:463:57//AF070717
 R-NT2RP3002276//HS_2260_A1_MF_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence. //0.0017:198:63//AQ292491
 R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17. //7.4e-93:510:93//X13546
 R-NT2RP3002304//Human BAC clone GS188P18, complete sequence. //6.3e-09:477:59//AC000115
 R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.087:388:58//AC004688
 R-NT2RP3002343

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R-NT2RP3002351//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //0.20:489:56//AC004617
 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene. //2.4e-104:516:94//Y15164
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds. //4.7e-102:524:95//AB014578
 R-NT2RP3002484
 R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS. //5.2e-17:232:75//Z73359
 R-NT2RP3002512
 R-NT2RP3002529//CIT-HSP-2340H2. TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence. //0.81:266:58//AQ057387
 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds. //3.3e-82:438:94//AB018272
 R-NT2RP3002549//Medicago truncatula ENBP1 gene, exons 1 to 12. //0.95:381:56//AJ002479
 R-NT2RP3002566//HS_2036_A1_D08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence. //0.18:162:64//AQ230627
 R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces. //5.1e-15:213:73//AC004956
 R-NT2RP3002590//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence. //0.00010:431:59//AB019236
 R-NT2RP3002602//Mus musculus stannin gene, complete cds. //1.6e-20:339:70//AF030522
 R-NT2RP3002603
 R-NT2RP3002631//Homo sapiens chromosome 21 PAC RPC IP704A9190Q2. //1.0:241:59//AJ006997
 R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds. //6.8e-24:331:76//M85300
 R-NT2RP3002660//H. sapiens partial gene for progesterone receptor and Aluelement DNA. //9.8e-43:273:82//Z49816
 R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA, partial sequence. //0.60:300:59//U82072
 R-NT2RP3002671//S.pombe chromosome III cosmid c553. //1.2e-20:399:66//AL023704
 R-NT2RP3002682//RPC11-44K6.TJ RPC11 Homo sapiens genomic clone R-44K6, genomic survey sequence. //4.7e-09:122:77//AQ202481
 50 R-NT2RP3002687//P.falciparum complete gene map of

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plastid-like DNA (IR-B).//1.1e-07:494:59//X95276
 R-NT2RP3002688//Human 7SL RNA sequence.//2.7e-32:290:79//X01037
 R-NT2RP3002701
 R-NT2RP3002713//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//0.95:334:59//AL031427
 R-NT2RP3002763//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567
 R-NT2RP3002770//R.prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710
 R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//AC004822
 R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.1e-20:161:77//AF003528
 R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972
 R-NT2RP3002818//HS_3053_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3053 Col=16 Row=A, genomic surveysequence.//0.19:220:60//AQ135025
 R-NT2RP3002861//P.falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276
 R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//AC005256
 R-NT2RP3002876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.6e-59:311:96//AL034380
 R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPCI1-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.6e-24:422:63//AC003035
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314
 R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//3.1e-16:471:64//AC005014
 R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500
 R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//3.4e-111:566:96//AC005754
 R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:58//AE001391
 R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666

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R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482
 R-NT2RP3002978//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//4.8e-05:249:63//AL031733
 R-NT2RP3002988//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.0097:246:67//Z97195
 R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, C7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown gene s.//1.9e-24:188:78//AF109905
 R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon Tall-1 integration site.//5.3e-07:376:63//L47211
 R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165_I_16, complete sequence.//1.4e-13:323:66//AC005669
 R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-10).//3.8e-42:265:91//Y16708
 R-NT2RP3003068//HS_3214_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=18 Row=N, genomic surveysequence.//0.025:207:64//AQ181894
 R-NT2RP3003071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
 R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T26A1, genomic survey sequence.//0.95:219:63//B27013
 R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153
 R-NT2RP3003121//Homo sapiens full length insert cDNA clone ZD62D10.//2.1e-47:242:98//AF086348
 R-NT2RP3003133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985
 R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646
 R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995
 R-NT2RP3003150

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R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems HumanBac Library) complete sequence. //5.5e-42:289:74//AC005294

R-NT2RP3003185//HS_2058_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=0, genomic survey sequence. //0.025:52:94//AQ231298

R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence. //4.8e-40:349:79//AC005701

R-NT2RP3003197//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 364I1, WORKING DRAFT SEQUENCE. //5.2e-10:180:71//AL031319

R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA. //1.8e-11:148:77//U51904

R-NT2RP3003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 892F13, WORKING DRAFT SEQUENCE. //6.6e-41:282:86//AL009183

R-NT2RP3003212//Homo sapiens full length insert cDNA clone ZB91B11. //1.7e-68:363:95//AF086173

R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5. //0.0018:279:64//AF100307

R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence. //1.0:346:57//AC005272

R-NT2RP3003251//Homo sapiens BAC clone RC060N22 from 7q21, complete sequence. //2.5e-10:436:62//AC003083

R-NT2RP3003264//CIT-HSP-2296M7. TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence. //5.8e-05:308:61//AQ005862

R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3b11m5. //9.4e-47:302:89//D17022

R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds. //7.4e-101:550:93//L36983

R-NT2RP3003290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE. //3.0e-22:228:78//AL031662

R-NT2RP3003301

R-NT2RP3003302//CIT-HSP-2319H19. TF CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence. //1.5e-69:367:95//AQ034950

R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //5.1e-08:398:64//AC005505

R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence. //0.00022:436:58//Z69660

R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 -complete genomic sequence, c

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omplete sequence. //1.5e-16:334:70//AC002287

R-NT2RP3003330//Homo sapiens full length insert cDNA YI24C02. //4.4e-96:458:99//AF075015

R-NT2RP3003344//HS_3235_B2_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence. //4.1e-18:197:80//AQ303203

R-NT2RP3003346

R-NT2RP3003353//CITBI-E1-2523B18. TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence. //8.3e-06:130:73//AQ278834

R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces. //1.9e-97:481:94//AC005519

R-NT2RP3003384//Homo sapiens clone DJ0038I10, WORKING DRAFT SEQUENCE, 5 unordered pieces. //2.3e-10:226:71//AC004820

R-NT2RP3003385

R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence. //2.8e-40:496:72//AL031585

R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA A. //1.5e-20:375:68//L23204

R-NT2RP3003411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4, WORKING DRAFT SEQUENCE. //1.0:180:61//Z97635

R-NT2RP3003427//RPCI11-45J23. TJ RPCI11 Homo sapiens genomic clone R-45J23, genomic survey sequence. //0.82:162:69//AQ195566

R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence. //1.1e-10:379:61//AC006031

R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds. //1.1e-95:479:96//AF004828

R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds. //1.3e-100:527:93//AB018268

R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence. //4.0e-08:495:59//AE001398

R-NT2RP3003500//W.suaveolens mitochondrial ATP9 gene. //0.0074:514:59//X77238

R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containing mRNA. //1.3e-31:217:88//U00952

R-NT2RP3003552

R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, complete cds. //0.98:321:61//AF057019

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R-NT2RP3003564
 R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22q12.1 contains STS. //0.0015:507:59//AL008638
 R-NT2RP3003576//Human Chromosome 16 BAC clone CIT9 87SK-A-61E3, complete sequence. //1.2e-39:359:79//AC003007
 R-NT2RP3003589//Plasmodium falciparum MAL3P8, complete sequence. //0.014:539:58//AL034560
 R-NT2RP3003625//Human DNA sequence from clone 1042 K10 on chromosome 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with probable rabGAP domains and Src homology domain 3). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence. //1.8e-44:448:77//AL022238
 R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence. //0.34:257:62//AC005291
 R-NT2RP3003659//O. fuscipennis 16S rRNA gene, partial. //0.021:145:65//Z93701
 R-NT2RP3003665//HS_3078_B2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, genomic survey sequence. //1.3e-75:397:95//AQ140580
 R-NT2RP3003672
 R-NT2RP3003686
 R-NT2RP3003701//Human BAC clone GS310A05 from 7q21-q22, complete sequence. //6.4e-17:464:62//AC002452
 R-NT2RP3003716//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE. //0.00072:425:62//AL034410
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds. //1.7e-101:492:97//AB018300
 R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C10, complete sequence. //3.7e-07:217:66//AC003009
 R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence. //8.1e-26:456:68//Z98052
 R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey sequence. //4.9e-09:117:77//B01736
 R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon12 and partial cds. //2.8e-106:551:95//AF077754
 R-NT2RP3003805
 R-NT2RP3003809//Homo sapiens full length insert cDNA clone YZ95A01. //3.6e-106:533:97//AF086107

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R-NT2RP3003819//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE. //6.0e-44:288:81//Z84487
 R-NT2RP3003825//Mus domesticus interleukin 1 receptor antagonist (IL-1RA) mRNA. //0.0014:410:58//M64404
 R-NT2RP3003828
 R-NT2RP3003831//***ALU WARNING: Human Alu-J subfamily consensus sequence. //2.3e-41:289:85//U14567
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence. //1.6e-108:541:97//AF070611
 R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence. //1.5e-46:457:74//AC002980
 R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence. //3.5e-06:356:62//Z98547
 R-NT2RP3003870//Homo sapiens full length insert cDNA clone ZD75H11. //8.2e-09:68:98//AF086402
 R-NT2RP3003876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE. //0.0027:180:66//AL031650
 R-NT2RP3003914//Dictyostelium discoideum DNA for transposable element Tdd-3 tandem array. //0.029:234:62//X53439
 R-NT2RP3003918
 R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds. //0.00087:164:67//AF029215
 R-NT2RP3003989
 R-NT2RP3003992//Sequence 1 from patent US 5591825. //0.56:235:59//I33465
 R-NT2RP3004013//HS_3018_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=17 Row=M, genomic survey sequence. //0.00026:421:60//AQ119904
 R-NT2RP3004016//Drosophila melanogaster DNA sequence (Pis DS03465 (D149) and DS08544 (D187)), complete sequence. //4.8e-12:308:62//AC004532
 R-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE. //0.42:190:64//AL021579
 R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence. //3.6e-21:332:69//AC006130
 R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //2.0e-05:476:57//AC005308
 R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complete sequence. //2.0e-86:486:93//AC005

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R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete sequence.//5.3e-11:230:69//AC002525
R-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5unordered pieces.//7.5e-93:551:92//AC005038

R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPCI5-940 J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.6e-104:317:100//AC006064

R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus).//0.73:168:60//U36532

R-NT2RP3004145//Homo sapiens full length insert cDNA clone ZE09H03.//2.3e-89:427:99//AF086542

R-NT2RP3004148//Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence.//0.013:134:70//U78721

R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//3.8e-10:101:87//AC004081

R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//1.5e-06:442:57//AC005533

R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.7e-07:220:69//D29763

R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete sequence.//7.3e-89:504:92//D42052

R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequence.//0.018:353:59//Z81498

R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence.//4.5e-06:407:60//AE001415

R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//2.8e-105:534:97//AC005385

R-NT2RP3004253//RPCI11-78J12.TJ RPCI11 Homo sapiens genomic clone R-78J12, genomic survey sequence.//4.0e-64:382:90//AQ281324

R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-60:417:84//AF013967

R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, complete cds.//2.7e-43:528:73//AF092536

R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.4e-06:435:62//AC004231

R-NT2RP3004341//CITBI-E1-2503F11.TR CITBI-E1 Homo sapiens genomic clone 2503F11, genomic survey sequence.//0.0018:210:65//AQ263365

R-NT2RP3004348//Homo sapiens chromosome 17, clone 50

hRPK.85_B_7, complete sequence.//7.1e-46:340:83//AC005695

R-NT2RP3004349//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//9.4e-29:263:79//AL020995

R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monoamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.0e-67:422:90//Z95125

10 R-NT2RP3004399//HS_3046_A1_E02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=1, genomic survey sequence.//0.00014:186:67//AQ137619

R-NT2RP3004424//RPCI11-59I14.TJ RPCI11 Homo sapiens genomic clone R-59I14, genomic survey sequence.//7.4e-71:370:95//AQ201461

R-NT2RP3004428//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282

20 R-NT2RP3004451//Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824

R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917

R-NT2RP3004466

R-NT2RP3004470//Homo sapiens chromosome 5, BAC clone 5m9 (LBNL H220), complete sequence.//8.3e-06:229:64//AC005895

R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504

R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925

R-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//3.9e-38:322:81//U47024

R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982

R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023

R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357

R-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260

R-NT2RP3004507

R-NT2RP3004527//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518

R-nnnnnnnnnnnn//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316

- R-NT2RP3004544
 R-NT2RP3004566
 R-NT2RP3004569//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709
 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083
 R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946
 R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234
 R-NT2RP3004617
 R-NT2RP3004618//F2H16TF IGF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414
 R-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-0-sulfotransferase (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679
 R-NT2RP4000008//H.sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749
 R-NT2RP4000023//CIT-HSP-2372A9.TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388
 R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015
 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266
 R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b In DGCRRegion, complete sequence.//0.56:462:58//AC000074
 R-NT2RP4000078//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00021:460:60//AC005506
 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//1.6e-08:518:58//AC004648
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//3.5e-106:536:96//AB011538
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952
 R-NT2RP4000147
 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681
 R-NT2RP4000151
 R-NT2RP4000159//*Caenorhabditis elegans* cosmid R02F11.//0.00011:261:63//AF016439
 R-NT2RP4000167//RPC111-59L8.TK RPC111 Homo sapiens genomic clone R-59L8, genomic survey sequence.//6.2e-26:163:93//AQ200049
 R-NT2RP4000185
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505:96//AB014600
 R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300
 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HS P-444n24, complete sequence.//1.2e-39:272:88//AC005261
 R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470
 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092
 R-NT2RP4000263//CIT-HSP-2336N24.TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515
 R-nnnnnnnnnnnn//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt].//0.12:326:61//S76368
 R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524
 R-NT2RP4000323//S.cerevisiae telomeric sequence DNA, clone YLP108CA-2-i.//0.048:107:69//M34311
 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281
 R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195
 R-NT2RP4000370//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//9.9e-25:348:72//AC005154
 R-NT2RP4000376//Rattus norvegicus phospholipase A2-activating protein (plap) mRNA, complete cds.//2.2e-69:391:89//U17901
 R-NT2RP4000381//Homo sapiens chromosome 17, clone

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hRPK.394_K_10, complete sequence.//0.066:197:63//A
C006080

R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens
genomic clone A-345F19, genomic survey sequence.//
0.10:79:75//B15527

R-NT2RP4000417//Homo sapiens full length insert cD
NA clone ZD52B10.//9.6e-96:468:97//AF086313

R-NT2RP4000424//Homo sapiens DNA sequence from PAC
127D3 on chromosome 1q23-25. Contains FM02 and FM
03 genes for Flavin-containing Monooxygenase2 and
Flavin-containing Monooxygenase 3 (Dimethylaniline
Monooxygenase(N-Oxide 3, EC1.14.13.8, Dimethylani
line Oxidase 3, FM0 II, FM0 3), and a gene for anot
her, unknown, Flavin-containing Monooxygenase fami
ly protein. Contains ESTs and GSSs, complete seque
nce.//1.8e-08:489:59//AL021026

R-NT2RP4000448//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC181 genomicsequence, WORKING DRAFT SEQU
ENCE, 8 unordered pieces.//3.3e-07:510:60//AC00550
5

R-NT2RP4000449//HS_2037_B2_A09_T7 CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2037 Col=18 Row=B, genomic surveysequenc
e.//1.3e-58:375:88//AQ243047

R-NT2RP4000455//Phocine herpesvirus type 1 glycopr
otein D (gd) gene, partial cds.//0.62:133:63//U922
71

R-nnnnnnnnnnnnnnn

R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chro
mosome 11 specific cosmid Homo sapiens genomic clo
ne cSRL-54b11, genomic survey sequence.//2.1e-19:1
45:88//B05082

R-nnnnnnnnnnnnnnn

R-NT2RP4000500

R-NT2RP4000515//Plasmodium falciparum 3D7 chromoso
me 12 PFYACB8-420 genomic sequence, WORKING DRAFT
SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC
005140

R-NT2RP4000517//Human Chromosome 16 BAC clone CIT9
87SK-A-61E3, complete sequence.//2.7e-21:230:77//AC
003007

R-NT2RP4000518//Homo sapiens DNA sequence from PAC
206D15 on chromosome1q24. Contains a Reduced Fola
te Carrier protein (RFC) LIKE gene, a mitochondria
l ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pse
udogene, an unknown gene and the last exon of the
JEM1 gene coding for the Basic-Leucine Zipper nucl
ear factor JEM-1. Contains ESTs, an STS and a BAC
end sequence (GSS), complete sequence.//0.0080:46
1:59//AL021068

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R-NT2RP4000519

R-NT2RP4000524

R-NT2RP4000528//Homo sapiens chromosome 17, clone
hRPK.138_P_22, complete sequence.//0.99:158:66//AC
005697

R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Co
smid Clone 33e In DGCRRegion, complete sequence.//
1.0:309:59//AC000078

10 R-NT2RP4000556//Rattus norvegicus cell cycle prote
in p55CDC gene, complete cds.//0.0031:126:72//AF05
2695

R-NT2RP4000588//Homo sapiens BAC clone RG208K23 fr
om 7q31, complete sequence.//1.0:186:64//AC004161

R-NT2RP4000614//Plasmodium falciparum DNA *** SEQU
ENCING IN PROGRESS ***from contig 3-62, complete s
equence.//1.4e-06:526:58//AL009013

R-NT2RP4000638//Homo sapiens chromosome 17, clone
hCIT.468_F_23, WORKINGDRAFT SEQUENCE, 3 unordered
pieces.//6.9e-48:497:75//AC004666

20 R-NT2RP4000648//CIT-HSP-230017.TR CIT-HSP Homo sap
iens genomic clone 230017, genomic survey sequenc
e.//0.22:110:68//AQ012747

R-NT2RP4000657//Lycodichthys dearborni type III an
tifreeze peptide gene,clone 5' LD-1/NotI-EcoRI subc
lone SphI-XbaI, partial cds.//0.0065:189:63//U2044
3

R-NT2RP4000704//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 409J21, WORKING DRAFT S
EQUENCE.//0.22:334:60//Z83824

30 R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Co
smid Clone 56c In DGCRRegion, complete sequence.//
2.2e-70:448:88//AC000080

R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sa
piens genomic clone 2310K14, genomic survey sequen
ce.//0.00013:289:61//AQ019669

R-NT2RP4000739//Homo sapiens chromosome 12p13.3, W
ORKING DRAFT SEQUENCE,21 unordered pieces.//0.53:2
54:61//AC004765

40 R-NT2RP4000781//P.cepacia fusaric acid-resistance
genes encoding 5 proteins, complete cds.//1.0:392:
59//D12503

R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21
(Genome Systems HumanBAC library) complete sequenc
e.//0.59:378:58//AC003037

R-NT2RP4000833//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone Y313F4, WORKING DRAFT S
EQUENCE.//3.4e-53:307:85//AL023808

50 R-NT2RP4000837//Homo sapiens T-cell receptor alpha
delta locus from bases 501613 to 752736 (section
3 of 5) of the Complete Nucleotide Sequence.//7.0e

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-50:367:77//AE000660
 R-NT2RP4000855
 R-NT2RP4000865//Homo sapiens chromosome 17, clone
 HRPC905N1, complete sequence.//1.5e-78:479:88//AC0
 03098
 R-NT2RP4000878//Mus musculus mRNA for myeloid asso
 ciated differentiation protein.//4.5e-09:186:69//AJ
 001616
 R-NT2RP4000879//Plasmodium falciparum 3D7 chromoso
 me 12 PFYAC812 genomic sequence, WORKING DRAFT SEQU
 ENCE, 8 unordered pieces.//7.8e-08:364:60//AC00415
 3
 R-ntnnnnnnnnnn//Human S-adenosylmethionine decarbo
 xylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M8
 8006
 R-ntnnnnnnnnnn//H.sapiens ung gene for uracil DNA-
 glycosylase.//7.6e-09:392:61//X89398
 R-NT2RP4000925//Rattus norvegicus Shal-related pot
 assium channel Kv4.3 mRNA, complete cds.//5.8e-45:
 264:92//U42975
 R-ntnnnnnnnnnn//epstein-barr virus simple repeat a
 rray (ir3).//0.00012:367:61//J02079
 R-NT2RP4000928//Arabidopsis thaliana genomic DNA,
 chromosome 5, P1 clone: MCL19, complete sequence.//
 1.0:138:68//AB006698
 R-NT2RP4000929//Human DNA sequence from PAC 293L6
 on chromosome 22, complete sequence.//0.45:288:62//
 Z82197
 R-NT2RP4000955//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 633019, WORKING DRAFT S
 EQUENCE.//1.1e-09:322:62//AL022302
 R-NT2RP4000973//Homo sapiens X-linked anhidrotic
 ectodermal dysplasia protein gene (EDA), exon 2 and
 flanking repeat regions.//2.3e-06:326:62//AF0035
 28
 R-NT2RP4000975
 R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3009 Col=15 Row=L, genomic survey sequenc
 e.//2.3e-14:117:89//AQ090957
 R-NT2RP4000984//Human immunodeficiency virus type
 1 envelope glycoprotein (env) gene, C2-V3 region,
 isolate HIV194UG011INT.01_d1PD, partial cds.//0.1
 1:219:62//U44882
 R-NT2RP4000989//Sequence 30 from patent US 555228
 1.//3.5e-25:154:97//I25669
 R-NT2RP4000996//Plasmodium falciparum strain Dd2 h
 eat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02
 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9(cg9),
 CG1 (cg1), CG6 (cg6), chloroquine resistance candi

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date protein (cg2), and CG7 (cg7) genes, complete
 cds.//3.8e-07:421:59//AF030694
 R-NT2RP4000997//Homo sapiens chromosome 17, clone
 104H12, complete sequence.//4.2e-37:499:72//AC0000
 03
 R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3163 Col=4 Row=0, genomic survey sequenc
 e.//2.8e-38:241:90//AQ168515
 R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORK
 ING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:3
 72:73//AC006023
 R-NT2RP4001010//Homo sapiens full length insert cD
 NA clone ZD38E12.//3.3e-09:153:74//AF086247
 R-NT2RP4001029//Mus domesticus nuclear binding fac
 tor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20
 086
 R-NT2RP4001041//Homo sapiens chromosome 5, BAC clo
 ne 282B7 (LBNL H192), complete sequence.//9.9e-84:4
 35:96//AC005216
 R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partia
 l cds.//6.2e-50:282:94//AB007859
 R-NT2RP4001064//H.sapiens NOS2 gene, exon 15.//0.7
 1:183:61//X85771
 R-NT2RP4001078//Human D-site binding protein gene,
 exon 4 and complete cds.//1.9e-114:569:97//U48213
 R-NT2RP4001079//Homo sapiens mRNA for putative Ca2
 +-transporting ATPase, partial.//2.4e-118:574:98//A
 J010953
 R-NT2RP4001080//Plasmodium falciparum chromosome
 2, section 66 of 73 of the complete sequence.//0.01
 3:430:58//AE001429
 R-ntnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 pro
 tein, partial cds.//1.8e-119:548:95//AB011164
 R-NT2RP4001095//Homo sapiens cosmids IM0525, LC123
 3, Qc3C1, LB1439, Qc12C11 and 220B3 from Xq28, com
 plete sequence.//2.8e-39:312:81//AF003626
 R-NT2RP4001100//Human DNA sequence from cosmid U85
 A3, between markers DXS366 and DXS87 on chromosome
 X contains rad21 and T-cell cyclophorin pseudogen
 es, STS.//8.7e-41:389:78//Z78021
 R-NT2RP4001117//Canis familiaris sec61 homologue m
 RNA, complete cds.//2.8e-12:292:68//M96629
 R-NT2RP4001122//Caenorhabditis elegans cosmid F44D
 12, complete sequence.//0.97:129:66//Z68298
 R-NT2RP4001126//HS_3146_A1_B05_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3146 Col=9 Row=C, genomic survey sequenc
 e.//0.013:268:63//AQ141093
 R-NT2RP4001138

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R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE. //1.8e-31:380:68//AL031668

R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces. //1.2e-83:325:92//AC005095

R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds. //8.1e-32:553:67//D67067

R-NT2RP4001150//AK011 Genomic DNA *Hordeum vulgare* 10 genomic clone tel44a similar to barley TAS, genomic survey sequence. //0.91:132:63//AQ248412

R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence. //4.0e-118:437:97//AB003468

R-NT2RP4001174//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence. //1.7e-33:289:82//AC002996

R-nnnnnnnnnnnn//*P. falciparum* mRNA for AARP2 protein. //0.93:187:64//Y08924

R-NT2RP4001207

R-NT2RP4001210//CIT-HSP-2042D13. TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence. //3.8e-06:268:63//B74772

R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism. //4.7e-16:371:66//M99593

R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence. //2.4e-06:288:61//AQ216635

R-NT2RP4001228//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS ***from MAL1P2, WORKING DRAFT SEQUENCE. //0.024:357:58//AL031745

R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=I, genomic survey sequence. //0.0033:301:63//AQ126918

R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence. //1.5e-11:140:80//AQ118389

R-NT2RP4001260//*Plasmodium falciparum* chromosome 2, section 63 of 73 of the complete sequence. //0.0013:486:59//AE001426

R-NT2RP4001274//RPCI11-24021. TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-24021, genomic survey sequence. //3.9e-25:142:99//AQ013887

R-nnnnnnnnnnnn//Homo sapiens full length insert cDNA clone ZD55D10. //1.2e-10:90:92//AF086334

R-NT2RP4001313//*Mus musculus* orphan nuclear hormon 50

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e receptor (CAR) gene, complete sequence. //7.7e-23:466:66//AF009326

R-NT2RP4001315//CIT-HSP-2312C6. TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence. //0.98:305:62//AQ018036

R-NT2RP4001339

R-NT2RP4001345

R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence. //0.00082:260:59//AB003097

R-NT2RP4001353//RPCI11-55N17. TJ RPCI11 Homo sapiens genomic clone R-55N17, genomic survey sequence. //0.74:106:66//AQ081821

R-NT2RP4001372

R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence. //1.5e-09:473:60//AC006080

R-NT2RP4001375

R-NT2RP4001379//CIT-HSP-2335A10. TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence. //9.4e-41:441:75//AQ040083

R-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence. //2.4e-22:276:73//AC004691

R-NT2RP4001407//*Plasmodium falciparum* 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.49:254:61//AC005140

R-NT2RP4001414

30. R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7. //6.6e-66:357:90//L14272

R-NT2RP4001442//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.11:307:59//AC005308

R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence. //0.0039:112:71//B05220

R-NT2RP4001474

40 R-NT2RP4001483

R-NT2RP4001498//*Plasmodium falciparum* (clone Dd2) heat shock protein 86 gene, complete cds. //1.2e-07:339:61//L34027

R-NT2RP4001502//HS_2187_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2187 Col=19 Row=F, genomic survey sequence. //1.3e-20:183:81//AQ214108

R-NT2RP4001507//*Arabidopsis thaliana* chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.15:333:62//AC005916

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R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226

R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086

R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710

R-nnnnnnnnnnn//Arabidopsis thaliana BAC T12H20.// 10 1.5e-11:517:60//AF080119

R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212

R-NT2RP4001567//RPCI11-61A2.TJ RPCI11 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771

R-NT2RP4001568

R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12(RPS12), putative cryptogene (GRII), 12S ribosomal RNA, and apocytochrome b (CY b) genes, primary transcripts, and cytochrome c oxidase subunit III (COIII) gene, complete cds.//1.6e-09:555:58//U14181

R-NT2RP4001574//HS_2247_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345

R-NT2RP4001575//Human DNA sequence from clone 1033 B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and CDSs, complete sequence.//1.1e-118:567:98//AL031228

R-NT2RP4001592//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.5e-09:370:61//AL031650

R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U115B9(Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364

R-NT2RP4001614

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R-NT2RP4001634//Homo sapiens full length insert cDNA clone YU73B11.//5.8e-101:526:94//AF087969

R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:97//AF007151

R-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092

R-NT2RP4001656//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384

R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397

R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629

R-NT2RP4001725//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380

R-nnnnnnnnnnn//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735

20 R-NT2RP4001739//RPCI11-74E7.TJ RPCI11 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408

R-NT2RP4001753//H.sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926

R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316

R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020

30 R-NT2RP4001803//HS_3087_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3087 Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405

R-NT2RP4001822.

R-NT2RP4001823

R-NT2RP4001828//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540

40 R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.5e-06:418:60//AE001372

R-NT2RP4001849//P.falciparum serine rich protein (SERP I) gene.//0.64:135:67//J03983

R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548

R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.8e-111:570:96//AC005014

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R-NT2RP4001896
 R-NT2RP4001901
 R-NT2RP4001927//*Borrelia burgdorferi* (section 32 of 70) of the complete genome.//1.0:242:60//AE001146
 R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523
 R-NT2RP4001946//*Plasmodium falciparum* 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157
 R-NT2RP4001950//RPCI11-69C18.TJ RPCI11 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641
 R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023
 R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148
 R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3' UTR region.//1.0e-46:242:98//U25276
 R-NT2RP4002018//RPCI11-76I23.TV RPCI11 Homo sapiens genomic clone R-76I23, genomic survey sequence.//7.9e-89:438:97//AQ268536
 R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297
 R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353
 R-NT2RP4002058//RPCI11-6901.TJ RPCI11 Homo sapiens genomic clone R-6901, genomic survey sequence.//0.23:163:64//AQ268418
 R-NT2RP4002071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386
 R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375
 R-NT2RP4002078//RPCI11-79I16.TV RPCI11 Homo sapiens genomic clone R-79I16, genomic survey sequence.//3.3e-87:452:95//AQ283131
 R-nnnnnnnnnnnnn
 R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619
 R-NT2RP4002408//CIT-HSP-2376023.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.//6.8e-62:320:96//AQ111163
 R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476

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R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//6.0e-56:660:71//AC002383
 R-NT2RP4002905//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934
 R-OVARC1000004//Homo sapiens chromosome 4 clone B3 68A9 map 4q25, complete sequence.//2.1e-43:326:74//AC005510
 R-OVARC1000006//HS_2253_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124
 R-OVARC1000013//HS_2212_A2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584
 20 R-OVARC1000014//Human DNA sequence from PAC 463A9, on chromosome Xq25 contains STS.//0.0053:356:62//Z80232
 R-OVARC1000017
 R-OVARC1000035//RPCI11-65E1.TJ RPCI11 Homo sapiens genomic clone R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194
 R-OVARC1000058//Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an Immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and taga and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721
 R-OVARC1000060//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397
 R-OVARC1000068//*P. falciparum* complete gene map of plastid-like DNA (IR-B).//0.00038:553:58//X95276
 R-OVARC1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387
 R-OVARC1000085//DNA encoding component HC5 of human proteasome.//2.7e-65:366:92//E03413
 R-nnnnnnnnnnnnn//CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391
 R-OVARC1000091
 R-OVARC1000092//CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520
 50 R-OVARC1000106

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- R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250
- R-OVARC1000114//Homo sapiens partial XPGC gene, exon 2.//9.5e-49:392:80//X71342
- R-OVARC1000133//Human Chromosome 16 BAC clone CIT987SK-A-362C6, complete sequence.//0.00020:243:65//U95740
- R-OVARC1000145//Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//1.8e-16:370:67//AC005385
- R-OVARC1000148//CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492
- R-OVARC1000151//M.musculus GEG-154 mRNA.//9.8e-21:192:81//X71642
- R-OVARC1000168//CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932
- R-OVARC1000191//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506
- R-OVARC1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.2e-111:556:96//AC004604
- R-OVARC1000209//Blacus sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF003501
- R-OVARC1000212//Mouse DNA for beta-casein.//0.56:225:63//X13484
- R-OVARC1000240//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//6.2e-38:193:82//AC005670
- R-OVARC1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194
- R-OVARC1000288//Human HepG2 3' region MboI cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131
- R-OVARC1000302//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971
- R-OVARC1000304//Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574
- R-OVARC1000309
- R-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236
- R-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614
- R-OVARC1000335//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0483I23; HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.034:429:60//AC005690
- R-OVARC1000347//Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308
- R-OVARC1000384//D.discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588
- R-OVARC1000408//Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812
- R-OVARC1000411//CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720
- R-OVARC1000414//Homo sapiens genomic DNA, 21q region, clone: 149C3X10, genomic survey sequence.//1.8e-32:296:75//AG002388
- R-OVARC1000420//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378
- R-OVARC1000427//D.discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382
- R-OVARC1000431//HS_2199_A2_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=1, genomic survey sequence.//1.3e-34:186:98//AQ093722
- R-OVARC1000437//Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662
- R-OVARC1000440//Homo sapiens BAC clone NH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043
- R-OVARC1000442//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381
- R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583
- R-OVARC1000461//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417
- R-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//1.1e-81:489:91//AF023451
- R-OVARC1000466//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526
- R-OVARC1000473//Homo sapiens full length insert cDNA clone YI53C10.//3.2e-92:317:100//AF085851
- R-OVARC1000479//Rattus norvegicus mRNA for TIP120,

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- complete cds. //2.7e-70:502:84//D87671
 R-OVARC1000486//Dictyostelium discoideum FusC (fus C) gene, partial cds. //0.52:411:58//AF019984
 R-OVARC1000496
 R-OVARC1000520//Homo sapiens PAC clone DJ412A9 from m 22, complete sequence. //3.8e-17:294:71//AC005005
 R-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces. //4.5e-109:547:96//AC005024
 R-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence. //3.0e-46:264:93//AC004510
 R-OVARC1000543//Caenorhabditis elegans cosmid F10C1. //0.00063:417:59//U49831
 R-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence. //1.5e-39:144:92//AL022069
 R-OVARC1000557//Homo sapiens chromosome 19, cosmid R32469, complete sequence. //1.5e-81:429:96//AC005197
 R-OVARC1000564//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence. //0.83:301:58//AC004223
 R-OVARC1000573//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lul gene and cytochrome C (CCp) pseudogene. //2.4e-44:300:88//U52111R-OVARC1000578//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence. //6.4e-48:436:78//AF001549
 R-OVARC1000588//Homo sapiens chromosome 19, cosmid F19847, complete sequence. //2.7e-32:313:78//AC005952
 R-OVARC1000605
 R-OVARC1000622//Homo sapiens PAC clone DJ0942I16 from 7q11, complete sequence. //6.2e-43:328:83//AC006012
 R-OVARC1000640//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces. //1.9e-47:514:73//AC005840
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds. //1.6e-29:162:100//AB011162
 R-OVARC1000678//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.50:270:60//AC005140
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 R-nnnnnnnnnnnn//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7. //1.4e-83:549:86//AJ001713
 R-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE. //3.2e-13:160:76//AL034424
 R-OVARC1000689//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds. //0.90:230:61//U32943
 R-OVARC1000700//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence. //5.1e-15:133:85//AC005754
 R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130_H_16, complete sequence. //6.9e-48:525:73//AC005585
 R-OVARC1000730//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence. //0.00019:198:63//AQ093513
 R-OVARC1000746//P. falciparum complete gene map of plastid-like DNA (IR-B). //0.98:154:65//X95276
 R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pTZ18R. //2.0e-30:187:78//M21185
 R-OVARC1000771
 R-OVARC1000781//Sequence 5 from Patent W09722695. //8.4e-47:401:77//A63552
 R-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence. //7.8e-111:567:96//AC004542
 R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds. //1.3e-17:119:95//L15189
 R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBNL H171), complete sequence. //2.3e-51:482:78//AC005574
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC. //3.6e-105:536:95//Y17711
 R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence. //2.7e-107:538:96//AC004494
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds. //3.6e-114:579:96//AF045584
 R-OVARC1000862//M. musculus FIF mRNA. //2.3e-20:346:73//X71978
 R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence. //9.1e-08:427:58//AE001416
 R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds. //5.6e-34:357:78//U20086

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R-OVARC1000885//Lycopersicon esculentum alcohol de hydrogenase homolog (GAD3) mRNA, partial cds.//0.4 7:305:60//U21801

R-OVARC1000886

R-OVARC1000891//HS_3082_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500

R-OVARC1000897//Human DNA sequence from clone 192P 9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989

R-OVARC1000912

R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150

R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1Region, complete sequence.//1.6e-77:465:90//AC002471

R-OVARC1000936//HS_2195_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108

R-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716

R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549

R-OVARC1000948//Hypera postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169

R-OVARC1000959//CIT-HSP-2371K16.TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323

R-OVARC1000960//Homo sapiens BAC clone GS293C05 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021

R-OVARC1000971//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//2.2e-07:223:70//X91255

R-OVARC1000984

R-OVARC1000996//Human DNA sequence from clone 272L 16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, Beta 3 (Nicein, Kalinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker DIS491 and a carepeat polymorphism, complete sequence.//1.3e-06:179:70//AL02

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R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//5.8e-71:332:87//AC003957

R-OVARC1001000//HS_3032_B1_G11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695

R-OVARC1001004//Homo sapiens from UWC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190

R-OVARC1001010//RPCI11-10P1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813

R-OVARC1001011//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520

R-OVARC1001032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345

R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence.//1.4e-18:451:64//AC005220

R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149

R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410

R-OVARC1001044

30 R-OVARC1001051//H.sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962

R-OVARC1001055//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.0e-30:292:76//AC006213

R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237

R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657

40 R-OVARC1001072//Gallus gallus chicken brain factor -2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276

R-OVARC1001074//HS_2205_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=G, genomic survey sequence.//1.3e-35:205:94//AQ184530

R-OVARC1001085

R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897

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R-OVARC1001113//Homo sapiens diaphanous 1 (HD1A1) mRNA, complete cds.//1.0e-73:386:95//AF051782
 R-OVARC1001117//Homo sapiens chromosome 7 clone UW GC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272
 R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBNL H73), complete sequence.//1.5e-44:390:77//AC005372
 R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.//0.81:461:57//AJ 10 235270
 R-OVARC1001161//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680
 R-OVARC1001162//CIT-HSP-2171J2. TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781
 R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15unordered pieces.//1.3e-28:427:70//AC004963
 R-OVARC1001169//RPCI11-36P6. TV RPCI-11 Homo sapiens genomic clone RPCI-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859
 R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549
 R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213
 R-OVARC1001180//Homo sapiens 12q24.1 NOVECTOR P443 K8 () complete sequence.//9.1e-41:516:72//AC005907 30
 R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796
 R-OVARC1001200//ALS=85 kda insulin-like growth factor binding protein-3complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462
 R-OVARC1001232//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794
 R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//1.4e-41:284:87//AC006071
 R-OVARC1001243//HS_2055_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142
 R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148
 R-OVARC1001268
 R-OVARC1001270//Plasmodium falciparum MAL3P6, comp 50

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lete sequence.//0.0031:295:62//Z98551
 R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence.//1.6e-107:544:97//AC004494
 R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPCI1-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062
 R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018
 R-nnnnnnnnnnnn//Sequence 13 from patent US 562481 8.//5.4e-85:577:84//I41142
 R-OVARC1001329//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402
 R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862
 R-OVARC1001339//Homo sapiens 12q13 PAC RPCI1-316M2 4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:366:83//AC004242
 R-OVARC1001341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818
 R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874
 R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261J17 (LBNL H190), complete sequence.//2.8e-46:424:78//AC005350
 R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//I34297
 R-OVARC1001360//Homo sapiens chromosome 17, clone hRPF.786_0_4, complete sequence.//0.20:335:60//AC005863
 R-OVARC1001369
 R-OVARC1001372//S. scrofa DNA for myogenin 3' flanking region (285 bp).//6.9e-29:249:83//X89210
 R-OVARC1001376//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//2.1e-50:491:73//AC004491
 R-OVARC1001381//Homo sapiens chromosome 17, clone hRPF.156_L_14, complete sequence.//9.3e-20:422:60//AC005821
 R-OVARC1001391
 R-nnnnnnnnnnnn
 R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//9.9e-110:561:95//AB006651
 R-OVARC1001419//CIT-HSP-2362F16. TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequen

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ce. //7.6e-47:242:98//AQ074668
 R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence. //2.3e-20:211:66//AC005157
 R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1. //0.18:148:66//M80341
 R-OVARC1001442
 R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence. //2.3e-19:181:81//AC002086
 R-OVARC1001476//CITBI-E1-2517B6. TR CITBI-E1 Homo sapiens genomic clone 2517B6, genomic survey sequence. //0.24:308:59//AQ278655
 R-OVARC1001480//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 753D4, WORKING DRAFT SEQUENCE. //0.99:294:62//AL031676
 R-OVARC1001489//E.caballus microsatellite DNA marker (clone ASB32). //0.87:81:71//X93546
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds. //9.3e-116:585:96//AF016507
 R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13F4 ~complete genomic sequence, complete sequence. //2.6e-40:285:86//AC002039
 R-OVARC1001525//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.0:320:59//AC006036
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete cds. //5.0e-110:566:95//AB016488
 R-OVARC1001547
 R-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene. //5.9e-33:216:92//AF031165
 R-OVARC1001600//Human Chromosome X, complete sequence. //3.0e-22:157:89//AC002418
 R-OVARC1001610//HS_3070_A2_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070 Col=12 Row=A, genomic survey sequence. //0.47:107:66//AQ103523
 R-OVARC1001611//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE. //0.17:236:63//AL034423
 R-OVARC1001615//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE. //1.3e-19:248:70//AL031658
 R-OVARC1001668//HS_3228_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=24 Row=I, genomic survey sequence. //4.6e-13:156:76//AQ188379
 R-OVARC1001702//CITBI-E1-2501P16. TR.1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey se

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quence. //1.6e-41:217:99//AQ241965
 R-OVARC1001703
 R-OVARC1001711//CITBI-E1-2502N10. TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence. //2.0e-14:220:72//AQ266194
 R-OVARC1001726//CIT-HSP-232001. TF CIT-HSP Homo sapiens genomic clone 232001, genomic survey sequence. //0.021:170:62//AQ038145
 R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (pl). //2.5e-72:422:90//X05276
 R-OVARC1001745//Human DNA sequence from clone 796I11 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence. //7.6e-44:314:84//AL031257
 R-nnnnnnnnnnnn//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds. //1.6e-08:396:60//M23166
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds. //3.5e-108:567:94//U97670
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 protein, complete cds. //6.3e-108:529:97//AB014575
 R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence. //0.24:205:64//Z99279
 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence. //4.6e-58:558:76//AC005066
 R-OVARC1001795
 R-OVARC1001802//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence. //1.1e-37:346:78//U89337
 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence. //3.0e-112:581:95//AL023694
 R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) pseudogene and an STS, complete sequence. //6.6e-41:345:81//AL031585R-OVARC1001813//CITBI-E1-2508J18. TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence. //1.6e-72:386:95//AQ263046
 R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence. //4.8e-41:320:83//AC002086
 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //3.4e-08:527:58//AC004688

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R-OVARC1001846//CIT-HSP-2014F15. TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905

R-OVARC1001861//M.musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350

R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611

R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding ex 10 on of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.//9.1e-20:206:80//AL031864

R-OVARC1001880//RPCI11-42I15.TJ RPCI11 Homo sapiens genomic clone R-42I15, genomic survey sequence.//3.9e-50:287:88//AQ052700

R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//6.1e-13:457:63//AC003950

R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749

R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246

R-OVARC1001911//Homo sapiens full length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315

R-OVARC1001916

R-OVARC1001928

R-OVARC1001942//S.cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166

R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U58826

R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:63//M99593,

R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//8.2e-38:385:75//AC005666

R-OVARC1001987

R-OVARC1001989//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841

R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286-R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934

R-OVARC1002066//Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence.//

0.23:210:61//AC004411

R-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.4e-99:546:92//AC006015

R-OVARC1002107//Human DNA sequence from PAC 417C15 on chromosome Xq25-Xq26. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174

R-OVARC1002127

R-OVARC1002138//CIT-HSP-2290018. TF CIT-HSP Homo sapiens genomic clone 2290018, genomic survey sequence.//2.4e-07:316:62//AQ003988

R-OVARC1002143//RPCI11-54M8.TJ RPCI11 Homo sapiens genomic clone R-54M8, genomic survey sequence.//2.3e-35:220:90//AQ083241

R-OVARC1002156

R-OVARC1002158//CITBI-E1-2514D4. TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//1.6e-12:140:79//AQ265720

R-OVARC1002165//CIT-HSP-2307C9. TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey sequence.//5.0e-59:291:99//AQ020420

R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060

R-PLACE1000004//D.discoideum gene for protein kinase.//0.00081:263:59//Z37981

R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507

R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557

R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone:T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253

R-PLACE1000031//Homo sapiens clone UWGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//AC006162

40 R-PLACE1000040//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855

R-PLACE1000048//Human BAC clone RG210I04, complete sequence.//4.7e-83:518:89//AC002462

R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.98:73:76//AC005505

R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154

R-PLACE1000066

50

3667

R-PLACE1000078//Homo sapiens chromosome 11 clone C
IT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordere
d pieces.//1.2e-87:456:95//AC005848

R-PLACE1000081

R-PLACE1000094//RPCI11-91K6.TV RPCI11 Homo sapiens
genomic clone R-91K6, genomic survey sequence.//2.
3e-83:409:98//AQ282619

R-PLACE1000133//Homo sapiens chromosome 17, clone
hRPK.746_E_8, complete sequence.//1.8e-06:420:57//A
C005358

R-PLACE1000142

R-PLACE1000184//Homo sapiens estrogen-related rece
ptor gamma mRNA, complete cds.//1.3e-112:594:94//A
F058291

R-PLACE1000185

R-PLACE1000213//CIT-HSP-2308A18. TR CIT-HSP Homo sa
piens genomic clone 2308A18, genomic survey sequen
ce.//8.2e-80:410:97//AQ022149

R-PLACE1000214//Plasmodium falciparum DNA *** SEQU
ENCING IN PROGRESS ***from contig 3-09, complete s
equence.//1.6e-05:548:59//AL008989

R-PLACE1000236//Human DNA sequence *** SEQUENCING
IN PROGRESS *** from clone 695020, WORKING DRAFT S
EQUENCE.//2.2e-16:118:91//AL032818

R-PLACE1000246//X.laevis mRNA for XLCL2 protein.//
6.5e-13:66:95//Z14122R-PLACE1000292//Human DNA seq
uence *** SEQUENCING IN PROGRESS *** from clone 11
1B22, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98
200

R-PLACE1000332//Homo sapiens chromosome 17, clone
hCIT.281_F_24, complete sequence.//1.8e-16:598:62/
/AC004706

R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 f
rom 7q21-q22, complete sequence.//2.3e-11:237:69//A
C005326

R-PLACE1000374//Arabidopsis thaliana chromosome 1
BAC F15K9 sequence, complete sequence.//8.7e-09:49
2:58//AC005278

R-PLACE1000380//Plasmodium falciparum chromosome
2, section 1 of 73 of the complete sequence.//0.5
9:354:59//AE001364

R-PLACE1000383//Mus musculus myotubularin related
protein 1 (Mtmr1) mRNA, complete cds.//0.55:65:84/
/AF073997

R-PLACE1000401//Homo sapiens clone GS166C05, WORKI
NG DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:15
2:83//AC005015

R-PLACE1000406//Arabidopsis thaliana genomic DNA,
chromosome 5, TAC clone: K21H1, complete sequence.
//0.51:346:58//AB020742

3668

R-PLACE1000420//Homo sapiens genomic DNA, chromoso
me 21q22.2 (Down Syndrome region), segment 2/15, W
ORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009

R-PLACE1000421//HS_2251_B2_G12_MR CIT Approved Hum
an Genomic Sperm Library D Homo sapiens genomic cl
one Plate=2251 Col=24 Row=N, genomic survey sequenc
e.//1.4e-82:430:95//AQ192807

R-PLACE1000424//Human PAC clone DJ515N1 from 22q1
1.2-q22, complete sequence.//1.8e-36:483:71//AC002
10 073

R-PLACE1000435//Homo sapiens chromosome 21q22.2 co
smid clone Q71A3, complete sequence.//2.6e-37:371:
76//AF015724

R-PLACE1000444//Homo sapiens chromosome 17, clone
hRPK.227_G_15, complete sequence.//1.0e-54:429:81
//AC005899

R-PLACE1000453//Murine genomic DNA; partially dige
sted Sau3A fragment, cloned into cosmid vector pEM
BLcos2, complete sequence.//0.66:103:72//AF059580

R-PLACE1000481//Human DNA sequence from clone 9600
17 on chromosome Xp11.21-11.22 Contains EST, CA re
peat (DXS991), STS, GSS, complete sequence.//0.019:
171:66//AL022166

R-PLACE1000492//Rat vacuolar protein sorting homol
og r-vps33b mRNA, complete cds.//3.2e-17:221:72//U
35245

R-PLACE1000540//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC492 genomic sequence, WORKING DRAFT SEQU
ENCE, 5 unordered pieces.//0.00045:480:60//AC00530
30 8

R-PLACE1000547//Homo sapiens chromosome 19, cosmid
F17987, complete sequence.//9.6e-32:231:85//AC004
790

R-PLACE1000562//, complete sequence.//1.8e-45:280:
92//AC005409

R-PLACE1000564//Human chromosome 16 creatine trans
porter (SLC6A8) and (CDM) paralogous genes, comple
te cds.//0.0079:180:65//U41302

R-PLACE1000583//Homo sapiens chromosome 17, clone
hRPK.799_N_11, complete sequence.//1.5e-37:414:74/
/AC005323

R-nnnnnnnnnnnnn//Human guanylate binding protein is
oform I (GBP-2) mRNA, complete cds.//1.9e-77:542:82
//M55542

R-PLACE1000596//Plasmodium falciparum 3D7 chromoso
me 12 PFYAC357 genomic sequence, WORKING DRAFT SEQU
ENCE, 7 unordered pieces.//0.00019:482:59//AC00550
6

R-PLACE1000599//Human germline T-cell receptor bet
a chain Dopamine-beta-hydroxylase-like, TRY1, TRY

3669

2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3). //5.6e-51:369:85//U66059

R-PLACE1000610//HS_3071_A1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence. //0.051:147:65//AQ103341

R-PLACE1000636//HS_3220_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence. //0.010:253:64//AQ181157

R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds. //1.6e-99:506:96//AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)). //4.5e-101:559:92//AJ005896

R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt]. //9.1e-10:331:63//S78219

R-PLACE1000712//Homo sapiens full length insert cDNA clone ZD76G10. //1.0e-69:345:98//AF086408

R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence. //1.0:174:62//AC002300

R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence. //1.0e-06:337:60//Z98547

R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence. //8.8e-26:236:80//B02791

R-PLACE1000755//HS_2183_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence. //0.47:151:65//AQ064202

R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces. //7.0e-38:492:74//AC004847

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds. //2.6e-101:513:96//AB014548

R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds. //0.078:180:68//U58970

R-nnnnnnnnnnnnn

R-PLACE1000798//Homo sapiens cosmid D66B10, chromo 50

3670

some 21 5' of IFNARI. //5.1e-26:348:72//AF039904

R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds. //1.4e-26:110:95//U02081

R-nnnnnnnnnnnnn//Homo sapiens full length insert cDNA clone ZD55D10. //1.4e-13:93:96//AF086334

R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6,8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits). //2.7e-09:484:59//L04272

R-PLACE1000863

R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //3.0e-05:274:60//AC005505

R-PLACE1000931//RPCI11-66P7.TK RPCI11 Homo sapiens genomic clone R-66P7, genomic survey sequence. //3.4e-73:369:97//AQ237489

R-PLACE1000948//RPCI11-64K15.TK RPCI11 Homo sapiens genomic clone R-64K15, genomic survey sequence. //6.6e-06:258:62//AQ239337

R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence. //8.3e-20:223:76//AC005553

R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces. //0.00030:448:59//AC005506

R-PLACE1000979

R-PLACE1001000//CIT-HSP-229718.TF CIT-HSP Homo sapiens genomic clone 229718, genomic survey sequence. //7.0e-07:64:95//AQ004997

R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds. //0.0078:215:64//D26607

R-PLACE1001010

R-PLACE1001015//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE. //1.5e-16:452:63//AL022318

R-PLACE1001024//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE. //0.99:186:63//AL024498

R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces. //2.5e-15:313:68//AC005377

R-PLACE1001062//Homo sapiens chromosome 17, clone hCIT54K19, complete sequence. //7.3e-16:119:84//AC003664

R-PLACE1001076

3671

R-PLACE1001088//Human DNA sequence from cosmid 203 C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696

R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139

R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372

R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480

R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412

R-PLACE1001168//HS_2036_A1_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=0, genomic survey sequence.//0.40:144:63//AQ230662

R-PLACE1001171

R-PLACE1001185

R-PLACE1001238//Human coxVIb gene, last exon and flanking sequence.//3.4e-36:349:76//X58139

R-PLACE1001241//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.11:258:61//AL008972

R-PLACE1001257//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B4P3; HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016

R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448

R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839

R-PLACE1001280//CIT-HSP-2328B24.TF CIT-HSP Homo sapiens genomic clone 2328B24, genomic survey sequence.//5.4e-24:147:76//AQ042129

R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642

R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682

R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286

R-PLACE1001323//Homo sapiens DNA sequence from PAC 50

3672

418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480

R-PLACE1001351//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399

10 R-PLACE1001366//Human Na⁺/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615

R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030

R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319

R-PLACE1001387

R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355

R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412

R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087

R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//0.12:53:84//AC006241

30 R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na⁺-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lul gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111

R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130

R-PLACE1001468//HS_3050_A2_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920

R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//7.2e-17:180:80//AC002368

R-PLACE1001502//RPCI11-24F2.TP RPCI-11 Homo sapiens genomic clone RPCI-11-24F2, genomic survey sequence.//0.15:203:66//B84401

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R-PLACE1001503//HS_2183_A1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic surveysequence. //1.3e-38:181:82//AQ022613

R-PLACE1001517//Homo sapiens hGAA1 mRNA, complete cds. //6.4e-56:339:90//AB006969

R-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE. //8.6e-59:304:97//AL031667

R-PLACE1001545//Homo sapiens chromosome 3, clone h 10 RPK.165_I_16, complete sequence. //2.6e-18:171:82//AC005669

R-PLACE1001551

R-PLACE1001570//M.capricolum DNA for CONTIG MC188. //0.0043:305:57//Z33135

R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //2.5e-82:408:98//AB020860

R-PLACE1001603//Homo sapiens KE05 protein mRNA, complete cds. //1.5e-40:295:84//AF064605

R-PLACE1001610//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces. //2.5e-39:307:82//AC005037

R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds. //4.9e-41:217:97//AF054174

R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds. //1.4e-08:178:65//M27878

R-PLACE1001634//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone H06C16, WORKING 30 DRAFT SEQUENCE. //0.00026:221:62//Z92791

R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence. //2.6e-83:441:95//AC005971

R-PLACE1001672//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8. //0.91:115:69//Z79253

R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds. //1.5e-111:545:97//AF069250

R-PLACE1001692//Homo sapiens clone RC228D17, WORKING 40 DRAFT SEQUENCE, 2 unordered pieces. //1.0e-46:478:75//AC005077

R-PLACE1001705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE. //0.79:91:73//Z99716

R-PLACE1001716//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence. //0.96:172:66//AC002349

R-PLACE1001720

R-PLACE1001729//Human interleukin-13 (IL-13) precu 50

3674

rsor gene, complete cds. //0.79:280:60//U31120

R-PLACE1001739//Homo sapiens chromosome 19, CIT-HS P-444n24, complete sequence. //1.0:109:65//AC005261

R-PLACE1001740//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence. //5.3e-11:249:67//AC006027

R-PLACE1001745

R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence. //6.0e-05:337:61//AC005509

R-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds. //1.3e-91:540:89//AF061243

R-PLACE1001756//Human BAC clone RC302F04 from 7q31, complete sequence. //0.074:344:62//AC002463

R-PLACE1001761

R-PLACE1001771//Homo sapiens full length insert cDNA clone ZD79C11. //4.4e-57:298:96//AF086426

R-PLACE1001781//T.thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819. //4.6e-05:282:61//M15711

R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces. //0.015:331:58//AC004710

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds. //4.1e-92:463:95//AF058953

R-PLACE1001821//***ALU WARNING: Human Alu-J subfamily consensus sequence. //3.6e-36:281:82//U14567

R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds. //9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (Dlx5) mRNA, complete cds. //0.0043:207:64//AF033011

R-PLACE1001912//RPC11-25F23.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-25F23, genomic survey sequence. //6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein G G2-1 mRNA, complete cds. //5.0e-73:363:98//AF070671

R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence. //0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H7, WORKING DRAFT SEQUENCE. //0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE. //1.4e-44:376:80//AL023755

R-PLACE1002046//CITBI-E1-2520J24.TF CITBI-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence

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nce.//4.5e-20:144:89//AQ280117
 R-PLACE1002052//Human DNA sequence from cosmid U16
 OA4, between markers DXS366 and DXS87 on chromosom
 e X contains STS.//0.025:362:57//Z80900
 R-PLACE1002066//Leishmania tarentolae maxicircle D
 NA fragment.//0.0034:197:62//X02438
 R-PLACE1002072//Homo sapiens chromosome 5, P1 clon
 e 854b11 (LBNL H44), complete sequence.//9.7e-06:4
 14:60//AC004763
 R-PLACE1002073
 R-PLACE1002090//Homo sapiens Chromosome 16 BAC clo
 ne CIT987-SKA-345G4 ~complete genomic sequence, c
 omplete sequence.//1.8e-06:278:63//AC002302
 R-PLACE1002115//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone Y214H10, WORKING DRAFT
 SEQUENCE.//6.0e-12:327:64//AL022344
 R-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, com
 plete cds.//5.1e-67:442:86//AF079527
 R-PLACE1002140//Homo sapiens DNA sequence from PAC
 454M7 on chromosome Xq25-26.3. Contains the OCRL1
 gene for Lowe Oculocerebrorenal Syndrome protein
 OCRL-1. Contains ESTs, STSs and GSSs, complete seq
 uence.//2.2e-80:403:97//AL022162
 R-PLACE1002150//Human DNA sequence from PAC 145B12
 on chromosome Xq27-Xq28. Contains EST, CA repeat
 and STS.//0.043:455:59//AL008706
 R-PLACE1002157//Human DNA sequence from Fosmid 65B
 7 on chromosome 22q11.2-qter. Contains exons 6-12
 of the SLC5A1 (SGLT1) gene for solute carrier fami
 ly 5 (sodium/glucose cotransporter) member 1 (High
 Affinity Sodium-Glucose Cotransporter), complete
 sequence.//9.8e-58:384:79//Z83849
 R-PLACE1002163//Canis familiaris MHC class IIA DLA
 -DQA (DQA 1 allele) gene, exon 2, partial cds.//0.
 82:96:70//U44785
 R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 f
 rom 7q31, complete sequence.//0.83:196:65//AC00445
 6
 R-PLACE1002205//Human DNA sequence from PAC 436M11
 on chromosome Xp22.11-22.2. Contains the serine t
 hreonine protein phosphatase gene PPEF1, and the fi
 rst coding exon of the RS1 gene for retinoschisis
 (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an
 STS and GSSs, complete sequence.//0.0017:193:61//Z
 94056
 R-PLACE1002213//Homo sapiens chromosome 19, fosmid
 37308, complete sequence.//8.0e-42:330:81//AC0041
 52
 R-PLACE1002227//Homo sapiens BAC clone BK085E05 fr
 om 22q12.1-qter, complete sequence.//2.1e-10:126:8

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0//AC003071
 R-PLACE1002256//Homo sapiens clone DJ0853H20, WORK
 ING DRAFT SEQUENCE, 5unordered pieces.//2.7e-06:47
 8:57//AC004907
 R-PLACE1002259//Human DNA sequence from cosmid U75
 A4 on chromosome X.//6.5e-81:501:88//Z82255
 R-PLACE1002319//Plasmodium falciparum 3D7 chromoso
 me 12 PFYAC181 genomicsequence, WORKING DRAFT SEQU
 ENCE, 8 unordered pieces.//0.00023:549:58//AC00550
 5
 R-PLACE1002342//Homo sapiens mRNA for KIAA0728 pro
 tein, partial cds.//4.9e-94:501:93//AB018271
 R-PLACE1002395//Homo sapiens chromosome 19, cosmid
 R34382, complete sequence.//1.4e-69:385:93//AC005
 329
 R-PLACE1002399//Human HepG2 3' region cDNA, clone
 hmd5d06.//2.4e-71:411:92//D16939
 R-PLACE1002433//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 173D1, WORKING DRAFT SE
 QUENCE.//0.85:176:63//AL031984
 R-PLACE1002437//Human BAC clone RG114A06 from 7q3
 1, complete sequence.//0.0040:213:63//AC002542
 R-PLACE1002438//CITBI-E1-2501M20.TF.1 CITBI-E1 Hom
 o sapiens genomic clone 2501M20, genomic survey se
 quence.//0.70:247:61//AQ242104
 R-PLACE1002450//Homo sapiens 959 kb contig between
 AML1 and CBR1 on chromosome 21q22; segment 1/3.//
 0.00060:471:59//AJ229041
 R-PLACE1002465//Homo sapiens clone DJ0673M15, WORK
 ING DRAFT SEQUENCE, 33unordered pieces.//2.5e-10:9
 8:81//AC004854
 R-PLACE1002474//Mus musculus matrilin-2 precursor
 mRNA, complete cds.//1.7e-25:199:71//U69262
 R-PLACE1002477//Human DNA sequence from PAC 50A13
 on chromosome Xp11. Contains ATP SYNTHASE LIPID BI
 NDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G
 2, ATP5G3) like pseudogene, ESTs and STSs. Contain
 s polymorphic CRepeat.//1.2e-11:382:63//Z92545
 R-PLACE1002493//Homo sapiens signal transducing ad
 aptor molecule 2A (STAM2) mRNA, complete cds.//1.1
 e-53:307:91//AF042273
 R-PLACE1002499//Plasmodium falciparum MAL3P6, comp
 lete sequence.//0.56:270:60//Z98551
 R-PLACE1002500//CIT-HSP-2337C20. TR CIT-HSP Homo sa
 piens genomic clone 2337C20, genomic survey sequen
 ce.//3.2e-42:297:85//AQ037614
 R-PLACE1002514//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 212A2, WORKING DRAFT SE
 QUENCE.//7.8e-16:221:73//Z95114
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 pro

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tein, partial cds.//1.6e-86:582:85//AB018256
 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//AC004774
 R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//0.0042:489:60//D16253
 R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178
 R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBNL H127), complete sequence.//2.5e-44:292:84//AC006084
 R-PLACE1002583//Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555
 R-PLACE1002591
 R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626
 R-PLACE1002604//Human cosmid LL12NC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:65//U63313
 R-PLACE1002625//HS_2233_B2_H04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663
 R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-46:272:94//AF079765
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180
 R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656
 R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I73723
 R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC GSHB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185
 R-PLACE1002772//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:82//AC006145
 R-PLACE1002782
 R-PLACE1002794
 R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981
 R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279
 R-PLACE1002816//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC libr

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ary) complete sequence.//6.3e-59:339:93//AC004466
 R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//M27877
 R-PLACE1002839//Homo sapiens PAC clone DJ0015123 from 22, complete sequence.//6.5e-25:301:74//AC004819
 R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519
 R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049
 R-PLACE1002881
 R-PLACE1002908//HS_3064_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=G, genomic survey sequence.//1.9e-09:156:72//AQ142985
 R-PLACE1002941
 R-PLACE1002962
 R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a carepeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721
 R-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755
 R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921
 R-PLACE1002996//HS_2064_A1_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211
 R-PLACE1003025//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//0.26:428:58//AC006145
 R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.3e-95:465:98//AC005920
 R-PLACE1003044
 R-PLACE1003092//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266
 R-PLACE1003100//HS_2244_A2_H12_MR CIT Approved Hum

- an Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=0, genomic surveysequence. //2.3e-42:288:86//AQ084224
- R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3unordered pieces. //0.00066:233:61//AC004885
- R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence. //0.019:429:57//AL034558
- R-PLACE1003145
- R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence. //3.2e-05:390:58//AC004616
- R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence. //2.4e-06:390:60//AB015479
- R-PLACE1003176
- R-PLACE1003190//Homo sapiens clone RC332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces. //4.0e-78:406:81//AC005095
- R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence. //0.016:411:57//Z98551
- R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomicsequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.00084:288:61//AC005139
- R-PLACE1003238//Homo sapiens full length insert cDNA clone ZD79H11. //7.6e-114:567:96//AF086432
- R-PLACE1003249//Human Chromosome X, complete sequence. //1.3e-45:317:85//AC002416
- R-PLACE1003256//Homo sapiens chromosome 17, clone HCIT421K24, complete sequence. //1.0e-45:328:85//AC004099
- R-PLACE1003258
- R-PLACE1003296//Diphtheria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence. //0.050:228:59//U39952
- R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences ofHPP1, -2, and -9. //1.7e-91:458:96//M27877
- R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence. //4.3e-34:370:71//Z82243
- R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence. //1.0:159:68//AQ020460
- R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomicsequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //1.1e-05:330:61//AC00415
- 3
- R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds. //3.4e-98:469:98//U92715
- R-PLACE1003361
- R-PLACE1003366//Homo sapiens CAG repeated sequence. //0.018:319:61//AJ006805
- R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence. //0.050:155:63//B20174
- R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence. //1.2e-62:434:83//AC004771
- R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds. //0.042:263:57//U89350
- R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10. //1.7e-83:429:96//AB020878
- R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence. //2.4e-13:175:76//AC005695
- R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence. //2.1e-05:340:61//AC005587
- R-PLACE1003454//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from contig 3-64, complete sequence. //0.47:411:58//AL009014
- R-PLACE1003478//M.capricolum DNA for CONTIG MC175. //0.51:253:59//Z33125
- R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence. //4.6e-37:319:81//AC006080
- R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence. //1.0e-40:251:90//AQ007480
- R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a. //2.7e-29:163:89//AF064859
- R-PLACE1003521//HS_3252_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic surveysequence. //0.00017:274:60//AQ221562
- R-PLACE1003528//HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic surveysequence. //6.6e-40:219:83//AQ230483
- R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes,

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and unidentified reading frames A61, 2 and 3.//8.3e-05:300:61//J01404
 R-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297
 R-PLACE1003566
 R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965
 R-PLACE1003583//Human DNA sequence from PAC 388N15 on chromosome Xq21.1.//3.5e-18:287:68//Z99571
 R-PLACE1003584
 R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032
 R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066
 R-PLACE1003596//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200
 R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081
 R-nnnnnnnnnnnnn
 R-PLACE1003618//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451
 R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688
 R-PLACE1003638//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312
 R-PLACE1003669//HS_3054_A2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=I, genomic survey sequence.//0.014:265:61//AQ132713
 R-PLACE1003704//HS_3213_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=G, genomic survey sequence.//0.80:195:61//AQ176784
 R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067
 R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607
 R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//

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2.7e-44:505:73//AL022336
 R-PLACE1003738//H. sapiens DNA sequence.//0.93:185:60//Z22357
 R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023
 R-PLACE1003762//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//4.6e-13:134:79//AC003070
 R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//5.4e-12:189:71//AC005919
 R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160
 R-PLACE1003783
 R-PLACE1003784//Homo sapiens chromosome 19, CIT-HS P-87m17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659
 R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ114933
 R-PLACE1003833//Homo sapiens full length insert cDNA clone ZE15C06.//4.4e-59:313:95//AF086558
 R-PLACE1003850
 R-PLACE1003858
 R-nnnnnnnnnnnnn
 R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 In DCCR Region, complete sequence.//8.7e-33:285:81//AC000072
 R-nnnnnnnnnnnnn
 R-PLACE1003886
 R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//0.73:127:65//AC004069
 R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810
 R-PLACE1003903//Homo sapiens full length insert cDNA clone ZD78D11.//8.1e-74:369:97//AF086422
 R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520
 R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.67:213:63//Z99281
 R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//8.7e-49:342:85//Z74022
 R-PLACE1003936//H. sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030
 R-PLACE1003968//Plasmodium falciparum DNA *** SEQU

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ENCING IN PROGRESS ***from contig 4-62, complete sequence. //1.3e-07:245:65//AL010247

R-PLACE1004104

R-PLACE1004114//Human PAC clone RG212D03, complete sequence. //5.0e-07:336:61//AC002485

R-PLACE1004118//HS_3092_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, genomic survey sequence. //0.80:207:60//AQ128151

R-PLACE1004128//Rattus norvegicus guanine nucleotide binding protein beta 4 subunit mRNA, partial cds. //1.8e-06:193:66//AF022085

R-PLACE1004149//HS_2253_A2_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, genomic survey sequence. //2.4e-59:315:95//AQ129711

R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPC I4-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence. //8.3e-53:299:76//AC005295

R-PLACE1004161

R-PLACE1004183//Homo sapiens for TOM1-like protein. //1.3e-80:434:93//AJ010071

R-PLACE1004197//RPC111-69N15.TK RPC111 Homo sapiens genomic clone R-69N15, genomic survey sequence. //0.0078:170:65//AQ265515

R-PLACE1004203//Homo sapiens semaphorin L (SEMA) mRNA, complete cds. //3.4e-105:501:98//AF030698

R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence. //6.1e-65:373:86//AL021326

R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21.1, complete sequence. //0.011:383:61//AC006031

R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems HumanBAC library) complete sequence. //3.4e-09:576:59//AC004470

R-PLACE1004258//HS_3034_A1_B12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, genomic survey sequence. //1.4e-35:359:77//AQ128936

R-PLACE1004270//CITBI-E1-2504K14.TR CITBI-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence. //2.7e-06:150:74//AQ261108

R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence. //0.025:116:72//AC005234

R-PLACE1004277//Homo sapiens two pore domain K⁺ channel (TASK-2) mRNA, complete cds. //4.4e-106:581:9

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1//AF084830

R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.59:231:60//AC005308

R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence. //5.8e-31:340:75//AC005920

R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces. //6.4e-90:572:86//AC005095

R-PLACE1004316//H. sapiens mRNA for apoptosis specific protein. //1.9e-113:590:94//Y11588

R-PLACE1004336//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE. //2.3e-65:292:82//AL033383

R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds. //2.4e-70:379:93//AF100153

R-PLACE1004376//CIT-HSP-2287M8.TF CIT-HSP Homo sapiens genomic clone 2287M8, genomic survey sequence. //0.47:173:61//AQ000837

R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic clone 2316J11, genomic survey sequence. //0.035:109:69//AQ037817

R-PLACE1004388//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-82, complete sequence. //4.2e-06:381:60//AL010149

R-PLACE1004405//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.20:270:60//AC005027

R-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence. //1.3e-96:516:94//AC005532

R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, complete sequence. //5.8e-10:279:65//AL031296

R-PLACE1004437//Human NAD⁺-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds. //2.9e-88:516:88//U49283

R-PLACE1004451//HS_2258_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, genomic survey sequence. //0.82:172:61//AQ221189

R-PLACE1004460

R-PLACE1004467//Syrian hamster carbamoyl phosphate synthetase-aspartate transcarbamylase-di hydroorotase (CAD) gene, exons 1 and 2. //1.2e-24:311:62//M31621

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R-PLACE1004471//Homo Sapiens Chromosome X clone bW XD75, complete sequence.//2.1e-34:333:70//AC004389
 R-PLACE1004473
 R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584
 R-PLACE1004506
 R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427
 R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071
 R-PLACE1004518
 R-PLACE1004548//Homo sapiens Xp22 BAC GS-551019 (Genome Systems Human BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride channel 4 gene, complete sequence.//4.9e-40:245:80//AC003666
 R-PLACE1004550
 R-PLACE1004564//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.7e-82:532:86//X75931
 R-PLACE1004629//Homo sapiens chromosome 7 clone UW GC:g3586a230 from 7p14-15, complete sequence.//0.015:437:59//AC004800
 R-PLACE1004645//CIT-HSP-2370D6.TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.033:76:75//AQ110136
 R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq 28, complete sequence.//2.0e-23:237:79//AF036876
 R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPC111-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.1e-09:94:87//AC005343
 R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//2.7e-24:263:74//U07561
 R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606
 R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3 -p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.3e-96:498:95//AB020860
 R-PLACE1004686
 R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3

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-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 2/11.//2.1e-33:290:80//AB020859
 R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9 A, complete sequence.//1.0:195:60//AL021448
 R-PLACE1004716//CITBI-E1-2519C14.TR CITBI-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965
 R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0022:360:60//AC005507
 R-PLACE1004736
 R-PLACE1004740
 R-PLACE1004751//Homo sapiens ubiquitin-protein ligase E3-alpha (UBR1) mRNA, partial cds.//5.4e-105:575:92//AF061556
 R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GS HB-555C13, complete sequence.//9.0e-26:317:76//AC002523
 R-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds.//8.5e-88:437:96//AF084367
 R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:138:65//AP000010
 R-PLACE1004793//Human endogenous retrovirus HERV-K (HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds, and 3' LTR.//5.1e-58:313:80//U60269
 R-PLACE1004813//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178
 R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140
 R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250
 R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence.//3.8e-61:353:89//AC004126
 R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666
 R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC Library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669
 R-PLACE1004836//HS_2270_A2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=0, genomic survey sequence

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e.//8.6e-51:267:96//AQ164110
 R-PLACE1004838//CIT-HSP-2343E10. TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544
 R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//192820
 R-PLACE1004868//Human Chromosome X clone bWDX342, complete sequence.//0.57:344:59//AC004072
 R-PLACE1004885//HS_3235_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193
 R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577
 R-PLACE1004902
 R-nnnnnnnnnnnn//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209
 R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//0.00084:373:60//AC004605
 R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936
 R-PLACE1004934//Homo sapiens clone RC062N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00030:198:66//AC005683
 R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788
 R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
 R-PLACE1004972
 R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
 R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
 R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
 R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925

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R-PLACE1005027
 R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
 R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711; WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
 R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
 R-PLACE1005077//H. sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
 R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495
 20 R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788
 R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401
 R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476
 R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195
 30 R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845
 R-PLACE1005128
 R-PLACE1005146
 R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140
 R-nnnnnnnnnnnn//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018
 R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787
 R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
 R-PLACE1005206//Homo sapiens full length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
 50 R-PLACE1005232//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE. //1.3e-34:286:81//Z84476

R-PLACE1005243

R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence. //0.66:180:60//Z49132

R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence. //1.3e-15:166:78//AC005067

R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence. //2.5e-34:358:74//AQ265720

R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P1, WORKING DRAFT SEQUENCE. //4.1e-07:495:60//AL031744

R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence. //1.1e-42:308:85//AQ169443

R-PLACE1005308

R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces. //0.0048:320:60//AC000383

R-PLACE1005327//chromosome 1 specific transcript KIAA0491. //5.4e-103:537:94//AB007960

R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence. //2.2e-94:536:91//AC004794

R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces. //5.3e-32:313:79//AC000380

R-PLACE1005373//Homo sapiens BAC129, complete sequence. //8.8e-10:229:68//U85195

R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence. //3.0e-44:434:77//AC005291

R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence. //8.8e-105:529:96//AC003991

R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence. //4.7e-39:302:82//AC002477

R-PLACE1005467//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE. //1.1e-40:328:81//Z93014

R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kd) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GS

Ss, complete sequence. //6.4e-68:409:90//AL022310

R-PLACE1005477//Human DNA sequence *** SEQUENCING

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IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE. //0.020:216:66//AL023693

R-PLACE1005480//Homo sapiens chromosome 19, CIT-HS P BAC 490g23 (BC338531), complete sequence. //2.8e-44:327:70//AC005392

R-PLACE1005481//Homo sapiens chromosome 17, clone hRPC.1164_0_3, complete sequence. //4.2e-23:284:74//AC004703

R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4. //0.19:468:60//AF031631

R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds. //1.6e-55:277:98//AF071185

R-PLACE1005526//Human mRNA for alpha-1 type II collagen. //0.10:227:63//X16468

R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE. //2.3e-76:395:96//AP000038

R-PLACE1005530//C.familiaris CA repeat sequence (isolate). //0.023:90:75//X86184

R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence. //2.0e-09:235:64//AL025928

R-PLACE1005554//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence. //0.069:305:60//AC005969

R-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence. //4.3e-105:587:91//AC004707

R-PLACE1005574//Human BAC 367D17 from chromosome 18, complete sequence. //1.5e-17:274:67//AC003971

R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence. //2.7e-15:191:77//AC004991

R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pDJ606g6, complete sequence. //6.4e-90:453:96//AC004126

R-PLACE1005603//Homo sapiens cosmid clone U169D2 from Xp22.1-22.2, complete sequence. //0.69:322:61//U72788

R-PLACE1005611//Borrelia burgdorferi plasmid cp18, OspE (ospE) gene, partial cds. //0.059:473:56//U42599

R-PLACE1005623//Homo sapiens full length insert cDNA clone ZD76B03. //1.6e-113:575:95//AF086405

R-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces. //5.6e-79:270:94//AC005840

R-PLACE1005639//Human BAC clone RG022J17 from 7q21, complete sequence. //8.2e-56:441:83//AC002382

R-PLACE1005646//Homo sapiens RNA helicase-related

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protein mRNA, completecds.//3.2e-110:585:93//AF083255
 R-PLACE1005656//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//8.6e-08:505:58//AC005701
 R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307:72//Z82203
 R-PLACE1005698//344B22.TV CIT978SKA1 Homo sapiens genomic clone A-344B22, genomic survey sequence.//10 0.030:91:70//B15144
 R-PLACE1005727//Human variable number tandem repeat (VNTR) region, allele 17R1 3' to collagen type I I (COL2A1) gene.//5.2e-10:587:59//L10171
 R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//0.0039:239:58//L78810
 R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.2e-21:270:72//U15635
 R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:64//U64601
 R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-45:268:87//D42087
 R-PLACE1005799//Human X chromosome mRNA for CCG1 protein inv. in cell proliferation.//0.030:91:78//X07024
 R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.4e-69:391:92//AC004827
 R-PLACE1005803
 R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.8e-21:175:75//AC002530
 R-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKINGDRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150
 R-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL031745
 R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8e-10:182:69//Y00763
 R-PLACE1005850
 R-PLACE1005851//Homo sapiens clone DJ0789I05, WORKING DRAFT SEQUENCE, 2unordered pieces.//5.5e-06:318:63//AC004887
 R-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//6.7e-28:366:72//X75931
 R-PLACE1005884//Human DNA sequence from cosmid V526F1, between markers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:64//Z70281

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R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomicsequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0094:449:59//AC005139
 R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic clone2509N21, genomic survey sequence.//4.8e-84:494:89//AQ261347
 R-PLACE1005923//RPCI11-65N9.TJ RPCI11 Homo sapiens genomic clone R-65N9,genomic survey sequence.//8.3e-97:520:93//AQ237243
 R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78//AL022719
 R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete sequence.//0.0035:176:62//AL032654
 R-PLACE1005934
 R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5cM, complete sequence.//0.00021:272:62//AF069716
 R-PLACE1005951
 R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:60//U37429
 R-PLACE1005955//Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//8.3e-08:128:70//D17131
 R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//7.0e-09:549:59//AF044863
 R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1e-51:394:81//AB002086
 R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPCI11-407G6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC005866
 R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//5.9e-27:299:74//U15177
 R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequence.//3.5e-07:164:67//AF046375
 R-PLACE1006011//Mus musculus poly-(ADPriboseyl)-transferase homolog PARPmRNA, complete cds.//1.1e-32:266:83//AF072521
 R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e In DGCRRegion, complete sequence.//1.8e-17:164:82//AC000077
 R-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//2.0e-49:557:72//U01139
 R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:128:81//X99906
 R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3unordered pieces.//3.3e-18:220:74//AC004885

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R-PLACE1006119//*Plasmodium berghei* (STRAIN ANKA) gamma-GCS gene, complete CDS.//0.0050:271:63//AJ005122

R-PLACE1006129//*Drosophila melanogaster*, chromosome 2R, region 31C1-31D6, P1 clone DS08879, complete sequence.//0.43:178:65//AC005454

R-PLACE1006139//*Homo sapiens* PAC clone DJ0659J06 from 7q33-q35, complete sequence.//7.5e-13:222:68//AC004849

R-PLACE1006143//*Plasmodium falciparum* MAL3P6, complete sequence.//0.00019:455:59//Z98551

R-PLACE1006157//*Plasmodium falciparum* DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034557

R-PLACE1006159//*Homo sapiens* chromosome 10 clone L A10NC01_124_D_3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:586:96//AC006103

R-PLACE1006164//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.0e-28:342:75//U91328

R-PLACE1006167//*Homo sapiens* full length insert cDNA clone ZE14E04.//4.6e-77:426:93//AF086555

R-nnnnnnnnnnn//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82//X14972

R-PLACE1006187//*Homo sapiens* cyclin E2 mRNA, complete cds.//1.6e-116:597:95//AF091433

R-PLACE1006195//*Homo sapiens* chromosome 19, fosmid 39554, complete sequence.//8.8e-11:148:74//AC004410

R-PLACE1006196

R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.//8.4e-44:332:85//AC000398

R-PLACE1006223//Human DNA sequence from cosmid U74 C11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:215:61//Z73362

R-PLACE1006225//*Caenorhabditis elegans* cosmid Y69H2, complete sequence.//9.7e-13:358:63//Z98877

R-PLACE1006236//*Plasmodium falciparum* MAL3P4, complete sequence.//0.00019:538:58//AL008970

R-nnnnnnnnnnn//*Homo sapiens* BAC clone RG118D07 from 7q31, complete sequence.//3.1e-96:497:95//AC004142

R-PLACE1006246//*Homo sapiens* clone NH0144M13, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.029:499:56//AC006034

R-PLACE1006248//*Homo sapiens* mRNA for KIAA0648 protein, partial cds.//9.2e-96:499:95//AB014548

R-PLACE1006262//*Homo sapiens* Xp22 CSHB-314C4 (Geno 50

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me Systems Human BAC library) complete sequence.//0.00043:160:66//AC004087

R-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL031320

R-PLACE1006318

R-PLACE1006325//*Plasmodium falciparum* MAL3P8, complete sequence.//1.0:426:57//AL034560

R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq21.//0.96:173:66//AL008987

R-PLACE1006357//*P. falciparum* complete gene map of plastid-like DNA (IR-B).//1.9e-07:491:58//X95276

R-PLACE1006360//*Plasmodium falciparum* chromosome 2, section 35 of 73 of the complete sequence.//0.25:484:56//AE001398

R-PLACE1006368//*Caenorhabditis elegans* cosmid Y38H6C, complete sequence.//1.0:240:59//AL031630

R-PLACE1006371//*Homo sapiens* chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//3.7e-101:574:91//AC004232

R-PLACE1006382

R-PLACE1006385//*Mus musculus* intersectin-EH binding protein Ibp2 mRNA, partial cds.//1.4e-50:350:86//AF057286

R-PLACE1006412//*Homo sapiens* clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//5.1e-51:339:82//AC004854

R-PLACE1006414//*Homo sapiens* 12p13.3 PAC RPCI5-927 J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-38:297:84//AC004804

R-PLACE1006438//*Homo sapiens* full length insert cDNA YH73H06.//7.6e-73:422:90//AF074985

R-PLACE1006445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//3.0e-07:376:61//AL031726

R-PLACE1006469

R-PLACE1006470//Mouse B1 repetitive sequence DNA.//1.0:96:66//M24152

R-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.0e-101:535:94//AL021977

R-PLACE1006492//*Homo sapiens* chromosome 17, clone hRPK.180_P_8, complete sequence.//0.78:44:95//AC005972

R-PLACE1006506//*R. norvegicus* BSP gene.//1.0:206:60//X86100

R-PLACE1006521//RPCI11-13L8.TV RPCI-11 *Homo sapiens* genomic clone RPCI-11-13L8, genomic survey sequence.//9.0e-17:414:61//B75158

R-PLACE1006531//*Plasmodium falciparum* coronin gen

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e, isolate 3D7.//0.98:186:63//AJ002197
 R-PLACE1006534//Anopheles gambiae complete mitochondrial genome.//0.051:412:61//L20934
 R-PLACE1006540//Homo sapiens clone UWCC:y55c025 from 6p21, complete sequence.//7.5e-41:470:70//AC004209
 R-PLACE1006552//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.57:355:57//Z98865
 R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.016:291:58//AC004710
 R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//2.9e-116:590:95//U97670
 R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.2e-45:209:88//AC004050
 R-PLACE1006626//C. elegans cosmid K12H4.//1.2e-16:344:64//L14331
 R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//2.8e-25:343:70//AC006128
 R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence.//0.00020:201:62//B90038
 R-PLACE1006673//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.4e-42:309:84//AC004882
 R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence.//6.4e-09:454:59//AC006024
 R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence.//0.56:226:63//AL022154
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence.//6.0e-101:486:98//AF038172
 R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.4e-68:381:93//AC005626
 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence.//6.2e-72:397:92//AF070622
 R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds.//1.6e-11:420:61//U20984
 R-PLACE1006782//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE.//0.60:321:58//Z98865
 R-PLACE1006792//Homo sapiens chromosome 4 clone CO026P05 map 4P16, complete sequence.//2.9e-40:379:7

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7//AC005599
 R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//6.2e-07:291:63//AC005083
 R-PLACE1006800//HS_2270_B1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence.//4.1e-76:367:99//AQ085793
 R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.00058:354:59//AC005507
 R-PLACE1006815//HS_3028_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence.//1.5e-33:251:77//AQ120174
 R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.4e-76:544:84//Z86062
 R-PLACE1006829
 R-PLACE1006860
 R-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//3.2e-107:549:95//AL033378
 R-PLACE1006878//Homo sapiens full length insert cDNA clone ZB55G05.//1.4e-46:241:97//AF086155
 R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LANL), complete sequence.//1.3e-38:283:85//AC004232
 R-nnnnnnnnnnnnn
 R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat.//4.1e-15:477:62//Z82203
 R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665N22 (Genome Systems Human BAC Library) complete sequence.//1.3e-42:305:87//AC005184R-PLACE1006932
 R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X.//0.0014:114:74//Z86061
 R-nnnnnnnnnnnnn//Mouse mRNA for germ cell specific protein APC-1, complete cds.//9.5e-85:590:83//D49482
 R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.//6.7e-42:295:86//AC005544
 R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//1.1e-19:302:71//AC002349

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R-PLACE1006966//HS_2219_B2_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequence.//0.019:180:63//AQ145873

R-PLACE1006989

R-PLACE1007014

R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPCI3-454B23, WORKING DRAFT SEQUENCE, 48 unordered pieces.//1.6e-23:362:70//AC005845

R-PLACE1007045//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//2.3e-90:584:86//AL023693

R-PLACE1007053//Homo sapiens clone DJ0810E06; WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.4e-108:550:96//AC004895

R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with abeta-galacturonidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (CAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//1.8e-103:552:93//AL021368

R-PLACE1007105//Mus musculus muskelin mRNA, complete cds.//2.7e-32:379:73//U72194

R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.14:422:57//AC004688

R-PLACE1007112//Cynips cornifex cytb gene.//0.020:427:58//AJ228479

R-PLACE1007132//Homo sapiens full length insert cDNA YH77E09.//5.7e-107:535:96//AF074987

R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.36:408:58//AC005050

R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA.//0.99:63:73//AF009283

R-PLACE1007226

R-PLACE1007238

R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//2.0e-91:534:89//D50495

R-PLACE1007242//CITBI-E1-2512M9.TF CITBI-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence.//1.3e-05:117:76//AQ279454

R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA.//0.21:284:58//U02970

R-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//6.9e-113:607:93//Y15908

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R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//4.4e-10:135:74//AC006080

R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//1.7e-36:435:72//AF069291

R-PLACE1007282//B.garinii (strain TIs1) p83/100 gene (partial).//0.95:183:60//X81533

R-PLACE1007286//RPCI11-13L8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158

R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195

R-PLACE1007317//Drosophila dasycnemia 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//U94253R-PLACE1007342

R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870

R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507

R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709

R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261

R-PLACE1007402//HS_2055_A2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=6 Row=G, genomic survey sequence.//0.0046:88:79//AQ234824

R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771

40 R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594

R-PLACE1007450//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304

R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081

R-PLACE1007460

50 R-PLACE1007478//Homo sapiens 12q13.1 PAC RPCI3-197 B17 (Roswell Park Cancer Institute Human PAC libra

3699

3700

- ry) complete sequence.//7.0e-08:335:60//AC004241
 R-PLACE1007484
 R-PLACE1007488//Glossina morsitans morsitans 16S r
 ibosomal RNA gene, mitochondrial gene for mitochon
 drial RNA, partial sequence.//2.5e-05:421:61//AF07
 2373
 R-PLACE1007507//Plasmodium falciparum MAL3P7, comp
 lete sequence.//2.3e-09:577:57//AL034559
 R-PLACE1007511//Homo sapiens chromosome 17, clone
 hRPC.1110_E_20, complete sequence.//1.2e-79:387:96 10
 //AC004231
 R-PLACE1007524//Homo sapiens chromosome 19, overla
 pping cosmids F18547, F11133, R27945, R28830 and R3
 2804, complete sequence.//3.4e-09:148:73//AC003682
 R-PLACE1007525//Homo sapiens Chromosome 16 BAC clo
 ne CIT987SK-44M2, complete sequence.//4.7e-38:297:
 82//AC004381
 R-PLACE1007544
 R-PLACE1007547//Human laminin alpha 4 chain (LAMA4
 *-1) mRNA, complete cds.//4.0e-17:108:97//U77706 20
 R-PLACE1007557//Human BAC clone RG343P13 from 7q3
 1, complete sequence.//2.2e-45:390:77//AC002465
 R-PLACE1007583//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 545L17, WORKING DRAFT S
 EQUENCE.//1.0e-56:302:95//AL031665
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequ
 ence.//1.5e-102:554:93//AF038179
 R-PLACE1007618
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequ
 ence.//1.4e-103:537:94//AF038176
 R-PLACE1007632//High throughput sequencing of huma
 n chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered
 pieces.//3.3e-76:289:94//AC005840
 R-PLACE1007645//Homo sapiens full length insert cD
 NA clone ZD76G10.//0.0080:96:77//AF086408
 R-PLACE1007649//CIT-HSP-2308A18.TR CIT-HSP Homo sa
 piens genomic clone 2308A18, genomic survey sequen
 ce.//1.1e-82:412:97//AQ022149
 R-PLACE1007677//Plasmodium falciparum chromosome
 2, section 4 of 73 of the complete sequence.//0.00 40
 41:470:57//AE001367
 R-PLACE1007688
 R-PLACE1007690//Human Chromosome 16 BAC clone CIT9
 87SK-A-418G10, complete sequence.//1.3e-22:162:91/
 /AC002044
 R-PLACE1007697
 R-PLACE1007705//Human DNA sequence *** SEQUENCING
 IN PROGRESS *** from clone 460J8, WORKING DRAFT SE
 QUENCE.//4.4e-121:624:95//AL031662
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP 50
 1) mRNA, complete cds.//1.8e-73:374:96//AF061243
 R-PLACE1007725//Caenorhabditis elegans cosmid F38A
 5.//0.070:186:60//U70854
 R-PLACE1007729//Human endogenous retrovirus HERV-K
 (HML6) proviral cloneHML6.17 putative polymerase a
 nd envelope genes, partial cds, and 3' LTR.//3.8e-5
 3:415:81//U60269
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 pro
 tein, complete cds.//2.1e-92:556:89//AB014585
 R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8
 sequence.//4.0e-43:302:77//AF015169
 R-PLACE1007743//Plasmodium falciparum MAL3P8, comp
 lete sequence.//1.0e-06:533:59//AL034560
 R-PLACE1007746//T.brucei mitochondrial maxicircle
 DNA encoding cytochrome c oxidase subunit I (COI),
 and NADH dehydrogenase subunits 4 and 5, complete
 cds.//0.28:386:58//M14820
 R-PLACE1007791//D.discoideum gene for protein kina
 se.//0.17:263:60//Z37981
 R-PLACE1007807//Human DNA sequence from clone 8780
 8 on chromosome Xq21.1-21.33. Contains an EST, STS
 s, a GSS and genomic marker DXS472, completesequen
 ce.//1.1e-72:324:88//AL031116
 R-PLACE1007810//Homo sapiens chromosome 7 common f
 ragile site, completesequence.//2.2e-14:325:67//AF
 017104
 R-PLACE1007829//Human BAC clone GS165104 from 7q2
 1, complete sequence.//0.00052:455:61//AC002379
 R-PLACE1007843//P.falciparum complete gene map of
 plastid-like DNA (IR-A).//0.0050:447:57//X95275 30
 R-PLACE1007846//Homo sapiens genomic DNA, chromoso
 me 21q22.2 (Down Syndrome region), segment 3/15, W
 ORKING DRAFT SEQUENCE.//2.2e-111:570:95//AP000010
 R-PLACE1007852//HS_3028_B2_F04_MR CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3028 Col=8 Row=L, genomic survey sequenc
 e.//1.3e-12:209:71//AQ131021
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 pro
 tein, complete cds.//6.6e-110:574:94//AB018309
 R-PLACE1007866//Homo sapiens DNA sequence from PAC
 454M7 on chromosome Xq25-26.3. Contains the OCRL1
 gene for Lowe Oculocerebrorenal Syndrome protein
 OCRL-1. Contains ESTs, STSs and GSSs, complete seq
 uence.//1.6e-43:551:70//AL022162
 R-PLACE1007877//Homo sapiens chromosome 5, BAC clo
 ne 34j15 (LBNL H169), complete sequence.//1.6e-22:2
 22:78//AC005754
 R-PLACE1007897//HS_3113_B2_E04_T7 CIT Approved Hum
 an Genomic Sperm Library D Homo sapiens genomic cl
 one Plate=3113 Col=8 Row=J, genomic survey sequenc

3701

e. //2.9e-72:381:95//AQ186905
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487. //8.8e-88:460:95//AB007956
 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKINGDRAFT SEQUENCE. //4.9e-23:172:78//AC003095
 R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence. //1.7e-27:303:75//AC006157
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds. //3.9e-102:513:95//AF084530
 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds. //2.2e-87:465:93//AF079529
 R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds. //4.8e-72:556:81//U13262
 R-PLACE1007990//E. tenella antigen LPNC61 mRNA, partial cds. //0.043:273:63//M30933
 R-PLACE1008000//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE. //8.8e-10:453:62//AL034346
 R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces. //9.0e-114:563:96//AC005628
 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds. //2.6e-44:509:72//L31840
 R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence. //0.32:137:66//AC005592
 R-PLACE1008080//Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence. //0.082:292:59//AC006232
 R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence. //5.4e-27:260:76//AC005036
 R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type I I (COL2A1) gene. //2.2e-07:444:59//L10157
 R-PLACE1008122//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence. //1.9e-11:384:63//AC005919
 R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces. //3.0e-10:189:66//AC004955
 R-PLACE1008132//Human HepG2 3' region cDNA, clone hmd5d06. //7.4e-47:320:86//D16939

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R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds. //2.6e-32:410:70//D14849
 R-PLACE1008181//Caenorhabditis elegans cosmid C31H2. //0.055:358:60//U41748
 R-PLACE1008198
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds. //4.8e-103:551:93//AB011102
 R-PLACE1008209//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE. //4.6e-16:250:71//AL034549
 R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.13:341:60//AC004688
 R-PLACE1008244//P. falciparum P.195 gene. //0.11:212:66//A04562
 R-PLACE1008273//Human MEST mRNA, complete cds. //0.00013:52:100//D78611
 R-nnnnnnnnnnnnn
 R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence. //1.5e-05:104:76//AC005272
 R-PLACE1008309//Human at-rich region adjacent to alpha satellite DNA. //0.70:138:63//M80308
 R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence. //0.00061:150:68//AC005886
 R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence. //4.8e-74:252:98//AC005176
 R-PLACE1008331//Genomic sequence from Human 13, complete sequence. //1.0:176:65//AC001226
 R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, 3' UTR. //2.5e-98:556:90//AF036145
 R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence. //1.2e-05:375:62//B36336
 R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE. //2.8e-10:466:61//AP000011
 R-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence. //1.0e-46:282:82//AC005244
 R-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE. //4.1e-101:529:94//AL034417
 R-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS p

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hase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces. //0.18:379:58//AC004604
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds. //1.6e-101:521:95//D86326
 R-PLACE1008405//Human cosmid CRI-JC2015 at D10S289 in 10sp13. //6.8e-22:328:71//U15177
 R-PLACE1008424
 R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11. //7.5e-101:505:96//AB020864
 R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence. //1.2e-11:118:78//AL022576
 R-PLACE1008437//H. sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE. //2.2e-06:159:69//Y12335
 R-PLACE1008455
 R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence. //1.2e-109:588:93//AC004526
 R-PLACE1008465//CIT978SK-A-28A11. TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence. //1.1e-10:133:77//B78696
 R-PLACE1008488
 R-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING DRAFT SEQUENCE. //7.3e-120:612:95//AL031778
 R-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds. //8.5e-96:510:93//AF045555
 R-PLACE1008532
 R-PLACE1008533
 R-PLACE1008568//HS_3218_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence. //0.0042:295:62//AQ214623
 R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence. //5.0e-26:254:66//AC003074
 R-PLACE1008621//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence. //4.0e-78:498:86//AC006120
 R-nnnnnnnnnnnnn
 R-PLACE1008626//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE. //5.5e-06:228:67//AL031297
 R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor. //3.4e-20:335:71//Y12836

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R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces. //0.55:326:58//AC004826
 R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence. //0.13:440:55//AC011096
 R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence. //1.3e-58:356:82//AC004001
 R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds. //2.4e-88:434:97//AF044333
 R-PLACE1008693//CIT-HSP-2025M9. TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence. //1.2e-41:300:82//B64742
 R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds. //4.8e-31:320:75//AF038406
 R-PLACE1008715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE. //0.074:478:58//AL022147
 R-PLACE1008748//CIT-HSP-2170P12. TR CIT-HSP Homo sapiens genomic clone 2170P12, genomic survey sequence. //8.5e-42:160:86//B90841
 R-PLACE1008757//Homo sapiens 12q24.2 PAC RPC14-765 H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //0.99:211:61//AC005864
 R-PLACE1008790//Rattus norvegicus clone1 polymeric immunoglobulin receptor mRNA 3' untranslated region, GA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats. //0.052:108:68//U00762
 R-PLACE1008798//Homo sapiens full length insert cDNA clone YZ86C05. //7.7e-58:285:100//AF086088
 R-PLACE1008807//CIT-HSP-2366014. TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence. //3.5e-35:223:89//AQ079210
 R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds. //2.3e-97:499:95//AF030933
 R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds. //9.7e-45:394:78//AF032668
 R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces. //2.9e-28:207:87//AC004581
 R-nnnnnnnnnnnnn//CIT-HSP-2172B3. TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence. //8.9e-30:166:97//B93289
 R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence. //3.5e-76:404:95//AC005

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R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3unordered pieces.//7.7e-37:585:67//AC004932

R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494_G_17, complete sequence.//0.0022:409:60//AC005820

R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308

R-PLACE1008925//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860

R-PLACE1008934

R-PLACE1008941//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//9.8e-84:429:92//AC005495

R-PLACE1008947

R-PLACE1009020

R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117

R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.0010:297:58//AL031391

R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//2.9e-06:160:70//AC004707

R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694

R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023

R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting proteinX, short form, complete CDS.//0.00075:79:83//AJ005074

R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783

R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206

R-PLACE1009099

R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025

R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140

R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//7.5e-06:426:58//Z98551

R-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929

R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AP000031

R-PLACE1009158//Homo sapiens full length insert cDNA clone YP10D03.//1.9e-105:539:95//AF085876

R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence.//2.8e-44:360:71//AC005972

R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046

20 R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925

R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//1.9e-46:572:69//Z84480

R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070

R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560

R-PLACE1009200//H. sapiens mRNA for sortilin.//1.0e-31:195:92//X98248

R-PLACE1009230//Homo sapiens chromosome 19, CIT-HS P BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392

R-PLACE1009246//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818

R-PLACE1009308

R-PLACE1009319//Homo sapiens 12q13.1 PAC RPC11-228 P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801

R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//3.3e-87:576:85//AC006120

R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE00117

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R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//6.8e-05:411:59//AC005140

R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989

R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-fMet, tRNA-Gln, tRNA-Ile and tRNA-Val. 10 //1.1e-08:444:60//X05915

R-PLACE1009388

R-PLACE1009398//Homo sapiens BAC clone GS011E15 from 5q31, complete sequence.//0.065:279:61//AC002427

R-nnnnnnnnnnnn//Homo sapiens clone NH0486I22, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038

R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//9.8e-112:561:96 20 //AC005919

R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120

R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598

R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L361 30 51

R-PLACE1009459

R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531

R-PLACE1009477//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.4e-46:284:91//AC006213

R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321

R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160

R-PLACE1009539//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427

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R-PLACE1009542//CIT-HSP-2166P10. TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614

R-PLACE1009571//RPCI11-61J16. TK RPCI11 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ202146

R-PLACE1009581

R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006

R-PLACE1009596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051

R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230

R-PLACE1009613//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266

R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222

R-PLACE1009622//CIT-HSP-2023D13. TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey sequence.//0.72:176:62//B81271

R-PLACE1009637//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276

R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10W6 (ESSAI project).//0.013:521:58//AL021811

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159

R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534

R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011

R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109

40 R-PLACE1009731//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024

R-PLACE1009794

50 R-nnnnnnnnnnnn//Human DNA sequence from clone 1189

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B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-proteinKinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins *S. pombe* C22F3.14C and *C. elegans* C16A3.8. Contains ESTs, an STS and GSSs, complete sequence. //7.5e-88:191:96//AL030996

R-PLACE1009845//Homo sapiens DNA sequence from PAC 10 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence. //8.7e-19:226:69//Z98172

R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence. //2.1e-29:230:76//AC002672

R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence. //0.99:203:61//AC004945

R-PLACE1009888//Homo sapiens chromosome 19, BAC CI 20 T-B-393i15 (BC301323), complete sequence. //5.3e-91:577:88//AC006116

R-nnnnnnnnnnnnn

R-PLACE1009921//Homo sapiens cosmid clone HDAB (1S149) insert DNA, complete cosmid. //4.7e-81:385:84//M63005

R-PLACE1009924//HS_3151_B1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3151 Col=19 Row=D, genomic survey sequence. //5.5e-47:240:99//AQ167412

R-PLACE1009925//CIT978SK-A-931F6.TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence. //0.00010:159:68//B51673

R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.081:238:65//AC005308

R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence. //1.0:353:58//AC002483

R-PLACE1009971//Homo sapiens full length insert cDNA clone ZD38E12. //3.7e-11:152:75//AF086247

R-PLACE1009992

R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence. //0.0019:305:61//AE001367

R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence. //1.8e-43:462:76//AC005874

R-PLACE1010023//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic cl 50

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one Plate=3018 Col=19 Row=P, genomic survey sequence. //0.00013:198:63//AQ093513

R-PLACE1010031//Human DNA sequence from clone 30W3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to *C. elegans* Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence. //7.4e-115:581:96//AL031775

R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein. //1.9e-05:136:74//X84692

R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic clone 2328B12, genomic survey sequence. //2.6e-60:324:94//AQ042094

R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //4.6e-87:543:88//AF065482

R-PLACE1010076//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0473M13; HTCS phase 1, WORKING DRAFT SEQUENCE, 4 unordered pieces. //6.3e-08:489:58//AC005699

R-PLACE1010083

R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone F19F22, genomic survey sequence. //0.14:400:59//B10583

R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein. //4.3e-91:562:87//X64411

R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II intergenic spacer region, mitochondrial sequence. //1.5e-08:357:60//AF039556

R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence. //4.0e-09:510:59//AE001374

R-PLACE1010106//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE. //1.4e-12:194:73//Z98304

R-PLACE1010134

R-PLACE1010148//HS_3128_A1_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, genomic survey sequence. //0.17:281:61//AQ140790

R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete cds. //3.1e-45:351:81//D38417

R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUENCE, 1 unordered pieces. //3.6e-06:207:66//AC004928

R-PLACE1010194//HS_2232_B1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2232 Col=19 Row=P, genomic survey sequence. //2.4e-08:134:74//AQ185425

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R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CYK18, K18, CK18) p pseudogene and an STS, complete sequence.//0.00035:383:61//AL031585

R-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL033377

R-PLACE1010261

R-PLACE1010270//H.sapiens CpG island DNA genomic M sel fragment, clone 85a6, reverse read cp85a6.rtl a.//0.068:171:63//Z63482

R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63//X59280

R-PLACE1010293//Homo sapiens chromosome 2 PAC RPCI 3-417E16 (Roswell ParkCancer Institute Human PAC library) complete sequence.//4.7e-91:522:90//AC004464

R-PLACE1010321

R-PLACE1010324//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57//AL021149

R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10 In IGLC Region, complete sequence.//7.9e-35:328:79//AC000024

R-PLACE1010341//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21unordered pieces.//1.3e-31:418:66//AC004971

R-PLACE1010362

R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:64//M77098

R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, complete sequence.//1.4e-105:543:95//AC004675

R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence.//0.00017:268:62//AC004137

R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial cds.//8.6e-79:556:83//AF003927

R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//7.3e-88:438:96//AF039081

R-PLACE1010492//HS_3169_B2_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, genomic survey sequence.//0.98:171:63//AQ169892

R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:407:62//AC006082

R-nnnnnnnnnnnnn

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R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic clone2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929

R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosomal protein var1.//1.7e-05:271:65//X02893

R-PLACE1010580

R-PLACE1010599

R-PLACE1010616//Human BAC clone RG343P13 from 7q31, complete sequence.//3.0e-13:151:75//AC002465

R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//AF096370

R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete sequence.//8.2e-34:322:79//AF053356

R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21unordered pieces.//2.3e-97:515:94//AC004846

R-PLACE1010629//HS_3003_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, genomic survey sequence.//5.6e-60:321:95//AQ130493

R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.//0.051:372:59//AE001382

R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds.//2.6e-92:497:93//AB011102

R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic clone 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089

R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequence.//9.4e-09:151:73//Z81467

R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clone 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536

R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//5.3e-08:478:58//U49822

R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//3.8e-55:300:95//AF092564

R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//Z95400

R-PLACE1010743

R-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//3.0e-103:511:97//AC005921

50 R-PLACE1010771

- R-PLACE1010786
 R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30unordered pieces.//1.8e-43:545:71//AC005682
 R-PLACE1010802//Phoebeis agarithe large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitorchondrial RNAs.//1.9e-09:492:59//AF044862
 R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence.//0.041:415:59//AC002524
 R-PLACE1010833
 R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomicsequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:512:55//AC004153
 R-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene ofhepatocellular colorectal and non-small cell lung cancer , segment 11/11.//4.9e-85:507:90//AB020868
 R-PLACE1010870//RPC111-59K21.TK RPC111 Homo sapiens genomic clone R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697
 R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//7.0e-100:501:96//AB011182
 R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489
 R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomicsequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00032:409:59//AC005505
 R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//3.2e-07:180:71//AB018488
 R-PLACE1010916//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL034557
 R-PLACE1010917
 R-PLACE1010925//HS_2027_B2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, genomic surveysequence.//1.6e-46:404:77//AQ247031
 R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds.//4.2e-65:402:89//AB011126
 R-nnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds.//1.9e-80:441:93//AF064243
 R-PLACE1010944
 R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533
 R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-51:518:74//AC005077
 R-PLACE1010960//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522
 R-PLACE1010965//Human mariner1 transposase gene, complete consensus sequence.//1.0e-64:444:84//U52077
 R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome;segment 3/4.//0.59:345:61//AJ235272
 R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242
 R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153
 R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483
 R-PLACE1011056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985
 R-PLACE1011057//CIT-HSP-2014F10.TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896
 R-PLACE1011090//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//0.12:489:59//AC005509
 R-PLACE1011109//Homo sapiens chromosome Y, clone 486, 0, 2, complete sequence.//8.4e-43:427:76//AC002531
 R-PLACE1011114//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone hl1-14).//1.7e-29:179:94//Y16709
 R-PLACE1011133//HS-1058-B1-H02-MF.abi CIT Human Genomic Sperm Library CHomo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//B44006
 R-PLACE1011143//H.sapiens CpG island DNA genomic Msel fragment, clone 127a4, forward read cpg127a4.f1a.//1.0:127:67//Z56550
 R-PLACE1011160//Homo sapiens HRIHFB2038 mRNA, partial cds.//2.4e-95:534:91//AB015333
 R-PLACE1011165//Human Cosmid g5129s232 from 7q31.3, complete sequence.//0.47:355:58//AC003968
 R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5unordered pieces.//1.3e-26:403:70//AC004820

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R-PLACE1011203//paramecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908

R-PLACE1011219//HS_3036_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic surveysequence.//2.6e-39:253:88//AQ104587

R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.3 2:279:60//AE000659

R-PLACE1011229//HS_3002_B1_E10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic surveysequence.//9.3e-31:317:74//AQ303626

R-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//1.2e-109:571:94//AC005014

R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//0.00027:337:61//M97514

R-PLACE1011291

R-PLACE1011296//H.sapiens steroid reductase pseudo gene.//4.2e-37:326:80//M68887

R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661

R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.0e-10:511:59//AE001398

R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344

R-PLACE1011340//Human BAC clone RC341D10 from 7p15-p21, complete sequence.//0.67:290:58//AC002530

R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310

R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140

R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102

R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013

R-PLACE1011465

R-PLACE1011472//Homo sapiens mRNA for KIAA0712 pro

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tein, complete cds.//7.9e-103:515:96//AB018255

R-PLACE1011492//A-837A4.TP CIT978SK Homo sapiens genomic clone A-837A4, genomic survey sequence.//6.5e-37:234:82//B14085

R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171_I_10, complete sequence.//0.99:267:60//AC004687

R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968

10 R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688

R-PLACE1011567//Plasmodium falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551

R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973

R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477

R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463

R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205

R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620

R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:414:91//AF070535

30 R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477

R-PLACE1011664//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905

R-PLACE1011675//CIT-HSP-2370W16.TR CIT-HSP Homo sapiens genomic clone 2370W16, genomic survey sequence.//1.3e-27:233:81//AQ108283

R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776

40 R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC11-36 OE11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806

R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526

R-PLACE1011729//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345

R-PLACE1011749//Homo sapiens clone RC315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:31

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4:81//AC005089

R-PLACE1011762//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//1.9e-35:538:68//AC002383

R-PLACE1011778//CIT-HSP-2326C17.TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782

R-PLACE1011783//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090

R-PLACE1011858//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321

R-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312, complete sequence.//2.1e-100:511:95//AC004478

R-PLACE1011875

R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193

R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398

R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090

R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617

R-PLACE1011962//CIT-HSP-2294L24.TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352

R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994

R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889

R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738

R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256

R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000

R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722

R-PLACE2000011//Homo sapiens clone 614 unknown mRNA 50

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A, complete sequence.//1.5e-103:524:95//AF091080

R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191

R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//3.0e-55:299:86//AC006236

R-PLACE2000021//CIT-HSP-2343C18.TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey sequence.//4.5e-54:295:94//AQ058140

10 R-PLACE2000033//H. sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907

R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4unordered pieces.//5.3e-34:200:79//AC005628

R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//AC003083

R-PLACE2000047//CIT-HSP-2373C2.TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389:79//AQ112243

R-PLACE2000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//0.0027:95:76//AL022315

R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147

R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10unordered pieces.//5.9e-40:310:84//AC004832

30 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219

R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC11-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910

R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285:84//AL031730

40 R-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559:97//AL031848

R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricular light chain, exon 1.//0.00041:347:61//X16325

R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067

R-PLACE2000132

50 R-PLACE2000136//Plasmodium falciparum DNA *** SEQU

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ENCING IN PROGRESS ***from contig 3-30, complete sequence. //0.0032:310:61//AL008974

R-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE. //1.1e-111:566:96//AL020995

R-PLACE2000164

R-PLACE2000170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08; HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces. //3.9e-40:390:76//AC005598

R-PLACE2000172

R-PLACE2000176

R-PLACE2000187//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE. //8.7e-45:298:87//AL008718

R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end. //5.6e-88:495:92//L02897

R-PLACE2000223

R-PLACE2000235//HS_3159_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3159 Col=11 Row=D, genomic survey sequence. //1.8e-88:454:96//AQ179271

R-PLACE2000246//Homo sapiens chromosome 3p clone R PCI4-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces. //9.1e-41:282:86//AC005902

R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and CTC repeat polymorphisms, complete sequence. //8.3e-35:305:80//Z97181

R-PLACE2000274//Human Chromosome 16 BAC clone CIT9 87SK-A-211C6, complete sequence. //3.5e-18:325:67//AC002394

R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence. //1.5e-39:287:85//AC003043

R-PLACE2000305//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 169I5, WORKING DRAFT SEQUENCE. //1.2e-43:295:85//Z93015

R-PLACE2000317//Human DNA sequence from clone 245G 19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence. //4.0e-05:284:65//Z92542

R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.5e-26:334:70//AC006147

R-PLACE2000342//Fugu rubripes cosmid 258N02 contains

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ning IGFII, TH, NAP2 genes. //4.0e-05:254:64//AL021880

R-PLACE2000347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE. //1.6e-82:504:88//AL022147

R-PLACE2000359//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 40E16, WORKING DRAFT SEQUENCE. //2.0e-36:314:80//AL031963

10 R-PLACE2000366//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE. //2.0e-48:389:80//AL031291

R-PLACE2000371

R-PLACE2000373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 324M8, WORKING DRAFT SEQUENCE. //0.61:231:61//AL008734

R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence. //3.5e-11:287:67//AC004917

20 R-PLACE2000394//Human DNA sequence from clone 465N 24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands, complete sequence. //6.8e-108:553:96//AL031432

R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces. //2.9e-26:326:73//AC005059

R-PLACE2000399

R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence. //6.5e-84:434:96//AC005216

30 R-PLACE2000411//P.clarkii mRNA; repeat region (ID 2R). //0.47:104:70//Z54273

R-PLACE2000419

R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions. //1.9e-40:447:74//AF003528

R-PLACE2000427

R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence. //3.5e-40:286:85//AC000379

R-PLACE2000435

40 R-PLACE2000438//Homo sapiens full length insert cDNA clone ZE04D01. //2.2e-107:523:98//AF086521

R-PLACE2000450

4.1e-42:328:79//AG006257

R-PLACE2000455

R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //5.1e-116:570:97//AC005740

R-PLACE2000465//Human BAC clone RC191D16, complete sequence. //6.3e-37:408:75//AC002460

50 R-PLACE2000477//M.musculus tex264 mRNA (3' region).

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//7.5e-06:117:76//X80427
 R-PLACE3000004
 R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976
 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267
 R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence.//2.3e-10:181:71//AC004648
 R-PLACE3000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156
 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026
 R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//9.2e-23:171:76//AC005200
 R-PLACE3000136//U. arctos microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645
 R-PLACE3000142//HS_3037_B2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023
 R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735
 R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237
 R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//6.9e-106:549:94//AC005277
 R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383
 R-PLACE3000157
 R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500
 R-PLACE3000160
 R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229:85//AC006130
 R-PLACE3000194
 R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//7.2e-61:394:89//AC005291
 R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for or neural cell adhesion molecule L1 (L1CAM), argin

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ine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//0.23:309:57//U52112
 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//1.1e-15:156:81//B54637
 10 R-PLACE3000208//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594
 R-PLACE3000218//HS_3185_B1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720
 R-PLACE3000220//Homo sapiens chromosome 17, clone HRPC1096F1, complete sequence.//2.4e-44:363:80//AC004167
 20 R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786
 R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-69:536:81//U95626
 R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//I35489
 R-PLACE3000244//M. musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169
 30 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:94//AB002307
 R-PLACE3000271//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379
 R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//AC004081
 R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//AC005328
 40 R-PLACE3000310//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884
 R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-44:289:90//U93037
 R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006
 R-PLACE3000331//Homo sapiens clone DJ0592C07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-43:23

- O: 84//AC005480
R-PLACE3000339
R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC I4-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:97//AC006055
R-PLACE3000350//Human DNA sequence from clone 243E 7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.5e-44:314:78//AL022323
R-PLACE3000352//HS_3095_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142
R-PLACE3000353//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z99712
R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197
R-PLACE3000363
R-PLACE3000365//Human BAC clone RG343P13 from 7q31, complete sequence.//4.6e-52:487:76//AC002465
R-PLACE3000373//HS_3202_B1_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699
R-PLACE3000388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722
R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6unordered pieces.//0.00098:444:60//AC005231
R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506
R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25unordered pieces.//8.0e-47:223:81//AC006023
R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003
R-PLACE3000405//Homo sapiens chromosome 7qtelo BAC F6, complete sequence.//2.4e-44:466:74//AF104455
R-PLACE3000406//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718
R-PLACE3000413
R-PLACE3000416//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612
R-PLACE3000425//Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal prot
- ein L29 pseudogene, ESTs and STSs.//1.1e-41:366:78//AL008627
R-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899
R-PLACE3000477
R-PLACE4000009//R. norvegicus mRNA encoding 45kDa protein which binds to heymann nephritis antigen gp330.//6.6e-17:344:68//Z11995
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352
R-PLACE4000034//cSRL-51C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-51C5, genomic survey sequence.//0.54:116:66//B04984
R-PLACE4000049//Human BAC clone GS165I04 from 7q21, complete sequence.//0.29:313:59//AC002379
R-PLACE4000052//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557
R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356
R-PLACE4000089//RPCI11-1511.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1511, genomic survey sequence.//3.2e-07:284:60//B82414
R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506
R-PLACE4000100
R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010
R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969
R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034
R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:

- 90//AL021939
R-PLACE4000192
R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631
R-PLACE4000233//Homo sapiens full length insert cDNA YH59G06.//1.8e-79:414:97//AF074981
R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//5.7e-59:558:76//AC005821
R-PLACE4000250//CIT-HSP-2335L20. TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381
R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.5e-39:311:83//AC005920
R-PLACE4000261//H.sapiens BF1P-g1H03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410
R-PLACE4000269//Homo sapiens chromosome 4 clone B3 68A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510
R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675
R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339
R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//8.2e-41:295:85//Z99495
R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640
R-PLACE4000326
R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//0.32:135:68//AC005587
R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829
R-PLACE4000369//HS_3181_A1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222
R-PLACE4000379//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312
R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913
R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e
-88:541:88//AL034377
R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143:83//AC000406
R-PLACE4000411
R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.028:91:78//AC005628
R-PLACE4000465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156
R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:357:61//AE001427
R-PLACE4000494//Homo sapiens 12p13.3 PAC RPCI5-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005865
R-PLACE4000522
R-PLACE4000548//Homo sapiens 12p13.3 PAC RPCI5-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342
R-PLACE4000558//Homo sapiens 12q24 BAC RPCI11-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//2.9e-44:465:75//AC002996
R-THYR01000026//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844
R-THYR01000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422
R-THYR01000035//HS_3018_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318
R-THYR01000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157
R-THYR01000070//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//1.1e-44:284:89//U14573
R-THYR01000072//***ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:83//U14567
R-THYR01000085
R-THYR01000092//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//3.3e-36:301:78//AF104455
R-THYR01000107//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528
R-THYR01000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300

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R-THYR01000121//Human chromosome 16 BAC clone CIT9 87SK-A-962B4, complete sequence. //6.6e-77:507:85//U 91318

R-THYR01000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces. //0.66:334:59//AC005840

R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds. //2.3e-88:449:96//AF087142

R-THYR01000132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SE 10
QUENCE. //1.1e-40:298:84//Z95114

R-THYR01000156//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence. //3.4e-37:425:73//AC005703

R-THYR01000163//RPCI11-1B20.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-1B20, genomic survey sequence. //8.4e-38:276:84//B63536

R-THYR01000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island. //1.1e-7
0:553:81//Z83841

R-THYR01000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 410I8, WORKING DRAFT SE
QUENCE. //6.7e-41:345:81//AL031732

R-THYR01000187//Human thymopoietin (TMP0) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta. //1.3e-43:356:80
//U18271

R-THYR01000190//Homo sapiens chromosome 17, clone HRPC843B9, complete sequence. //2.6e-40:386:77//AC0
04139

R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease. //1.1e-108:535:97//AJ005698

R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds. //1.4e-113:559:97//AB014552

R-THYR01000206//Rat PMSG-induced ovarian mRNA, 3's sequence, N4. //4.0e-43:318:86//D84482

R-THYR01000221//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence. //2.7e-44:452:76//AC002115

R-THYR01000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence. //4.8e-58:447:81//AC000039

R-THYR01000242

R-THYR01000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete 50

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sequence. //3.4e-56:300:84//Z95152

R-THYR01000270

R-THYR01000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SE
QUENCE. //4.8e-113:584:96//AL031664

R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds. //1.1e-98:566:91//AB016068

R-THYR01000320//HS_2033_B1_A07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=B, genomic survey sequence. //0.97:211:63//AQ233366

R-THYR01000327//Sequence 1 from patent US 5541298. //2.8e-52:289:93//I24058

R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds. //1.1e-111:559:96//AB018333

R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds. //4.6e-47:317:87//U29091

R-THYR01000368//HS_3049_A1_E12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=I, genomic survey sequence. //7.0e-11:111:83//AQ126777

R-nnnnnnnnnnnnn

R-THYR01000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence. //2.4e-101:545:93//AC006019

R-THYR01000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces. //1.6e-4
6:233:88//AC006078

30 R-THYR01000395//Mouse MIPP mRNA for a placenta-expressed gene. //2.3e-57:395:85//X58523

R-THYR01000401

3.3e-111:546:97//AF051907

R-THYR01000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces. //2.7e-44:28
9:89//AC005231

R-THYR01000452//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence. //6.7e-27:222:82//AC005668

40 R-THYR01000471//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SE
QUENCE. //2.4e-36:369:76//AL021391

R-THYR01000484//Homo sapiens clone DJ1099N07, complete sequence. //1.6e-43:288:81//AC004962

R-THYR01000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //1.6e-95:
512:94//AC005740

R-THYR01000501//HS_2208_A1_G11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence

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e.//0.0063:189:63//AQ091586
 R-THYR01000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987
 R-THYR01000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798
 R-THYR01000558
 R-THYR01000569
 R-THYR01000570//Homo sapiens full length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408
 R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587
 R-THYR01000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPolB) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.36:170:67//AF006072
 R-THYR01000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675
 R-THYR01000605
 R-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//AC005546
 R-THYR01000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-06:249:63//AL022323
 R-THYR01000641//P.falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998
 R-THYR01000658//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572
 R-nnnnnnnnnnnn
 R-THYR01000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005
 R-THYR01000676//Homo sapiens chromosome 4 clone B7M12 map 4q25, complete sequence.//1.2e-06:227:64//AC004069
 R-THYR01000684
 R-THYR01000699
 R-THYR01000712
 R-THYR01000734//Human BAC clone RC191D16, complete sequence.//3.7e-14:468:64//AC002460
 R-THYR01000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533
 R-THYR01000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//I25660
 R-THYR01000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558
 R-THYR01000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequenc

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e.//1.2e-81:391:99//AQ038226
 R-THYR01000787//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//9.4e-07:494:58//AC004617
 R-THYR01000793
 R-THYR01000796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014
 R-THYR01000805//Human Chromosome 11 pac pDJ610i20, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555
 R-THYR01000815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199
 R-THYR01000829//Sequence 7 from patent US 5716622.//0.97:362:61//I87788
 R-THYR01000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-57:522:76//AC004738
 R-THYR01000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849
 R-THYR01000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592
 R-THYR01000865//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549
 R-THYR01000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719
 R-THYR01000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015
 R-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//9.6e-109:566:94//AF079529
 R-THYR01000934//Homo sapiens full length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378
 R-THYR01000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229
 R-THYR01000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//M28639
 R-THYR01000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440
 R-THYR01000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006

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R-THYR01000983//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//0.99:71:78//AC005562
R-THYR01000984//Homo sapiens Chromosome 11q12.2 PA C clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-4 2:320:84//AC006078
R-THYR01000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466
R-THYR01001003//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727
R-THYR01001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466
R-THYR01001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677
R-THYR01001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882
R-THYR01001093
R-THYR01001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070
R-THYR01001120
R-THYR01001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417
R-THYR01001133//CIT-HSP-2381I10.TR CIT-HSP Homo sapiens genomic clone 2381I10, genomic survey sequence.//4.7e-12:237:67//AQ111077
R-THYR01001134
R-THYR01001142//H.sapiens CpG island DNA genomic Msel fragment, clone 81d1, reverse read cpg81d1.rtl a.//0.95:214:60//Z56037
R-THYR01001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:2 62:77//B04145
R-THYR01001177
R-THYR01001189//Homo sapiens DNA from chromosome 1 9, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973
R-THYR01001204
R-THYR01001213//Human Alu repeat sequence A6.//3.8 e-38:236:88//U12581
R-THYR01001262//Homo sapiens, clone hRPK.16_A_1, complete sequence.//8.7e-53:442:79//AC006227
R-THYR01001271//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0224P12; HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630
R-THYR01001290
R-THYR01001313//H.sapiens CpG island DNA genomic Msel fragment, clone 195h3, forward read cpg195h3.f t1b.//0.046:126:66//Z57783
R-THYR01001320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207
R-THYR01001321//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558
R-nnnnnnnnnnnnn
R-THYR01001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288
R-THYR01001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:47 1:92//B05884
R-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8 e-109:584:94//AC005660
R-THYR01001374
R-THYR01001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953
R-THYR01001403//Human PAC clone DJ222H05 from Xq25 -q26, complete sequence.//8.7e-38:307:82//AC002377
R-THYR01001405
R-THYR01001406//RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297
R-THYR01001411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 80N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123
R-THYR01001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA(PAC 1118i22) from chromosome 11; HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-8 9:506:86//AJ002553
R-THYR01001434//Microcentus caryae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877
R-THYR01001458//Human DNA sequence from clone 453C 12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578
R-THYR01001480//Homo sapiens clone DJ0756H11, WORK

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ING DRAFT SEQUENCE, 5unordered pieces.//1.2e-99:517:95//AC006001

R-THYR01001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085

R-THYR01001534//HS_2242_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326

R-THYR01001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876

R-THYR01001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077

R-THYR01001559//Homo sapiens 12q24.2 PAC RPCI5-944 M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868

R-THYR01001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomicsequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308

R-THYR01001573//M.avium rpsL gene.//0.98:131:66//X80120

R-THYR01001584//A.longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653

R-THYR01001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808

R-THYR01001602//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//4.4e-13:320:67//AC005919

R-THYR01001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249

R-THYR01001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190

R-THYR01001637//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

R-THYR01001656//HS_2201_B2_A08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic surveysequence.//0.096:162:63//AQ293168

R-THYR01001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59kDa isoform.//4.8e-110:562:95//AJ225089

R-THYR01001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequen

3734

ce.//1.5e-17:224:68//AQ042426

R-THYR01001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYR01001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYR01001721//, complete sequence.//1.3e-101:571:92//AC005500

R-nnnnnnnnnnnnn

R-THYR01001745//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

R-THYR01001746//Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 3.//0.54:260:61//M88244

R-THYR01001772//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYR01001793

R-THYR01001809//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYR01001854//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYR01001895//Human Chromosome 11p14.3 PAC clone 6-106f23, complete sequence.//4.4e-12:419:61//AC005137

R-THYR01001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b In DGCRRegion, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Luman mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114I09 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D21079

R-Y79AA1000131//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0548N01; HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene

3735

similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence. //1.1e-106:474:98//AL031864
 R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence. //1.0e-10:78:97//B68074
 R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces. //6.5e-59:386:90//AC004854
 R-Y79AA1000230//Cytauxzoon felis 18S ribosomal RNA. //1.0:167:62//L19080
 R-Y79AA1000231//HS_3009_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=0, genomic survey sequence. //6.4e-52:348:88//AQ090225
 R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds. //0.65:127:65//D10558
 R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 22. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence. //4.7e-40:300:84//Z98047
 R-Y79AA1000313//Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island. //5.0e-14:136:83//Z92540
 R-Y79AA1000328
 R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence). //0.55:189:65//X54107
 R-Y79AA1000346//Human MEST mRNA, complete cds. //0.00013:52:100//D78611
 R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein. //8.8e-36:300:81//X84692
 R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VT4 protein pseudogene, EST, GSS, complete sequence. //5.7e-45:403:80//AL022163
 R-Y79AA1000368
 R-Y79AA1000405//RPCI11-16B12.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-16B12, genomic survey sequence. //0.10:171:65//B88000
 R-Y79AA1000410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE. //4.1e-50:361:83//Z93097
 R-Y79AA1000420//Plasmodium falciparum merozoite surface

3736

protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds. //0.071:474:57//AF033037
 R-Y79AA1000469//Homo sapiens clone NH0140K04, complete sequence. //1.8e-86:221:90//AC005033
 R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence. //2.1e-14:179:72//AC004057
 R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces. //4.5e-43:321:83//AC005282
 R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence. //0.0012:275:59//AC006143
 R-Y79AA1000540//Z. diploperennis repetitive DNA (clone ZEAR 260). //0.0017:258:62//X53609
 R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C). //6.1e-32:390:70//X14972
 R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence. //0.96:224:61//AC002325
 R-Y79AA1000627//Homo sapiens full length insert cDNA ZA77G02. //6.3e-100:533:94//AF075117
 R-Y79AA1000705//RPCI11-76G7.TV RPCI11 Homo sapiens genomic clone R-76G7, genomic survey sequence. //4.6e-88:429:98//AQ268433
 R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds. //2.7e-112:586:95//AF093670
 R-Y79AA1000748

3737

R-Y79AA1000752
 R-Y79AA1000774//CIT-HSP-2
 288K24. TF CIT-HSP Homo sa
 piens genomic clone 2288K
 24. genomic survey sequen
 ce. //5.3e-45:316:86//AQ00
 5014
 R-Y79AA1000782//Human mRN
 A for KIAA0246 gene, part
 ial cds. //5.0e-17:107:100 10
 //D87433
 R-Y79AA1000784//Plasmodiu
 m falciparum 3D7 chromoso
 me 12 PFYAC181 genomicseq
 uence, WORKING DRAFT SEQU
 ENCE, 8 unordered pieces.
 //0.00034:520:55//AC00550
 5
 R-Y79AA1000794//Human DNA
 sequence *** SEQUENCING 20
 IN PROGRESS *** from clon
 e 989H11, WORKING DRAFT S
 EQUENCE. //0.015:322:60//Z
 83851
 R-Y79AA1000800//M. musculu
 s tex264 mRNA (3' region).
 //1.1e-06:104:78//X80427
 R-nnnnnnnnnnnnnnn//CIT-HSP-2
 295G6. TF CIT-HSP Homo sap
 iens genomic clone 2295G 30
 6, genomic survey sequenc
 e. //0.67:152:62//AQ007605
 R-Y79AA1000805//Human Chr
 omosome 11 Cosmid cSRL30h
 11, complete sequence. //
 3.1e-26:423:68//U73642
 R-Y79AA1000824//Human DNA
 sequence *** SEQUENCING
 IN PROGRESS *** from clon
 e 329A5, WORKING DRAFT SE 40
 QUENCE. //1.1e-08:449:61//
 Z97832
 R-Y79AA1000827//Triticum
 aestivum heat shock prote
 in 101 kDa (HSP101) mRNA,
 complete cds. //1.0:101:6
 9//AF083344
 R-Y79AA1000850//Homo sapi
 ens small optic lobes hom
 olog (SOLH) mRNA, complet 50

3738

e cds. //0.40:386:59//U856
 47
 R-Y79AA1000962//CIT-HSP-2
 298N11. TR CIT-HSP Homo sa
 piens genomic clone 2298N
 11, genomic survey sequen
 ce. //0.00019:253:65//AQ01
 3111
 R-Y79AA1000968//Rattus no
 rvegicus initiation facto
 r eIF-2B gamma subunit (eI
 F-2B gamma) mRNA, complet
 e cds. //1.7e-58:446:80//U
 38253
 R-Y79AA1000969.
 R-Y79AA1000976//CIT-HSP-2
 350C4. TF CIT-HSP Homo sap
 iens genomic clone 2350C
 4, genomic survey sequenc
 e. //3.3e-60:295:100//AQ06
 1422
 R-Y79AA1000985//Mus muscu
 lus pericentrin mRNA, com
 plete cds. //5.9e-38:348:7
 6//U05823
 R-Y79AA1001023
 R-Y79AA1001041
 R-Y79AA1001048
 R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clo
 ne CIT987SK-A-427H10, complete sequence. //1.2e-60:5
 37:78//AC004626
 R-Y79AA1001068//Homo sapiens P1 clone GSP13996 fro
 m 5q12, complete sequence. //2.3e-41:405:77//AC0050
 31
 R-Y79AA1001077
 R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPCI1-228
 P16 (Roswell Park Cancer Institute Human PAC Libra
 ry) complete sequence. //2.0e-09:534:59//AC004801
 R-Y79AA1001105//Staphylococcus epidermidis trimetho
 prim resistance plasmid pSK639. //0.0072:309:63//U4
 0259
 R-Y79AA1001145//RPCI11-59N12. TK RPCI11 Homo sapien
 s genomic clone R-59N12, genomic survey sequence. /
 /3.7e-07:256:64//AQ200068
 R-Y79AA1001167//Homo sapiens genomic DNA, chromoso
 me 21q22.2 (Down Syndrome region), segment 5/15, W
 ORKING DRAFT SEQUENCE. //0.55:223:61//AP000012
 R-Y79AA1001177//Human gene for Gi3 alpha protein,
 intron 7 through exon9, variant U6 gene, and snRNP
 E protein pseudogene LH87. //7.0e-09:203:69//X5404

- 8
R-Y79AA1001185
R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPCI11-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-32:277:81//AC005912
R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924
R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112
R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5unordered pieces.//0.19:106:72//AC004988
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//3.4e-109:549:95//AJ005892
R-Y79AA1001281
R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//Y17126
R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372
R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355
R-Y79AA1001384//W.makrii mitochondrial CYTB and tRNA genes.//0.070:209:65//X66594
R-Y79AA1001391//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS ***from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745
R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.99:241:63//AC004221
R-Y79AA1001402//Homo sapiens Chr.14 PAC RPCI4-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80//AC005924
R-Y79AA1001493
R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12Contains ESTs and GSSs, complete sequence.//1.3e-35:207:95//AL034430
R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336
R-nnnnnnnnnnnn//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and anSTS, complete sequence.//0.70:365:60//AL023574
R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L361
- 51
R-Y79AA1001555
R-Y79AA1001585
R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X; contains STS.//6.6e-19:241:76//Z94722
R-Y79AA1001603//H.sapiens CpG island DNA genomic Msel fragment, clone 72f8, forward read cpg72f8.ft1a.//3.3e-21:131:96//Z62766
10 R-Y79AA1001613
R-Y79AA1001647//Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975
R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008
R-Y79AA1001679//O. cuniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743
R-nnnnnnnnnnnn//RPCI11-42M5.TJ RPCI11 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792
20 R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178
R-Y79AA1001705
R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139
R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402
30 R-nnnnnnnnnnnn//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044
R-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//2.3e-90:557:89//U74297
R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z95152
R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I14369
R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence.//0.0089:527:58//AB016874
R-Y79AA1001874
R-Y79AA1001875//M. musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650
50

3741

R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and CDSs, complete sequence. //1.0:138:68//AL022577

R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA. //0.71:153:67//X04465

R-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 172B20, WORKING DRAFT SEQUENCE. //1.0:178:64//AL022319

R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces. //6.3e-49:377:81//AC005011

R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA. //4.0e-32:174:99//L77612

R-Y79AA1002103//CIT-HSP-2328I21. TR CIT-HSP Homo sapiens genomic clone 2328I21, genomic survey sequence. //1.9e-44:245:96//AQ044502

R-Y79AA1002115//CITBI-E1-2514F10. TF CITBI-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence. //1.8e-24:249:78//AQ265752

R-Y79AA1002125//RPCI11-15J6. TV RPCI-11 Homo sapiens genomic clone RPCI-11-15J6, genomic survey sequence. //8.5e-21:147:91//B75354

R-Y79AA1002139

R-Y79AA1002204

R-nnnnnnnnnnnn//Human ankyrin C (ANK-3) mRNA, complete cds. //0.040:319:59//U13616

R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4). //0.99:106:65//X65415

R-Y79AA1002210

R-Y79AA1002211//H.sapiens NGAL gene. //1.0:311:59//X99133

R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE. //5.9e-07:535:57//AL034557

R-Y79AA1002229

R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds. //6.1e-117:564:98//AB014592

R-Y79AA1002246

R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds. //1.3e-92:453:97//AB013384

R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey sequence. //1.9e-56:384:87//AQ171331

R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds. //2.5e-108:403:99//AB014534

3742

R-Y79AA1002311//Homo sapiens chromosome 10 clone C1T987SK-1173112 map 10q25, complete sequence. //1.1e-07:368:61//AC005887

R-Y79AA1002351

R-Y79AA1002361//H.sapiens CpG island DNA genomic Msel fragment, clone 65b9, reverse read cpg65b9.rtl a. //0.57:59:79//Z62206

R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence. //2.0e-98:385:99//AC005920

R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence. //5.4e-59:490:76//AC004662

R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence. //6.3e-08:103:80//AC004087

R-Y79AA1002431

R-nnnnnnnnnnnn//Mouse transcriptional control element. //0.064:84:71//M17284

20 R-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence. //1.6e-103:525:96//AC006116

R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence. //9.7e-38:302:83//AC006238

R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B). //0.23:266:61//X95276

【1125】 相同性検索結果データ4.

5'末端クローン配列に対するHuman Unigene相同性検索結果データ

30 各データは、クローン配列名、トップヒットデータのTitle、P値:比較配列の長さ (base):相同性(%), トップヒットデータのAccession No.の順に//で区切って記載した。なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069

F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds. //0.82:170:64//Hs.2864:L40157

F-HEMBA1000020//Homo sapiens beta 2 gene. //4.0e-74:529:83//Hs.150244:U83668

F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078

F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247

F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae] //0.00019:192:65//Hs.7900:W22411

50 F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI33675

- 9
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417
910
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66
734
F-HEMBA1000129//Human phosphatidylinositol 3-kinase
catalytic subunit p110delta mRNA, complete cds//
0.27:342:61//Hs.14207:U86453
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 pro
tein, partial cds//6.8e-169:791:98//Hs.27197:AB018 10
340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 pro
tein, partial cds//1.4e-37:243:88//Hs.2397:Z70200
F-HEMBA1000156//ESTs, Weakly similar to The KIAA01
38 gene product is novel. [H.sapiens]//5.3e-80:38
3:98//Hs.135552:AI215187
F-HEMBA1000158//Homo sapiens OPA-containing protei
n mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF0
71309
F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23 20
079
F-HEMBA1000180//ESTs, Moderately similar to RETROV
IRUS-RELATED POL POLYPROTEIN [H.sapiens]//1.3e-18:
111:96//Hs.163863:W28729
F-HEMBA1000185//H.sapiens ERF-2 mRNA//1.0:125:68//
Hs.78909:U07802
F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:AI2
40133
F-HEMBA1000201//Human Inl1 mRNA, complete cds//6.5
e-75:440:92//Hs.155626:U04847
F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA5275
29
F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequ
ence//1.1e-57:529:68//Hs.8136:U81984
F-HEMBA1000227//Human RNA-binding protein CUG-BP/h
Nab50 (NAB50) mRNA, complete cds//1.3e-05:311:64//
Hs.81248:U63289
F-HEMBA1000231
F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23
377
F-HEMBA1000244//H.sapiens mRNA for cytokine induci
ble nuclear protein//0.0022:350:60//Hs.74019:X8370
3
F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47
460
F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA58856
2
F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA0
35568
F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA 50
813186
F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64
406
F-HEMBA1000290//Human novel homeobox mRNA for a DN
A binding protein//3.8e-07:412:61//Hs.37035:U07664
F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:AI2
06095
F-HEMBA1000303
F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA7
28946
F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:AI1
24898
F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA
305965
F-HEMBA1000333//Human mRNA for KIAA0206 gene, part
ial cds//0.84:395:56//
Hs.79299:D86961
F-HEMBA1000338//ESTs, Moderately similar to novel
stromal cell protein [M.musculus]//2.4e-38:317:80/
/Hs.99189:X84712
F-HEMBA1000351//Human Line-1 repeat mRNA with 2 op
en reading frames//0.020:334:59//Hs.23094:W19503
F-HEMBA1000355//Myosin, heavy polypeptide 11, smoo
th muscle//0.11:336:61//Hs.78344:AF001548
F-HEMBA1000356//H.sapiens ERF-2 mRNA//0.031:317:59
//Hs.78909:U07802
F-HEMBA1000357//Human mRNA for KIAA0118 gene, part
ial cds//1.2e-50:441:78//Hs.154326:D42087
F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H7401
30 0
F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 f
rom 7q33-q35//0.99:433:58//Hs.159899:AC004853
F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70/
/Hs.2820:X64878
F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA
741320
F-HEMBA1000390//Homo sapiens BAC clone RG119C02 fr
om 7p15//2.3e-141:712:95//Hs.22900:AC004520
F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequ
ence//1.7e-47:461:74//Hs.139088:AF070533
40 F-HEMBA1000396//ESTs, Weakly similar to hypothetic
al protein [H.sapiens]//1.2e-26:351:70//Hs.138992:
C14008
F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52
915
F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:AI07
9253
F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:AI0
32875
F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 sp

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ecific transcript KIAA0501//7.6e-31:616:66//Hs.159
897:AB007970
F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA55
9034
F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA57739
8
F-HEMBA1000456//Fanconi anemia complementation gro
up C//0.58:362:59//Hs.37953:X66893
F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:AI0
32875
F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49
590
F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA
127853
F-HEMBA1000469
F-HEMBA1000488//Homo sapiens HIV-1 inducer of shor
t transcripts bindingprotein (FBI1) mRNA, complete
cds//0.15:253:58//Hs.104640:AF000561
F-HEMBA1000490//Homo sapiens kinectin mRNA, comple
te cds//0.71:539:56//Hs.82709:Z22551
F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA
864970
F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRN
A, complete cds//2.5e-39:312:77//Hs.5247:AF029750
F-HEMBA1000504//Homo sapiens mRNA for osteoblast s
pecific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155
095:D13666
F-HEMBA1000505//Homo sapiens KE04p mRNA, complete
cds//1.0:197:62//Hs.131962:AF064093
F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA6596
46
F-HEMBA1000518
F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:AI2
81881
F-HEMBA1000520//ESTs, Weakly similar to coded for
by C. elegans cDNA CEESB82F [C.elegans]//2.9e-16:1
32:84//Hs.155871:AA533783
F-HEMBA1000523//ESTs, Highly similar to TESTIS-SP
ECIFIC PROTEIN PBS13 [Mus musculus]//2.1e-25:192:8
7//Hs.22383:R51067
F-HEMBA1000531//ESTs, Weakly similar to heat shock
protein [H.sapiens]//2.4e-57:288:97//Hs.116022:AA
455706
F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, co
mplete cds//2.8e-47:153:88//Hs.113283:AF018080
F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA
180809
F-HEMBA1000542//Human lysyl oxidase-like protein m
RNA, complete cds//0.088:581:57//Hs.65436:U24389
F-HEMBA1000545//Human kpni repeat mrna (cdna clone

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pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K
00629
F-HEMBA1000555//Human mRNA for KIAA0242 gene, part
ial cds//0.75:283:58//Hs.77495:D87684
F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA
495729
F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 pro
tein, partial cds//3.8e-64:665:72//Hs.137168:AB018
303
10 F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:AI3
38977
F-HEMBA1000568//EST//0.12:270:61//Hs.134833:AI0910
46
F-HEMBA1000569//H.sapiens mRNA encoding GPI-anchor
ed protein p137//3.8e-19:409:62//Hs.119283:Z48042
F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826
681
F-HEMBA1000588//ESTs, Weakly similar to weakly sim
ilar to myosin heavy chain [C.elegans]//7.7e-41:21
7:96//Hs.55084:AA479162
20 F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-as
sociated protein//2.3e-44:228:97//Hs.155218:AJ0075
09
F-HEMBA1000592//ESTs, Weakly similar to sorting ne
xin 1 [H.sapiens]//1.7e-27:463:65//Hs.13794:AA2032
41
F-HEMBA1000594//Human clone 230971 defective marin
er transposon Hsmar2 mRNA sequence//4.0e-68:574:79
//Hs.159176:U92019
30 F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:AI
092535
F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 pro
tein, partial cds//3.7e-120:561:99//Hs.5003:AB0079
25
F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complet
e cds//5.2e-34:592:68//Hs.153563:AF011333
F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSO
MAL PROTEIN L20 [E.coli]//7.4e-22:166:84//Hs.2625
2:AA643235
40 F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 pro
tein, partial cds//2.1e-138:639:99//Hs.60103:AB014
590
F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA
176174
F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:6
1//Hs.89603:J05582
F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:AI1
23912
F-HEMBA1000673//H.sapiens mRNA for translin associ
ated protein X//1.7e-47:366:79//Hs.96247:X95073
50

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F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878
 F-HEMBA1000686
 F-HEMBA1000702
 F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309
 F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:AI039850
 F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630
 F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:AI21081881
 F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491
 F-HEMBA1000747
 F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:AI091568
 F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:H52716
 F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239
 F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803
 F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216
 F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300
 F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536
 F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542
 F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367
 F-HEMBA1000843
 F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.89764:X69962
 F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572
 F-HEMBA1000867
 F-HEMBA1000869//ESTs//5.1e-33:166:77//Hs.141186:R99609
 F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237
 F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047
 F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660
 F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154
 F-HEMBA1000910//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha

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-Trypsin Inhibitor Heavy Chain LIKE gene; alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//2.8e-11:309:65//Hs.4943:Z98046
 F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537
 F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:221:64//Hs.109804:D64142
 F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete cds//3.8e-09:360:62//Hs.36850:AB011119
 F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repair protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596
 F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [Homo sapiens]//0.0039:54:92//Hs.58338:AA609476
 20 F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase//0.93:132:66//Hs.82285:X54199
 F-HEMBA1000960//ESTs, Moderately similar to !!!! A LU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369
 F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87//Hs.84775:M23161
 F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI30127903
 F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775
 F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314
 F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DCKi) mRNA, complete cds//1.3e-05:424:59//Hs.159564:AF061936
 F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.0036:389:60//Hs.12734038:AB007961
 F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132
 F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:193:84//Hs.24756:U43895
 F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835
 F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.9e-43:472:74//Hs.46468:U45984
 F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//H

s.75758:X58529

F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//1.4e-140:661:98//Hs.158287:ABO07937

F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572

F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.78160:AF010238

F-HEMBA1001022

F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.8e-28:376:72//Hs.159897:AB007970

F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:745:57//Hs.94592:AB005142

F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515

F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881

F-HEMBA1001052//EST//0.94:149:67//Hs.131216:AI017971

F-HEMBA1001059//N-ACETYL GALACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-165:777:98//Hs.159479:U06088

F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813

F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.119571:X14420

F-HEMBA1001077//ESTs, Moderately similar to transcription intermediary factor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297

F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//0.013:385:58//Hs.69949:M94172

F-HEMBA1001085//Human hSIAH2 mRNA, complete cds//0.55:338:59//Hs.20191:U76248

F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:303:78//Hs.83987:U09284

F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017

F-HEMBA1001099

F-HEMBA1001109//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.4e-61:341:85//Hs.5247:AF029750

F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA12497

F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete cds//0.066:649:56//Hs.5347:AB007940

F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.5e-10:231:68//Hs.27349:AB007917

F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747

F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.2e-73:527:77//Hs.159277:AB018341

F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete cds//0.020:141:65//Hs.7482:AB014582

F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457

F-HEMBA1001174//ESTs//1.4e-63:363:92//Hs.132798:AA922226

F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//5.0e-54:555:71//Hs.55165:AA573499

F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463

F-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:569:57//Hs.48824:D87717

F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694

F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748

F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058

F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62//Hs.7647:M94046

F-HEMBA1001265

F-HEMBA1001281

F-HEMBA1001286//Natriuretic peptide precursor B//0.76:163:63//Hs.937:AL021155

F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-30:530:64//Hs.154050:AC004131

F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//Hs.119534:AJ224741

F-HEMBA1001299//Small inducible cytokine A5 (RANTE S)//2.2e-27:271:77//Hs.155464:AF088219

F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//3.3e-53:272:97//Hs.154563:AI129590

F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related protein [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201

F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873

F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cds//0.23:562:58//Hs.22039:AB018301

F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homolog//2.5e-31:165:99//Hs.152213:L20861

F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROTEIN INFAB1-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-08:185:68//Hs.108

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- 734: AI073427
 F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013
 F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569
 F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358
 F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794
 F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074
 F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156
 F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353
 F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.0e-132:643:97//Hs.124217:AA020848
 F-HEMBA1001388
 F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660
 F-HEMBA1001398
 F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117
 F-HEMBA1001407//ESTs//0.53:390:57//Hs.150447:AI017798
 F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108
 F-HEMBA1001413
 F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605
 F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040
 F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726
 F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053
 F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031
 F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]//6.8e-47:550:71//Hs.55165:AA573499
 F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds//0.82:312:58//Hs.7019:AB005666
 F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107
 F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:A
- A442412
 F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-51:323:88//Hs.40100:AB002390
 F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds//6.2e-104:489:99//Hs.14409:AB011144
 F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451
 F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219
 F-HEMBA1001510//H. sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054
 F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-105:773:82//Hs.23094:M19503
 F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902
 F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:AI376869
 F-HEMBA1001526
 F-HEMBA1001533//EST//1.0:75:73//Hs.145360:AI252476
 F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580
 F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205
 F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//7.0e-175:678:99//Hs.159597:AJ012449
 F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184
 F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:AI357228
 F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918
 F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210
 F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:AI016400
 F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:AI361870
 F-HEMBA1001636//ESTs, Moderately similar to !!!! A LU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:AI338536

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F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899
 F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204
 F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560
 F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283
 F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121
 F-HEMBA1001661
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943
 F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953
 F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788
 F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060
 F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760
 F-HEMBA1001709//EST//0.85:131:65//Hs.131451:AI023995
 F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:AI302836
 F-HEMBA1001712//EST//0.26:214:59//Hs.159088:AI383114
 F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452
 F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554
 F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197
 F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:AI028363
 F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:AI000415
 F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:AI052250
 F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924
 F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328
 F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]//0.76:218:60//Hs.135553:N41598
 F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622
 F-HEMBA1001784//Homo sapiens mRNA for KIAA0474 pro

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tein, complete cds//6.4e-09:265:67//Hs.158232:AB007943
 F-HEMBA1001791
 F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570
 F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817
 F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.5e-175:809:98//Hs.118164:AB007969
 F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305
 F-HEMBA1001815
 F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.158174:U66561
 F-HEMBA1001820//EST//0.057:214:62//Hs.148715:AI223845
 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.66392:AF064244
 F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:AF071309
 F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078
 F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293
 F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds//2.8e-185:865:98//Hs.78946:AB014517
 F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121
 F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D. melanogaster]//3.2e-39:293:84//Hs.152332:AI141922
 F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D. melanogaster]//8.1e-70:367:95//Hs.15423:T84036
 F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.158095:AB007953
 F-HEMBA1001896
 F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346
 F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:AI312633

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F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302
 F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511
 F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145
 F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:AI377295
 F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221
 F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:AI219882
 F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943
 F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360
 F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242
 F-HEMBA1001962//ESTs//0.0012:289:59//Hs.125492:AA938930
 F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708
 F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs//4.6e-156:720:99//Hs.11050:AL031178
 F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732
 F-HEMBA1001987//ESTs, Moderately similar to hTAFII68 [H. sapiens]//2.8e-29:151:100//Hs.124106:AA948100
 F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581
 F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487
 F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582
 F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426
 F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907
 F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:AI049827
 F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057 50

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F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU S UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776
 F-HEMBA1002084
 F-HEMBA1002092
 F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832
 F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:AI190276
 F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:AI129973
 F-HEMBA1002119
 F-HEMBA1002125//H. sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802
 F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393
 F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980
 F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263
 F-HEMBA1002151
 F-HEMBA1002153//EST//0.014:328:60//Hs.149115:AI244695
 F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976
 F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965
 F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590
 F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219
 F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245
 F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141
 F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363
 F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589
 F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970
 F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696
 F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767
 F-HEMBA1002215//ESTs, Highly similar to TESTIN 2

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PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.5990
 6:AA001281
 F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0488//2.4e-57:375:71//Hs.676
 19:AB007957
 F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partia
 l cds//7.9e-47:377:80//Hs.43681:AL022394
 F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812
 455
 F-HEMBA1002241
 F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA8
 88887
 F-HEMBA1002257//Homo sapiens diacylglycerol kinase
 iota (DGKi) mRNA, complete cds//1.1e-152:731:97//
 Hs.159564:AF061936
 F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI
 125420
 F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophos
 phorylase (GFPP) mRNA, complete cds//1.0:395:60//H
 s.150926:AF017445
 F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H9
 5404
 F-HEMBA1002321//Homo sapiens oxidized low-density
 lipoprotein receptor mRNA, complete cds//0.17:338:
 60//Hs.77729:AB010710
 F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:A
 1201982
 F-HEMBA1002337//Human mRNA for KIAA0118 gene, part
 ial cds//0.93:220:61//Hs.154326:D42087
 F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 pro
 tein, partial cds//7.8e-187:872:98//Hs.6162:AB0183
 14
 F-HEMBA1002348//EST//1.0e-19:285:70//Hs.121860:AA7
 76692
 F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200
 996
 F-HEMBA1002363//Homo sapiens chromosome-associated
 protein-E (hCAP-E) mRNA, complete cds//2.4e-189:8
 72:99//Hs.119023:AF092563
 F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA5
 35216
 F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA
 535144
 F-HEMBA1002417//Homo sapiens chromosome 19, cosmid
 R28784//2.2e-159:775:97//Hs.25527:AC005954
 F-HEMBA1002419//EST, Moderately similar to ROD CGM
 P-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUB
 UNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141
 F-HEMBA1002430//Human clone 23695 mRNA sequence//
 2.7e-06:563:59//Hs.90798:U79289

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F-HEMBA1002439//EST, Weakly similar to LINE-1 REVE
 RSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67
 //Hs.162154:AA528561
 F-HEMBA1002458//ESTs, Weakly similar to hypothetic
 al protein B, 6.8K [H.sapiens]//1.3e-71:346:98//H
 s.136121:W26490
 F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R5
 3160
 F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate
 10 receptor 2D subunit precursor (NMDAR2D) mRNA, comp
 lete cds//0.00024:240:64//Hs.113286:U77783
 F-HEMBA1002469//Human mRNA for KIAA0122 gene, part
 ial cds//1.3e-109:603:92//Hs.154583:D50912
 F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCL
 E//0.025:261:63//Hs.89631:U48508
 F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 pro
 tein, partial cds//2.8e-45:331:83//Hs.6189:AB01113
 3
 F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA30
 3235
 F-HEMBA1002495
 F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W7
 9161
 F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 pr
 otein//4.8e-13:164:74//Hs.19949:X98173
 F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, co
 mplete cds//6.1e-79:460:83//Hs.113283:AF018080
 F-HEMBA1002513//Homo sapiens mRNA for histone deac
 etylase-like protein (JM21)//9.0e-159:738:98//Hs.6
 30 764:AJ011972
 F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA
 420795
 F-HEMBA1002538//ESTs//0.97:68:73//Hs.134672:AI0879
 51F-HEMBA1002542//Homo sapiens mRNA for chemokine
 LEC precursor, complete
 cds//6.1e-46:238:87//Hs.10458:AF088219
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA,
 partial cds//1.1e-138:655:98//Hs.68900:AF016903
 F-HEMBA1002552//Human Hep27 protein mRNA, complete
 cds//2.8e-08:173:68//Hs.102137:U31875
 F-HEMBA1002555//Homo sapiens mRNA for APC 2 protei
 n, complete cds//0.00020:603:57//Hs.20912:AB012162
 F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA
 431205
 F-HEMBA1002561//Human clone 23574 mRNA sequence//
 4.7e-17:268:72//Hs.79385:U90905
 F-HEMBA1002569//Homo sapiens protein associated wi
 th Myc mRNA, completecds//4.3e-142:457:99//Hs.1514
 11:AF075587
 50 F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquit

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ous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132
 F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
 F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169
 F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351
 F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334
 F-HEMBA1002629//Human density enhanced phosphatase-1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886
 F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
 F-HEMBA1002651
 F-HEMBA1002659//Human vascular endothelial growth factor related proteinVRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142
 F-HEMBA1002661//Human Line-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503
 F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
 F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368
 F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457
 F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1)mRNA, partial cds//1.8e-11:541:60//Hs.124161:AF065164
 F-HEMBA1002696//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221
 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924
 F-HEMBA1002712
 F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
 F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521
 F-HEMBA1002730//Homo sapiens microsomal glutathion

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e S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867
 F-HEMBA1002742//EST//0.97:138:60//Hs.160545:AI271596
 F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372
 F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786
 F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126
 F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947
 F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
 F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
 F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N90326
 F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
 F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
 F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185
 F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
 F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119
 F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:AI279904
 F-HEMBA1002833
 F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550
 F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823
 F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
 F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AI279429
 F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679
 F-HEMBA1002921
 F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001

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F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:N77915
 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148
 F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene PC326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053
 F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703
 F-HEMBA1002944//Human putative endothelin receptor type B-like protein mRNA, complete cds//0.83:326:58//Hs.27747:U87460
 F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.126762:AA913925
 F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099
 F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092
 F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828
 F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA54219
 F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)//1.5e-37:247:89//Hs.188:L20971
 F-HEMBA1002997//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564
 F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525
 F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:81//Hs.155464:AF088219
 F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486
 F-HEMBA1003034//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.4e-70:330:78//Hs.113283:AF018080
 F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//Hs.159425:AJ001454
 F-HEMBA1003037//EST//0.53:59:74//Hs.148011:AI26800
 F-HEMBA1003041//ESTs, Weakly similar to F58C11.6 [C.elegans]//1.7e-64:337:95//Hs.105907:AA186514
 F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182
 F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438
 F-HEMBA1003067

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F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1 (IH1)mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164
 F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:542:62//Hs.48998:AB007865
 F-HEMBA1003078//CYTOCHROME P450 1VF3//2.0e-29:452:67//Hs.106242:AB002454
 F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461
 F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881
 F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721
 F-HEMBA1003096//ESTs, Weakly similar to HMG-box transcription factor [M.musculus]//0.98:216:61//Hs.97865:AA405872
 F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721
 F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U07802
 F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:507:58//Hs.12432:AF070575
 F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.038:288:63//Hs.6162:AB018314
 F-HEMBA1003136
 F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279
 F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:850:99//Hs.63931:AJ005670
 F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete cds//1.1e-24:171:83//Hs.141874:AB014588
 F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740
 F-HEMBA1003179//EST, Weakly similar to hypothetical protein in purB 5' region [E.coli]//4.7e-20:118:97//Hs.118831:AA211895
 F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523
 F-HEMBA1003199//SOX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135
 F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412
 F-HEMBA1003204//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.6e-33:154:85//Hs.113283:AF018080
 F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765
 F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784
 F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA1813

3763

10
F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA4170
12
F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA
A, complete cds//0.00054:432:58//Hs.132206:AF03969
4
F-HEMBA1003250
F-HEMBA1003257//Homo sapiens fibroblast growth fac
tor 18 (FGF18) mRNA, complete cds//4.3e-08:426:64/
/Hs.49585:AF075292
F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA8
67991
F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA6
05020
F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864
F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA
781867
F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-
1,4-galactosyltransferase mRNA, complete cds//2.9e
-146:539:97//Hs.13225:AF038662
F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 pro
tein, complete cds//1.6e-167:799:98//Hs.12836:AB01
1109
F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R4491
2
F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770
160
F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:A
A521012
F-HEMBA1003314//Homo sapiens mRNA for leucine zipp
er bearing kinase, complete cds//1.5e-189:865:99//
Hs.124224:AB001872
F-HEMBA1003322//H.sapiens mRNA for sigma 3B protei
n//4.5e-49:399:80//Hs.154782:X99459
F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA0
56254
F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA9
13328
F-HEMBA1003330
F-HEMBA1003348//Human mRNA for KIAA0331 gene, comp
lete cds//4.8e-26:256:78//Hs.146395:AB002329
F-HEMBA1003369//Homo sapiens DNA from chromosome 1
9p13.2 cosmids R31240, R30272 and R28549 containing
the EKLf, CCDH, CRTc, and RAD23A genes, genomic s
equence//0.37:187:65//Hs.80265:AD000092
F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA
226159
F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI2638
19
F-HEMBA1003376//Clathrin, light polypeptide (Lcb)/ 50

3764

/2.3e-29:606:64//Hs.73919:X81637
F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:H58
017
F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N9555
2
F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202
488
F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633
813
10 F-HEMBA1003403//Adducin 2 (beta) {alternative prod
ucts}//5.0e-05:445:61//Hs.90951:U43959
F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70266:Z783
09
F-HEMBA1003417//Glutamate-cysteine ligase (gamma-g
lutamylcysteine synthetase), regulatory (30.8kD)//
9.5e-05:541:58//Hs.89709:L35546
F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:A
A564962
F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, co
mplete cds//2.0e-149:686:99//Hs.25812:AF058696
20 F-HEMBA1003447//Human mRNA for KIAA0380 gene, comp
lete cds//0.43:271:60//Hs.47822:AB002378
F-HEMBA1003461//Glycoprotein Ib (platelet), beta p
olypeptide//4.8e-08:775:58//Hs.3847:U59632
F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA
058578
F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 pro
tein, partial cds//0.16:321:60//Hs.13999:AB014600
F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA
30 057443
F-HEMBA1003531//Human mRNA for KIAA0033 gene, part
ial cds//4.9e-51:451:78//Hs.22271:D26067
F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI
392811
F-HEMBA1003545//ISL1 transcription factor, LIM/hom
eodomain, (islet-1)//5.0e-75:736:73//Hs.505:U07559
F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R2
3311
F-HEMBA1003555//Human nucleotide-binding protein m
RNA, complete cds//3.6e-33:562:64//Hs.81469:U01833
F-HEMBA1003556
F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA7
67122
F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI
342327
F-HEMBA1003569//Human metastasis-associated mtal m
RNA, complete cds//2.0e-58:455:66//Hs.101448:U3511
3
F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA6
48972

3765

F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
 F-HEMBA1003581//ESTs, Highly similar to TALIN [Mus musculus]//3.6e-19:108:99//Hs.18420:AA599232
 F-HEMBA1003591//ESTs, Weakly similar to R74.5 [C.elegans]//5.2e-85:487:92//Hs.57937:W68285
 F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405
 F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T4082 10
 7
 F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916
 F-HEMBA1003615//ESTs, Highly similar to phosphorylation regulatory protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782
 F-HEMBA1003617//Homo sapiens mRNA for HRIHFB2157, partial cds//7.9e-171:501:97//Hs.124956:AB015344
 F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT protein PIASx-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:AF077954
 F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750
 F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159
 F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans sudD gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF013591
 F-HEMBA1003640//ESTs//1.1e-11:267:66//Hs.34359:AI122791
 F-HEMBA1003645
 F-HEMBA1003646
 F-HEMBA1003656
 F-HEMBA1003662
 F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381
 F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906
 F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:464:61//Hs.79706:U53204
 F-HEMBA1003684//ESTs, Weakly similar to zinc finger protein C2H2-171 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072
 F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cds//9.5e-74:606:77//Hs.9028:AF039691
 F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cds//0.81:254:62//Hs.32316:AB011116 50

3766

F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995
 F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:692:68//Hs.91916:AF035317
 F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921
 F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839
 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frames//8.6e-102:753:81//Hs.23094:M19503
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:242:62//Hs.153325:AC005390
 F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:AI198946
 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:430:69//Hs.8136:U81984
 F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920
 F-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//1.7e-24:224:81//Hs.18171:AA524327
 F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L39064
 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel (KCNN3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815
 F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.119537:M88108
 F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:AI379721
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds//3.3e-85:586:87//Hs.6051:AB014516
 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:AI204220
 F-HEMBA1003838//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314
 F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:AI005167
 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:144:66//Hs.21355:AB002367
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete cds//4.3e-30:580:63//Hs.27621:U5284

- 0
F-HEMBA1003879//Nuclear cap binding protein, 80kD/
/6.7e-10:87:95//Hs.89563:D32002
F-HEMBA1003880
F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 pro
tein, partial cds//4.2e-18:302:67//Hs.23711:AB0182
95
F-HEMBA1003893//ESTs, Weakly similar to HYPOTHETIC
AL 27.8 KD PROTEIN INVMA7-RPS31A INTERGENIC REGION
[S.cerevisiae]//1.2e-49:295:92//Hs.114673:W72675 10
F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA9
76236
F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 pro
tein, partial cds//0.081:345:58//Hs.78494:AB011097
F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:AI0
32875
F-HEMBA1003937//Human mRNA for KIAA0391 gene, comp
lete cds//2.9e-38:313:69//Hs.154668:AB002389
F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R5
9562
F-HEMBA1003942//EST, Weakly similar to 24 KD PROTE
IN [Xenopus laevis]//0.0029:222:61//Hs.144236:W523
80
F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W2005
5
F-HEMBA1003953//Zinc finger protein 7 (K0X 4, clon
e HF.16)//0.00014:271:66//Hs.2076:M29580
F-HEMBA1003958//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//2.1e
-44:243:76//Hs.91146:N73230
F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H7856
7
F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:AI1
38965
F-HEMBA1003978
F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009
F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA4
24456
F-HEMBA1003989//Homo sapiens HIV-1 inducer of shor
t transcripts bindingprotein (FBI1) mRNA, complete 40
cds//0.022:349:58//Hs.104640:AF000561
F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA3
58468
F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676
493
F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA
812573
F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:AI
379721
F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 pro 50
tein, complete cds//5.2e-51:359:84//Hs.15519:AB018
315
F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:AI2
39930
F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:AI3
12281
F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA5
84160
F-HEMBA1004048//Transforming growth factor beta//
0.026:462:57//Hs.6101:M60315
F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA
584638
F-HEMBA1004055//Human chromosome 3p21.1 gene seque
nce//1.5e-10:457:58//Hs.82837:L13435
F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fu
cosyltransferase, complete cds//1.5e-46:199:80//H
s.46328:D87942
F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA7
57426
20 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA7701
07
F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:
302:57//Hs.75666:M28713
F-HEMBA1004111//Human G protein-coupled receptor
(STRL22) mRNA, completecds//4.3e-39:335:79//Hs.464
68:U45984
F-HEMBA1004131//Human mRNA for KIAA0202 gene, part
ial cds//1.9e-24:610:61//Hs.80712:D86957
F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA7
80064 30
F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:AI4197
59
F-HEMBA1004138//H.sapiens mRNA for RanGTPase activ
ating protein 1//0.00055:343:62//Hs.5923:X82260
F-HEMBA1004143
F-HEMBA1004146
F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:AI18
6056
F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 pro
tein, complete cds//1.8e-15:591:60//Hs.159277:AB01
8341
F-HEMBA1004168//Homo sapiens geminin mRNA, complet
e cds//1.5e-134:649:97//Hs.59988:AF067855
F-HEMBA1004199
F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:AI3
75427
F-HEMBA1004202//ESTs, Weakly similar to GTP-BINDIN
G PROTEIN YPTM1 [Zea mays]//1.2e-35:205:94//Hs.100
92:AI189282
F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA

- 626040
F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//
Hs.54515:U50748
F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA1
92514
F-HEMBA1004227//ESTs, Weakly similar to F55A11.4
[C.elegans]//0.012:156:67//Hs.163588:AI073878
F-HEMBA1004238
F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA6
79571
F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA7
58522
F-HEMBA1004248//Homo sapiens insulin induced prote
in 1 (INSIG1) gene, complete cds//1.1e-28:295:72//
Hs.56205:U96876
F-HEMBA1004264//Human HCF1 gene related mRNA seque
nce//3.1e-07:553:60//Hs.83634:U52112
F-HEMBA1004267//Homo sapiens mRNA for KIAA0688 pro
tein, complete cds//4.9e-73:490:77//Hs.141874:AB01
4588
F-HEMBA1004272
F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA8764
44
F-HEMBA1004275//Human mRNA for KIAA0333 gene, part
ial cds//0.71:118:65//Hs.155313:AB002331
F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 pro
tein, complete cds//1.0:364:56//Hs.118738:AB018343
F-HEMBA1004286//Homo sapiens TGF beta receptor ass
ociated protein-1 mRNA, complete cds//6.9e-187:86
8:99//Hs.101766:AF022795
F-HEMBA1004289
F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA5734
84
F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:AI27
0047
F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:AI336
314
F-HEMBA1004321//Zinc finger protein 136 (clone pHZ
-20)//2.3e-40:452:65//Hs.69740:U09367
F-HEMBA1004323//EST//0.44:134:64//Hs.145464:AI2045
32
F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22)
mRNA, complete cds//0.017:209:64//Hs.43627:U35612
F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA
614062
F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA1
66888
F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 pro
tein, complete cds//0.49:80:73//Hs.139648:AB014606
F-HEMBA1004341
- F-HEMBA1004353//Homo sapiens mRNA for c-myc bindin
g protein, complete cds//2.7e-39:270:86//Hs.80686:
D89667
F-HEMBA1004354//Human CHL1 potential helicase (CHL
R1), complete cds//1.3e-46:190:92//Hs.27424:U75968
F-HEMBA1004356//Thyrotropin-releasing hormone rece
ptor//0.15:296:62//Hs.3022:D85376
F-HEMBA1004366//ESTs, Weakly similar to transposon
LRE2 reverse transcriptase homolog [H.sapiens]//
7.8e-10:396:61//Hs.33688:AA020928
F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R6880
0
F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//
8.0e-28:359:67//Hs.112180:AF039019
F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N5125
0
F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA5
84818
F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42
199
F-HEMBA1004408//ESTs, Weakly similar to The ha1539
protein is related to cyclophilin. [H.sapiens]//1.
4e-20:144:88//Hs.121076:AI246426
F-HEMBA1004429//Fucosyltransferase 1 (galactoside
2-alpha-L-fucosyltransferase, Bombay phenotype inc
luded)//4.8e-18:248:72//Hs.69747:M35531
F-HEMBA1004433//Small inducible cytokine A5 (RANTE
S)//8.2e-39:248:81//Hs.155464:AF088219
F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, co
mplete cds//5.6e-87:650:81//Hs.113283:AF018080
F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z4160
6
F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequ
ence//4.9e-17:223:71//Hs.8136:U81984
F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N3945
0
F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA
992600
F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H9
3431
F-HEMBA1004506//Human Line-1 repeat mRNA with 2 op
en reading frames//9.0e-89:758:76//Hs.23094:M19503
F-HEMBA1004507//ESTs, Weakly similar to T19B10.6
[C.elegans]//1.4e-61:296:99//Hs.114622:AA693492
F-HEMBA1004509//Homo sapiens suppressor of white a
pricot homolog 2 (SWAP2) mRNA, complete cds//0.01
4:265:61//Hs.43543:AF042800
F-HEMBA1004534//Filamin 1 (actin-binding protein-2
80)//5.0e-74:678:74//Hs.76279:X53416
F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA8

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05381
 F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552
 F-HEMBA1004554
 F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331
 F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802
 F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA4798 10
 25
 F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF010238
 F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661
 F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft)mRNA, complete cds//0.42:186:66//Hs.84136:U70370
 F-HEMBA1004610//ESTs, Moderately similar to !!!! A LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606
 F-HEMBA1004617//EST//0.027:188:61//Hs.159094:AI383198
 F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178
 F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416
 F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:AI360891
 F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:AI3 30
 46780
 F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:AI017522
 F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083
 F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796
 F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582
 F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141
 F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:AI093252
 F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homologue//0.64:313:61//Hs.118578:X80821
 F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892
 F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515
 F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019 50

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F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903
 F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909
 F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515
 F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004
 F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frames//2.0e-61:663:71//Hs.23094:M19503
 F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813
 F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504
 F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626
 F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.153563:AF011333
 F-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082
 F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060
 F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120
 F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frames//4.5e-115:909:78//Hs.23094:M19503
 F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:57//Hs.41587:U63139
 F-HEMBA1004771
 F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235
 F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:AI222106
 F-HEMBA1004795
 F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952
 F-HEMBA1004806//EST//0.080:142:65//Hs.160268:AI148971
 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042
 F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646
 F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:A

- I300481
 F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511
 F-HEMBA1004850//EST//0.033:253:64//Hs.158782:AI376601
 F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150
 F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987
 F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
 F-HEMBA1004880//H.sapiens mRNA for retrotransposon //1.2e-30:264:79//Hs.6940:Z48633
 F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698
 F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
 F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106
 F-HEMBA1004918//EST//0.78:122:61//Hs.145491:AI254348
 F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172
 F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947
 F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:AI224959
 F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331
 F-HEMBA1004934
 F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
 F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813
 F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:AI174478
 F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274
 F-HEMBA1004972
 F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914
 F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:AI361946
 F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013
 F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:AI244750
 F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA55358
- 9
 F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:AI394026
 F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429
 F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548
 F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560
 F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237
 F-HEMBA1005039//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627
 F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193
 F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802
 F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:AI264462
 F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2(XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587
 F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381
 F-HEMBA1005079//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785
 F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561
 F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:AI031916
 F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304
 F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106
 F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:AI032875
 F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA

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- 593021
F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA8
84216
F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA9
10914
F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282
197
F-HEMBA1005202
F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:43
1:58//Hs.144029:Y13436
F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W265
47
F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37
081
F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N4830
2
F-HEMBA1005241//Homo sapiens neuronal thread prote
in AD7c-NTP mRNA, complete cds//6.0e-54:399:79//H
s.129735:AF010144
F-HEMBA1005244//ESTs//2.5e-14:85:100//Hs.128744:AI
191922
F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393
896
F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 pro
tein, partial cds//4.7e-151:705:98//Hs.72660:AB011
157
F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI
261380
F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA
001777
F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequ
ence//7.7e-22:338:65//Hs.12451:U97018
F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149
232
F-HEMBA1005304//Small inducible cytokine A5 (RANTE
S)//1.7e-45:322:85//Hs.155464:AF088219
F-HEMBA1005311
F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI
279516
F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N2
1615
F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA
937117
F-HEMBA1005331//Human checkpoint suppressor 1 mRN
A, complete cds//0.00075:310:63//Hs.111597:U68723
F-HEMBA1005338//Homo sapiens mRNA for matrilin-4,
partial//4.4e-153:740:97//Hs.129361:AJ007581
F-HEMBA1005353//EST//5.4e-09:222:68//Hs.119508:AA4
85732
F-HEMBA1005359//Zinc finger protein 137 (clone pHZ 50
7
-30)//5.7e-100:500:88//Hs.151689:U09414
F-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1)
mRNA, complete cds//2.5e-70:572:73//Hs.43265:AF071
787
F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI
417905
F-HEMBA1005374//Human melanoma antigen recognized
by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.15406
9:U06452
10 F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI1
93053
F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA8
04448
F-HEMBA1005394//ESTs, Weakly similar to No definit
ion line found [C.elegans]//1.0e-130:620:98//Hs.10
8990:N25951
F-HEMBA1005403//ESTs, Weakly similar to No definit
ion line found [C.elegans]//7.7e-151:727:97//Hs.17
118:AI033807
20 F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H2
4513
F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70
347
F-HEMBA1005411
F-HEMBA1005423//Homo sapiens cyclin-dependent kina
se inhibitor (CDKN2C)mRNA, complete cds//3.3e-171:
537:99//Hs.4854:AF041248
F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323
F-HEMBA1005443//Zinc finger protein 157 (HZF22)//
30 9.0e-34:259:72//Hs.89897:U28687
F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI2
76783
F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA
533107
F-HEMBA1005469//Human (clone E5.1) RNA-binding pro
tein mRNA, complete cds//3.1e-29:155:99//Hs.75104:
L37368
F-HEMBA1005472//Human Line-1 repeat mRNA with 2 op
en reading frames//1.4e-88:481:92//Hs.23094:M19503
F-HEMBA1005474//Small inducible cytokine A5 (RANTE
S)//4.2e-29:257:78//Hs.155464:AF088219
F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRN
A, complete cds//5.3e-09:414:60//Hs.132206:AF03969
4
F-HEMBA1005497//Glucocorticoid receptor alpha (alt
ernative products)//8.7e-41:588:69//Hs.102761:U250
29
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 f
rom 7q11.23-q21//1.1e-28:318:73//Hs.159530:AC00495
7

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- F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635
- F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911
- F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353
- F-HEMBA1005513//ESTs, Weakly similar to males-abse nt on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220
- F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693
- F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575
- F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280
- F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:76//Hs.155464:AF088219
- F-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471
- F-HEMBA1005530
- F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376
- F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461
- F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903
- F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257
- F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507
- F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932
- F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873
- F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538
- F-HEMBA1005582
- F-HEMBA1005583
- F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381
- F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS//0.54:439:59//Hs.2137:D49357
- F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323
- F-HEMBA1005606//EST//2.0e-60:324:94//Hs.5062:D1960
- 9
- F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982
- F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280
- F-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845
- F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535
- F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734
- F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199
- F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956
- F-HEMBA1005666
- F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142
- F-HEMBA1005679//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629
- F-HEMBA1005680
- F-HEMBA1005685
- F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406
- F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678
- F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143
- F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)//2.6e-20:151:88//Hs.77393:D14697
- F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754
- F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
- F-HEMBA1005755//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627
- F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219
- F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
- F-HEMBA1005813//ESTs//0.012:209:63//Hs.113365:R77747
- F-HEMBA1005815//Human calpain-like protease (htra-

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- 3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346
 F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
 F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
 F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frames//7.9e-42:690:66//Hs.23094:M19503
 F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:470:56//Hs.79706:U53204
 F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
 F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953
 F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
 F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984
 F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766
 F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
 F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX42B (HPX42B) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
 F-HEMBA1005931//ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880
 F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588
 F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
 F-HEMBA1005963
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516
 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:AI127530
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526
 F-HEMBA1006002
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151
 F-HEMBA1006031
 F-HEMBA1006035
 F-HEMBA1006036//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.141186:R99609
 F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.143321:AI139422
 F-HEMBA1006081
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.161195:AI418788
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313
 F-HEMBA1006100//ESTs//7.1e-22:273:73//Hs.144407:AA737799
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA77968
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:AI027222
 F-HEMBA1006130//Human HOX4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372
 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:AI281881
 F-HEMBA1006155
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:N40575
 F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
 F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046
 F-HEMBA1006252
 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:AI140706
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631
 F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA88140
 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
 F-HEMBA1006283
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:AI189964

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F-HEMBA1006291
 F-HEMBA1006293
 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:AI032142
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244
 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:AI351026
 F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POBI) mRNA, complete cds//0.0028:422:59//Hs.80667:AF010233
 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922
 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:AI042531
 F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//2.1e-49:395:80//Hs.23094:M19503
 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:AI077477
 F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:AI281881
 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830
 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:AI206835
 F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264
 F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:AI209194
 F-HEMBA1006445
 F-HEMBA1006446//EST//0.14:200:59//Hs.160695:AI282889
 F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369
 F-HEMBA1006467

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F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:AI091453
 F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:AA875998
 F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081
 F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532
 10 F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897
 F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.128621:AA910431
 F-HEMBA1006492
 F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:AI248625
 F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389
 F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566
 F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein]reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185
 F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002
 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:AI30160081
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs.21301:AF093419
 F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638
 F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898
 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:AI198425
 40 F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136
 F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.144372:AI346522
 F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479
 F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778
 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219
 F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB0182

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F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862
F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:AI032875
F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN INSDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:AI391502
F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:AI1343331
F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589
F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185
F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003
F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, completecds//3.9e-28:108:93//Hs.6196:U40282
F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615
F-HEMBA1006653
F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//2.9e-92:438:98//Hs.8173:AC005189
F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317
F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56//1.6e-16:122:90//Hs.5092:Y12065
F-HEMBA1006676
F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575
F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145
F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:AI128198
F-HEMBA1006708
F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545
F-HEMBA1006717//ESTs//2.6e-31:286:78//Hs.55573:W37226
F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105
F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087
F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2(XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587
- F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325
F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720
F-HEMBA1006779//EST//9.1e-26:395:69//Hs.145366:AI252657
F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250
F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:AI369798
10 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-37:781:64//Hs.23094:M19503
F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U79298
F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723
F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:AI051551
F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624
20 F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970
F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327
F-HEMBA1006865
F-HEMBA1006877//ESTs, Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERC7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938
30 F-HEMBA1006885//ESTs, Highly similar to HYPOTHETICAL 29.1 KD PROTEIN INURA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214
F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592
F-HEMBA1006914//EST//0.065:366:62//Hs.162914:AA666199
F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989
40 F-HEMBA1006926//Human I kappa B mRNA, complete cds//0.90:545:59//Hs.154764:U16258
F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539
F-HEMBA1006936//ESTs//0.00014:60:93//Hs.8737:W22712
F-HEMBA1006938//ESTs//4.7e-51:256:98//Hs.143651:AI150382
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:AJ010841
- 50

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F-HEMBA1006949//H.sapiens mRNA for retrotransposon
//6.9e-43:385:76//Hs.6940:Z48633
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory d
omain mRNA, complete cds//1.8e-144:740:94//Hs.1493
4:AF004828
F-HEMBA1006976//H.sapiens mRNA for Gal-beta(1-3/1-
4)GlcNAc alpha-2,3-sialyltransferase//1.9e-79:447:
89//Hs.75268:X74570
F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA
600968
F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054
723
F-HEMBA1007002
F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282
F-HEMBA1007018//Homo sapiens dynein light intermed
iate chain 2 (LIC2) mRNA, complete cds//2.5e-78:82
7:70//Hs.43003:AF035812
F-HEMBA1007045
F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI37065
9
F-HEMBA1007052
F-HEMBA1007062
F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212
F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:H3
7845
F-HEMBA1007078//Human arginine-rich nuclear protei
n mRNA, complete cds//6.7e-75:417:91//Hs.80510:M74
002
F-HEMBA1007080
F-HEMBA1007085//Guanylate cyclase 2D, membrane (re
tina-specific)//1.3e-06:568:61//Hs.1974:M92432
F-HEMBA1007087//Human mevalonate pyrophosphate dec
arboxylase (MPD) mRNA, complete cds//0.95:541:57//H
s.3828:U49260
F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA
039595
F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA1963
54
F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA
643182
F-HEMBA1007129
F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W4
6172
F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA
757136
F-HEMBA1007151
F-HEMBA1007174//Homo sapiens epsin 2b mRNA, comple
te cds//6.6e-64:318:97//Hs.22396:AF062085
F-HEMBA1007178//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//4.2e

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-39:248:90//Hs.157148:AA311921
F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:A
A305965
F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 pro
tein, complete cds//5.6e-158:478:98//Hs.3363:D8698
7
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA6092
52
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 pro
tein, partial cds//1.6e-177:839:98//Hs.27197:AB018
340
F-HEMBA1007243//Hypoxanthine phosphoribosyltransfe
rase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.
82314:M31642
F-HEMBA1007251//Human plectin (PLEC1) mRNA, comple
te cds//0.19:210:67//Hs.79706:U53204
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequ
ence//1.0:144:64//Hs.12432:AF070575
F-HEMBA1007267//Human homolog of yeast mutL (hPMS
1) gene, complete cds//0.99:239:60//Hs.111749:U136
95
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N3
4836
F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:H0
6475
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA5845
29
F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA96863
7
F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI3
00062
F-HEMBA1007301//Collagen, type I, alpha 1//1.5e-0
9:406:61//Hs.111913:Z74615
F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890
506
F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:N63634
F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R8424
1
F-HEMBA1007327//ESTs, Weakly similar to HOST CELL
FACTOR C1 [H.sapiens]//3.5e-09:144:76//Hs.20597:W5
8370
F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA
494130
F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA
911006
F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA
916568
F-HEMBA1000008//H.sapiens mRNA for translin associ
ated protein X//1.1e-43:370:78//Hs.96247:X95073

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F-HEM BB1000018//Nuclear factor of kappa light poly peptide gene enhancerin B-cells 1 (p105)//1.0:108:70//Hs. 83428: M58603
 F-HEM BB1000024//EST//5.4e-07:137:70//Hs. 125389: AA878307
 F-HEM BB1000025//EST//0.99:362:58//Hs. 121221: AA757392
 F-HEM BB1000030//H. sapiens mRNA for cylicin II//1.3e-10:525:62//Hs. 3232: Z46788
 F-HEM BB1000036
 F-HEM BB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:98//Hs. 20815: AF084928
 F-HEM BB1000039//EST//0.0034:97:73//Hs. 141684: W35358
 F-HEM BB1000044//ESTs//0.0048:218:63//Hs. 123161: AA807319
 F-HEM BB1000048//EST//0.00025:222:62//Hs. 122474: AA765131
 F-HEM BB1000050//ESTs//5.6e-28:293:75//Hs. 136839: H93717
 F-HEM BB1000054//Human Line-1 repeat mRNA with 2 open reading frames//3.3e-54:259:88//Hs. 23094: M19503
 F-HEM BB1000055//ESTs//0.0017:289:62//Hs. 125755: AA286923
 F-HEM BB1000059//Homo sapiens mRNA for KIAA0761 protein, partial cds//5.9e-59:286:84//Hs. 93121: AB018304
 F-HEM BB1000083
 F-HEM BB1000089//EST//0.0016:192:66//Hs. 137093: AA917621
 F-HEM BB1000099//ESTs//5.7e-20:213:76//Hs. 57883: AA218645
 F-HEM BB1000103//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs. 103948: K00627
 F-HEM BB1000113//EST//4.6e-23:221:76//Hs. 142065: AA173763
 F-HEM BB1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs. 6315: Y15521
 F-HEM BB1000136//ESTs//2.3e-101:507:96//Hs. 12659: AA195207
 F-HEM BB1000141//ESTs//2.1e-15:283:69//Hs. 126257: AI279044
 F-HEM BB1000144//EST//4.5e-52:298:91//Hs. 149580: AI281881
 F-HEM BB1000173//Zinc finger protein 74 (Cos52)//2.4e-63:285:82//Hs. 3057: X92715
 F-HEM BB1000175//EST//1.0:101:65//Hs. 162898: AA659646

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F-HEM BB1000198//EST//0.99:179:56//Hs. 116880: AA662457
 F-HEM BB1000215//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.4e-15:139:82//Hs. 101414: AB011129
 F-HEM BB1000217//ESTs//3.4e-06:81:88//Hs. 121151: T66277
 F-HEM BB1000218//EST//0.11:136:63//Hs. 134683: AI092013
 F-HEM BB1000226//Fragile X mental retardation 1//0.99:126:65//Hs. 89764: X69962
 F-HEM BB1000240//H. sapiens mRNA for Nup88 protein//1.0:334:57//Hs. 90734: Y08612
 F-HEM BB1000244//ESTs//3.2e-15:139:81//Hs. 134549: AI078483
 F-HEM BB1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:98//Hs. 151411: AF075587
 F-HEM BB1000258//EST//0.0091:325:60//Hs. 97533: AA435884
 F-HEM BB1000264//Human CHL1 potential helicase (CHL R1), complete cds//1.4e-33:100:100//Hs. 27424: U75968
 F-HEM BB1000266//Homo sapiens mRNA for myosin phosphatase target subunit1 (MYPT1)//0.0019:373:60//Hs. 16533: D87930
 F-HEM BB1000272//ESTs//1.3e-93:440:99//Hs. 109224: N46684
 F-HEM BB1000274//ESTs//0.41:221:65//Hs. 71990: AA151796
 F-HEM BB1000284//EST//0.00024:108:73//Hs. 100725: F13689
 F-HEM BB1000307//EST//3.6e-10:149:73//Hs. 140415: AA778574
 F-HEM BB1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.00092:252:65//Hs. 41153: AB018326
 F-HEM BB1000317//Thrombospondin 1//7.1e-05:342:59//Hs. 87409: X14787
 F-HEM BB1000318//EST//0.014:184:61//Hs. 155758: AI311870
 F-HEM BB1000335//EST//0.99:187:63//Hs. 137424: AA243729
 F-HEM BB1000336//EST//1.0:209:63//Hs. 150410: AI003611
 F-HEM BB1000337//EST//0.086:133:66//Hs. 128207: AA972330
 F-HEM BB1000338//EST//7.1e-07:129:72//Hs. 140488: AA767127
 F-HEM BB1000339//Small inducible cytokine A5 (RANTE

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S)//1.2e-36:336:76//Hs.155464:AF088219
 F-HEM BB1000341
 F-HEM BB1000343//EST//0.66:163:63//Hs.150822:AI3027
 29
 F-HEM BB1000354//ESTs//7.1e-61:292:100//Hs.152266:A
 A926874
 F-HEM BB1000369//ESTs, Highly similar to t-BOP [M.m
 usculus]//0.013:157:64//Hs.129982:AI420970
 F-HEM BB1000374//ESTs//8.7e-53:454:79//Hs.133518:R6
 9934
 F-HEM BB1000376//ESTs//5.9e-14:87:97//Hs.163973:AA7
 44348
 F-HEM BB1000391//ESTs//0.033:237:64//Hs.135289:AI09
 2963
 F-HEM BB1000399//Homo sapiens mRNA for cell cycle c
 heckpoint protein//9.4e-165:762:98//Hs.16184:AJ001
 642
 F-HEM BB1000402//EST//0.013:291:59//Hs.149191:AI246
 155
 F-HEM BB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA
 947194
 F-HEM BB1000420//EST//6.3e-52:258:98//Hs.136434:AA5
 57925
 F-HEM BB1000434//Homo sapiens neuronal thread prote
 in AD7c-NTP mRNA, complete cds//9.4e-73:364:83//H
 s.129735:AF010144
 F-HEM BB1000438//ESTs//0.073:446:58//Hs.134632:AI22
 3429
 F-HEM BB1000441//Interleukin 10//1.7e-38:336:77//H
 s.2180:M57627
 F-HEM BB1000449//EST//5.5e-21:356:67//Hs.157848:AI3
 62501
 F-HEM BB1000455//ESTs//0.092:147:65//Hs.106446:N932
 27
 F-HEM BB1000472
 F-HEM BB1000480//EST//0.98:83:71//Hs.146462:AI12489
 8
 F-HEM BB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79
 206
 F-HEM BB1000490//ESTs//2.5e-27:200:79//Hs.56825:AI0
 57560
 F-HEM BB1000491
 F-HEM BB1000493//ESTs//0.019:103:69//Hs.138358:T661
 78
 F-HEM BB1000510//Glucocorticoid receptor alpha {alt
 ernative products}//1.6e-46:409:77//Hs.102761:U250
 29
 F-HEM BB1000518//ESTs//3.7e-06:187:64//Hs.140989:R6
 8413
 F-HEM BB1000523//ESTs//0.69:332:59//Hs.106845:W1954

3790

3
 F-HEM BB1000530//H.sapiens mRNA for extracellular m
 atrix protein collagentype XIV, C-terminus//2.1e-3
 8:138:96//Hs.36131:Y11710
 F-HEM BB1000550//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//7.7e-3
 1:554:67//Hs.157142:U85996
 F-HEM BB1000554//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0484//4.0e-27:282:75//Hs.158
 095:AB007953
 F-HEM BB1000556//Homo sapiens mRNA for KIAA0750 pro
 tein, complete cds//2.0e-33:537:65//Hs.5444:AB0182
 93
 F-HEM BB1000564
 F-HEM BB1000573//H.sapiens HCG II mRNA//7.5e-27:19
 7:76//Hs.146333:X81001
 F-HEM BB1000575//Von Hippel-Lindau syndrome//2.7e-7
 2:255:79//Hs.78160:AF010238
 F-HEM BB1000586//Dystrophin (muscular dystrophy, Du
 chenche and Becker types), includes DXS142, DXS164,
 DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, D
 XS272//0.011:338:59//Hs.79012:M18533
 F-HEM BB1000589//PLATELET GLYCOPROTEIN V PRECURSOR/
 //2.4e-22:228:79//Hs.73734:Z23091
 F-HEM BB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71
 990
 F-HEM BB1000592//EST//0.0038:51:88//Hs.148022:AI269
 323
 F-HEM BB1000593//Homo sapiens chromosome 7q22 seque
 nce//4.7e-109:503:99//Hs.3386:AF053356
 F-HEM BB1000598//Ribosomal protein L5//3.5e-29:537:
 66//Hs.118781:U66589
 F-HEM BB1000623//H.sapiens mRNA for GAIP protein//
 0.89:376:59//Hs.22698:X91809
 F-HEM BB1000630//Homo sapiens KIAA0404 mRNA, partia
 l cds//0.074:168:61//Hs.105850:AB007864
 F-HEM BB1000631//ESTs//1.7e-06:247:64//Hs.156864:AI
 346481
 F-HEM BB1000632//Human mRNA for KIAA0351 gene, comp
 lete cds//5.1e-50:811:65//Hs.29963:AB002349
 F-HEM BB1000637//Sialophorin (gpl115, leukosialin,
 CD43)//2.4e-79:304:85//Hs.80738:X52075
 F-HEM BB1000638//EST//0.0076:92:75//Hs.125496:AA883
 735
 F-HEM BB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSO
 R//3.5e-45:477:74//Hs.51048:X68830
 F-HEM BB1000649//Homo sapiens histone H2A.1b mRNA,
 complete cds//7.4e-52:533:75//Hs.51011:L19778
 F-HEM BB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA
 618531

3791

F-HEM BB1000665//EST//0.44:152:63//Hs.149534:AI2809
24
F-HEM BB1000671//Human Line-1 repeat mRNA with 2 op
en reading frames//2.2e-79:280:85//Hs.23094:M19503
F-HEM BB1000673//ESTs//0.99:177:59//Hs.149864:N8047
4
F-HEM BB1000684//Protein kinase, interferon-inducib
le double stranded RNA dependent//2.6e-31:220:87//H
s.73821:M35663
F-HEM BB1000693//Homo sapiens neuroanl mRNA, comple
te cds//5.3e-120:575:97//Hs.158300:AF040723
F-HEM BB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33
125
F-HEM BB1000706//EST//8.6e-14:373:61//Hs.138281:R55
703
F-HEM BB1000709//EST//0.99:110:65//Hs.162437:AA5775
10
F-HEM BB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-7
7:635:77//Hs.123109:X56741
F-HEM BB1000726//EST//1.3e-43:257:84//Hs.162197:AA5
35216
F-HEM BB1000738//EST//5.9e-13:259:64//Hs.159699:AI4
17328
F-HEM BB1000749//EST//3.1e-42:271:87//Hs.162197:AA5
35216
F-HEM BB1000763
F-HEM BB1000770//ESTs, Weakly similar to MOESIN/EZR
IN/RADIXIN HOMOLOG [D.melanogaster]//0.021:111:72/
/Hs.38178:AA921830
F-HEM BB1000774//ESTs, Weakly similar to mTERF [H.s
apiens]//2.5e-116:580:97//Hs.5009:AA081390
F-HEM BB1000781//Human MEK kinase 3 mRNA, complete
cds//5.3e-47:426:74//Hs.86201:U78876
F-HEM BB1000789//Homo sapiens mRNA for KIAA0677 pro
tein, complete cds//3.0e-65:672:71//Hs.155983:AB01
4577
F-HEM BB1000790//ESTs//1.2e-52:344:86//Hs.35254:AI1
33727
F-HEM BB1000794//ESTs//0.00098:289:59//Hs.138782:N7
3572
F-HEM BB1000807//ESTs//2.1e-91:434:99//Hs.61334:AI2
98375
F-HEM BB1000810//ESTs//0.038:92:71//Hs.148763:AA668
871
F-HEM BB1000821//EST//0.94:129:62//Hs.162299:AA5551
54
F-HEM BB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA
832421
F-HEM BB1000826//ESTs//4.8e-13:343:65//Hs.153429:AI
283069

3792

F-HEM BB1000827
F-HEM BB1000831
F-HEM BB1000835//EST//4.3e-27:201:85//Hs.141451:N29
915
F-HEM BB1000840//EST//6.3e-75:380:96//Hs.142557:AA4
64948
F-HEM BB1000848//Human Line-1 repeat mRNA with 2 op
en reading frames//1.4e-135:875:85//Hs.23094:M1950
3
F-HEM BB1000852//Phosphoribosyl pyrophosphate amido
transferase//0.12:292:61//Hs.311:U00238
F-HEM BB1000870//EST//0.00091:246:62//Hs.126502:AA9
13831
F-HEM BB1000876//Homo sapiens ELISC-1 mRNA, partial
cds//4.9e-34:200:94//Hs.128434:AF085351
F-HEM BB1000883//ESTs//0.42:107:67//Hs.154173:AI379
823
F-HEM BB1000887
F-HEM BB1000888//ESTs//1.0:137:67//Hs.8121:AA521290
F-HEM BB1000890//ESTs//1.0:116:65//Hs.7105:T23433
F-HEM BB1000893//EST//0.0079:408:58//Hs.146504:AI12
9834
F-HEM BB1000908//EST//9.2e-21:205:79//Hs.132635:AI0
32875
F-HEM BB1000910//Human mRNA for KIAA0231 gene, part
ial cds//0.16:327:60//Hs.7938:D86984
F-HEM BB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA
487049
F-HEM BB1000915//ESTs//2.5e-90:423:99//Hs.135254:AI
095468
F-HEM BB1000917//EST//2.8e-49:241:100//Hs.162216:AA
548089
F-HEM BB1000927//Hippocalcin//1.2e-31:528:65//Hs.89
692:D16593
F-HEM BB1000947
F-HEM BB1000959//Cytochrome P450, 51 (lanosterol 14
-alpha-demethylase)//9.3e-48:572:72//Hs.2379:U2394
2
F-HEM BB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA
142938
F-HEM BB1000975//ESTs//0.78:180:66//Hs.104789:AA417
124
F-HEM BB1000981
F-HEM BB1000985//Homo sapiens actin binding protein
MAYVEN mRNA, complete cds//6.7e-07:308:62//Hs.1229
67:AF059569
F-HEM BB1000991//EST//0.12:125:66//Hs.22945:R43713
F-HEM BB1000996//ESTs//6.9e-05:273:63//Hs.133116:AI
054055
F-HEM BB1001004//Homo sapiens mRNA for KIAA0665 pro

3793

tein, complete cds//0.62:193:62//Hs.119004:AB01456
5
F-HEM BB1001008//EST//4.7e-09:203:65//Hs.105221:AA
89025
F-HEM BB1001011//Human Chromosome 16 BAC clone CIT9
87SK-A-635H12//2.4e-17:384:67//Hs.108604:AC002310
F-HEM BB1001014//EST, Weakly similar to putative p1
50 [H.sapiens]//0.21:284:60//Hs.161547:W04991
F-HEM BB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA
284247
F-HEM BB1001024//ESTs, Highly similar to t-BOP [M.m
usculus]//0.11:242:61//Hs.129982:AI420970
F-HEM BB1001037//EST//0.0057:192:66//Hs.149987:AI29
1177
F-HEM BB1001047//ESTs//1.6e-22:360:70//Hs.120734:W5
8721
F-HEM BB1001051//H.sapiens mRNA for FAN protein//3.
8e-29:160:98//Hs.78687:X96586
F-HEM BB1001056//Homo sapiens mRNA for KIAA0618 pro
tein, complete cds//1.0e-42:149:96//Hs.15832:AB014
518
F-HEM BB1001058//Small inducible cytokine A5 (RANTE
S)//1.1e-45:349:82//Hs.155464:AF088219
F-HEM BB1001060//ESTs//1.6e-62:464:81//Hs.138663:N2
4942
F-HEM BB1001063
F-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, pa
rtial cds//9.9e-148:736:95//Hs.12953:AF034803
F-HEM BB1001096//EST//0.017:154:66//Hs.130403:AA909
272
F-HEM BB1001102//ESTs//2.1e-18:120:95//Hs.163767:RO
6293
F-HEM BB1001105//Human BRCA2 region, mRNA sequence
CG016//0.30:84:75//Hs.112434:U50529
F-HEM BB1001112//ESTs, Highly similar to PROTEIN T
RANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familia
ris]//9.3e-38:341:77//Hs.14038:R06800
F-HEM BB1001114//EST//6.4e-07:296:62//Hs.128420:AA9
75062
F-HEM BB1001117//EST//1.6e-99:464:99//Hs.130493:AA9
28139
F-HEM BB1001119
F-HEM BB1001126
F-HEM BB1001133//H.sapiens mRNA for translin associ
ated protein X//1.2e-28:739:61//Hs.96247:X95073
F-HEM BB1001137
F-HEM BB1001142//Human mRNA for KIAA0331 gene, comp
lete cds//2.1e-23:340:69//Hs.146395:AB002329
F-HEM BB1001151//ESTs//2.6e-30:252:79//Hs.6880:W268
54

3794

F-HEM BB1001153//ESTs//7.6e-16:97:96//Hs.113307:H16
716
F-HEM BB1001169//ESTs//1.4e-32:374:71//Hs.161682:AA
206863
F-HEM BB1001175//Human mRNA for ankyrin motif, comp
lete cds//7.1e-36:509:66//Hs.73073:D78334
F-HEM BB1001177//ESTs, Weakly similar to HYPOTHETI
CAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA
2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:10
0//Hs.86878:AA599183
F-HEM BB1001182//Electron-transfer-flavoprotein, be
ta polypeptide//0.94:199:64//Hs.74047:X71129
F-HEM BB1001199
F-HEM BB1001208//ESTs//0.12:120:69//Hs.130093:AA928
802
F-HEM BB1001209//EST//0.00028:215:65//Hs.118276:W15
258
F-HEM BB1001210//EST//2.9e-05:297:60//Hs.88840:AA28
1452
F-HEM BB1001218//Homo sapiens mRNA for KIAA0585 pro
tein, partial cds//8.5e-37:260:76//Hs.72660:AB0111
57
F-HEM BB1001221//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0507//0.00046:650:58//Hs.158
241:AB007976
F-HEM BB1001234//ESTs, Highly similar to 65 KD YES
-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:1
00//Hs.127835:AI378790
F-HEM BB1001242//Homo sapiens mRNA for LAX-1, compl
ete cds//1.2e-31:458:67//Hs.129918:AB005754
F-HEM BB1001249//EST//0.26:203:63//Hs.140791:AA9359
09
F-HEM BB1001253//ESTs//4.0e-91:433:98//Hs.120636:AA
325219
F-HEM BB1001254//ESTs//2.0e-24:180:85//Hs.136391:HO
4977
F-HEM BB1001267//Ataxia telangiectasia mutated (inc
ludes complementation groups A, C and D)//6.1e-24:1
46:78//Hs.51187:U82828
F-HEM BB1001271//ESTs//2.5e-05:686:58//Hs.115423:AI
359248
F-HEM BB1001282//GA-binding protein transcription f
actor, beta subunit 2(47kd)//0.39:531:57//Hs.7891
5:U13045
F-HEM BB1001288//ESTs, Highly similar to HYPOTHETI
CAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Cae
norhabditis elegans]//4.9e-10:91:89//Hs.16606:W810
21
F-HEM BB1001289//ESTs//6.4e-100:467:99//Hs.151720:A
1287890

3795

F-HEM BB1001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848

F-HEM BB1001302

F-HEM BB1001304//ESTs//0.98:109:68//Hs.138972:AA047725

F-HEM BB1001314//ESTs//7.4e-39:285:77//Hs.144749:AI217339

F-HEM BB1001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219

F-HEM BB1001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503

F-HEM BB1001326//ESTs//0.00030:257:63//Hs.62208:H12380

F-HEM BB1001331//ESTs, Weakly similar to DFS70 [H. sapiens]//1.0e-48:332:87//Hs.43071:AA206222

F-HEM BB1001335

F-HEM BB1001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB01135

F-HEM BB1001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694

F-HEM BB1001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878

F-HEM BB1001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142

F-HEM BB1001356//EST//0.32:292:59//Hs.135771:AI005648

F-HEM BB1001364

F-HEM BB1001366//EST//7.8e-24:367:69//Hs.138765:N70347

F-HEM BB1001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219

F-HEM BB1001369//EST//0.17:211:63//Hs.120066:AA707973

F-HEM BB1001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099

F-HEM BB1001384

F-HEM BB1001387//ESTs//0.61:215:60//Hs.145915:AI34230

F-HEM BB1001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503

F-HEM BB1001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988

F-HEM BB1001424//EST//0.20:307:58//Hs.135336:AI049827

F-HEM BB1001426//Homo sapiens clone 23579 mRNA sequ 50

3796

ence//8.3e-17:205:72//Hs.83466:AF038174

F-HEM BB1001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175

F-HEM BB1001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345

F-HEM BB1001443

F-HEM BB1001449//Homo sapiens sodium bicarbonate co transporter (HNBC1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216

F-HEM BB1001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038

F-HEM BB1001458//EST//1.7e-09:106:83//Hs.141422:N20920

F-HEM BB1001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220

F-HEM BB1001464//Homo sapiens Coch-5B2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740

F-HEM BB1001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303

F-HEM BB1001500//ESTs//8.1e-28:312:74//Hs.18498:N52088

F-HEM BB1001521//Homo sapiens mRNA for alpha(1,2) fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942

F-HEM BB1001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815

30 F-HEM BB1001531//ESTs//4.3e-33:403:75//Hs.44862:N38735

F-HEM BB1001535//ESTs//0.0029:47:93//Hs.124864:AA663093

F-HEM BB1001536//ESTs//0.0047:120:68//Hs.144858:R67748

F-HEM BB1001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D. melanogaster]//3.7e-20:297:73//Hs.42457:AA523306

40 F-HEM BB1001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315

F-HEM BB1001562//ESTs//0.95:161:61//Hs.145075:AI208240

F-HEM BB1001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953

F-HEM BB1001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080

F-HEM BB1001585

F-HEM BB1001586//EST//0.84:132:64//Hs.145264:AI2187

- 08
F-HEM BB1001588//Human clone 23695 mRNA sequence//
6.6e-20: 327: 67//Hs. 90798: U79289
F-HEM BB1001603//ESTs//1.3e-12: 84: 96//Hs. 13380: R604
14
F-HEM BB1001618//ESTs//4.4e-11: 349: 63//Hs. 132046: AA
693680
F-HEM BB1001619//ESTs//2.1e-06: 246: 63//Hs. 63428: AA0
58314
F-HEM BB1001630//EST//1.4e-07: 334: 62//Hs. 145698: AI2 10
66713
F-HEM BB1001635//ESTs//0.92: 282: 60//Hs. 126980: AA934
077
F-HEM BB1001637//ELK1, member of ETS oncogene famil
y//1.1e-27: 395: 64//Hs. 116549: AL009172
F-HEM BB1001641//EST//0.11: 53: 81//Hs. 112445: AA59427
9
F-HEM BB1001653//EST//0.91: 124: 64//Hs. 144213: T40480
F-HEM BB1001665//Human mRNA for apolipoprotein E re
ceptor 2, complete cds//7.0e-13: 473: 63//Hs. 54481: D 20
86407
F-HEM BB1001668//ESTs//0.94: 83: 69//Hs. 146202: AI2525
19
F-HEM BB1001673//Homo sapiens mRNA for KIAA0646 pro
tein, complete cds//2.3e-172: 803: 98//Hs. 24439: AB01
4546
F-HEM BB1001684//ESTs, Highly similar to Tbc1 [M.mu
sculus]//5.4e-20: 110: 100//Hs. 106104: AA599496
F-HEM BB1001685//EST//2.2e-05: 112: 73//Hs. 130984: AI0
15430
F-HEM BB1001695//Human novel homeobox mRNA for a DN
A binding protein//1.6e-08: 425: 62//Hs. 37035: U07664
F-HEM BB1001704//EST//5.8e-20: 295: 69//Hs. 140231: AI0
54398
F-HEM BB1001706
F-HEM BB1001707//EST//0.091: 241: 60//Hs. 136830: AA769
219
F-HEM BB1001717//ESTs//2.9e-06: 325: 60//Hs. 150063: AI
298064
F-HEM BB1001735//Small inducible cytokine A5 (RANTE 40
S)//3.2e-46: 326: 83//Hs. 155464: AF088219
F-HEM BB1001736//ESTs, Weakly similar to E04D5.1
[C.elegans]//5.4e-99: 485: 97//Hs. 120581: W25578
F-HEM BB1001747//ESTs//8.3e-87: 421: 98//Hs. 137051: AA
884244
F-HEM BB1001749//Homo sapiens neuronal thread prote
in AD7c-NTP mRNA, complete cds//3.5e-75: 315: 83//H
s. 129735: AF010144
F-HEM BB1001753//ESTs//0.00013: 35: 100//Hs. 139643: H0
6263
- F-HEM BB1001756//ESTs//2.3e-89: 433: 98//Hs. 128868: AA
931077
F-HEM BB1001760//ESTs//6.5e-06: 503: 58//Hs. 21766: AI3
57639
F-HEM BB1001762//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0507//2.9e-13: 498: 60//Hs. 158
241: AB007976
F-HEM BB1001785//EST//0.16: 262: 60//Hs. 162526: AA5841
02
F-HEM BB1001797//ESTs//0.37: 201: 63//Hs. 91559: AA8063
70
F-HEM BB1001802//ESTs//1.6e-06: 447: 58//Hs. 134672: AI
087951
F-HEM BB1001812//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0487//1.3e-54: 311: 81//Hs. 923
81: AB007956
F-HEM BB1001816//ESTs//2.2e-39: 302: 84//Hs. 35985: AA7
83017
F-HEM BB1001831//Homo sapiens PAM C00H-terminal int
eractor protein 1 (PCIP1) mRNA, complete cds//7.6e
-164: 763: 98//Hs. 159396: AF056209
F-HEM BB1001834//TRICHOHYALIN//7.1e-05: 548: 60//Hs. 8
2276: L09190
F-HEM BB1001836//Human mRNA for KIAA0033 gene, part
ial cds//4.0e-34: 272: 86//Hs. 22271: D26067
F-HEM BB1001839//Pyruvate carboxylase//0.050: 686: 59
//Hs. 89890: S72370
F-HEM BB1001850//EST//0.0035: 204: 61//Hs. 7311: T23858
F-HEM BB1001863//Small inducible cytokine A5 (RANTE
S)//3.0e-48: 357: 82//Hs. 155464: AF088219
F-HEM BB1001867//ESTs//2.2e-40: 265: 88//Hs. 146323: AI
251752
F-HEM BB1001868//ESTs//5.2e-06: 131: 73//Hs. 123362: AA
811371
F-HEM BB1001869//ESTs//1.0e-86: 429: 96//Hs. 141208: AA
825503
F-HEM BB1001872
F-HEM BB1001874//H. sapiens mRNA for CHD5 protein//
0.0033: 388: 60//Hs. 19923: Y12478
F-HEM BB1001875//H. sapiens mRNA for RNA helicase (M
yc-regulated dead boxprotein)//0.32: 346: 60//Hs. 100
555: X98743
F-HEM BB1001880//EST//4.0e-28: 171: 92//Hs. 151194: AI1
25868
F-HEM BB1001899//ESTs//0.17: 242: 62//Hs. 136969: AA830
918
F-HEM BB1001905
F-HEM BB1001906//ESTs//5.6e-49: 290: 92//Hs. 127298: H0
9155
50 F-HEM BB1001908//Human monocytic leukaemia zinc fin

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ger protein (MOZ) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742
 F-HEM BB1001910//EST, Weakly similar to albumin [H. sapiens]//0.047:206:62//Hs.159777:Z19955
 F-HEM BB1001911
 F-HEM BB1001915//ESTs//0.92:136:71//Hs.144465:R68882
 F-HEM BB1001921//EST//2.0e-19:398:67//Hs.44789:N36113
 F-HEM BB1001922//ESTs//4.3e-05:370:59//Hs.123669:AA 10 805245
 F-HEM BB1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398
 F-HEM BB1001930//EST//0.043:157:63//Hs.161927:AA483904
 F-HEM BB1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-55:444:80//Hs.154326:D42087
 F-HEM BB1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875
 F-HEM BB1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-21:333:66//Hs.40100:AB002390
 F-HEM BB1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.020:384:60//Hs.8546:U97669
 F-HEM BB1001952//EST//7.0e-13:302:63//Hs.120089:AA708101
 F-HEM BB1001953//ATL-derived PMA-responsive (APR) peptide//0.97:252:60//Hs.96:D90070
 F-HEM BB1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418
 F-HEM BB1001962//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053
 F-HEM BB1001967//H. sapiens mRNA for urea transporter//9.7e-52:322:88//Hs.66710:X96969
 F-HEM BB1001973//Myelin oligodendrocyte glycoprotein [alternative products]//2.1e-48:426:78//Hs.53217:Z48051
 F-HEM BB1001983
 F-HEM BB1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051
 F-HEM BB1001990//ESTs//0.25:171:64//Hs.7961:AA401205
 F-HEM BB1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103
 F-HEM BB1001997//EST//5.3e-33:294:76//Hs.161041:H82636
 F-HEM BB1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964
 F-HEM BB1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093

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F-HEM BB1002009//ESTs//0.066:441:58//Hs.125313:AI201685
 F-HEM BB1002015//EST//2.3e-18:310:68//Hs.145899:AI274951
 F-HEM BB1002042//CYTOCHROME P450 IVB1//2.9e-11:446:62//Hs.687:X16699
 F-HEM BB1002043//ESTs, Weakly similar to T06E6.d [C. elegans]//1.0:217:60//Hs.3487:AA425553
 F-HEM BB1002044
 F-HEM BB1002045
 F-HEM BB1002049//Homo sapiens mRNA for KIAA0713 protein, partial cds//0.082:201:61//Hs.88756:AB018256
 F-HEM BB1002050//Breakpoint cluster region protein BCR//0.84:267:59//Hs.2557:Y00661
 F-HEM BB1002068//Homo sapiens mRNA for KIAA0612 protein, partial cds//8.1e-07:402:61//Hs.112499:AB014512
 F-HEM BB1002069
 F-HEM BB1002092//EST//5.1e-15:180:75//Hs.127928:AA969239
 F-HEM BB1002094//EST//2.0e-52:264:98//Hs.71763:AA146625
 F-HEM BB1002115//EST//0.0083:244:64//Hs.125353:AA877080
 F-HEM BB1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027
 F-HEM BB1002139//ESTs//0.64:145:71//Hs.157821:AI362013
 F-HEM BB1002142//ESTs//0.013:311:59//Hs.150037:AI292214
 F-HEM BB1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254
 F-HEM BB1002189//EST//0.26:81:70//Hs.147726:AI220208
 F-HEM BB1002190//Alcohol dehydrogenase 2 (class I), beta polypeptide//0.16:608:58//Hs.4:X03350
 F-HEM BB1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:100//Hs.301:U18934
 F-HEM BB1002217//Homo sapiens mRNA for zinc finger protein 10//3.7e-25:405:67//Hs.104115:X52332
 F-HEM BB1002218//EST//0.015:241:61//Hs.105298:AA489813
 F-HEM BB1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:71//Hs.155464:AF088219
 F-HEM BB1002247
 F-HEM BB1002249//Homo sapiens haemopoietic progenitor or homeobox HPX42B (HPX42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006
 F-HEM BB1002254//Homo sapiens mRNA for KIAA0594 protein, partial cds//5.0e-47:437:77//Hs.154872:AB01150

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F-HEM BB1002255//ESTs//0.017:255:61//Hs.126786:U74314
F-HEM BB1002266//Homo sapiens retinoblastoma-associated protein HEC mRNA, complete cds//0.17:511:57//Hs.58169:AF017790
F-HEM BB1002280//EST//4.0e-35:182:98//Hs.127701:AA864998
F-HEM BB1002300
F-HEM BB1002306//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.3e-14:228:72//Hs.46468:U45984
F-HEM BB1002327//EST//4.3e-21:242:75//Hs.72377:AA161083
F-HEM BB1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7e-77:399:96//Hs.105837:AA536054
F-HEM BB1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M21188
F-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//1.4e-155:724:98//Hs.42644:AJ010841
F-HEM BB1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:L16991
F-HEM BB1002359//Human Rev interacting protein Rip-1 mRNA, complete cds//1.7e-06:66:96//Hs.154762:U00943
F-HEM BB1002364//EST//4.7e-16:201:73//Hs.149925:AI288838
F-HEM BB1002371//EST//2.4e-07:319:61//Hs.136459:AA577796
F-HEM BB1002381
F-HEM BB1002383//vasoactive intestinal peptide receptor 2//0.98:190:63//Hs.2126:L36566
F-HEM BB1002387//EST//2.1e-07:253:61//Hs.145993:AI277784
F-HEM BB1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
F-HEM BB1002415//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.0e-32:371:73//Hs.159897:AB007970
F-HEM BB1002425//Fc fragment of IgA, receptor for//2.7e-32:156:82//Hs.54486:X54150
F-HEM BB1002442
F-HEM BB1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-53:461:77//Hs.154326:D42087
F-HEM BB1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
F-HEM BB1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
F-HEM BB1002477//Human Grb2-associated binder-1 mRNA 50
A, complete cds//6.0e-89:493:92//Hs.159605:U43885
F-HEM BB1002489//Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds//0.019:228:63//Hs.74304:AF001691
F-HEM BB1002492//EST//0.24:149:62//Hs.146790:AI149051
F-HEM BB1002495//Fc fragment of IgE, high affinity I, receptor for; betapolypeptide//1.3e-22:331:71//Hs.30:M89796
F-HEM BB1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
F-HEM BB1002509//ESTs//0.017:220:63//Hs.155263:AI273725
F-HEM BB1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354
F-HEM BB1002520//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-50:580:72//Hs.23094:M19503
F-HEM BB1002522//EST//0.010:172:62//Hs.147224:AI205719
F-HEM BB1002531
F-HEM BB1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:88//Hs.155464:AF088219
F-HEM BB1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102
F-HEM BB1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648
F-HEM BB1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
F-HEM BB1002579//EST//1.0:77:68//Hs.147935:AI250286
F-HEM BB1002582//ESTs//0.00032:178:68//Hs.139163:AA226095
F-HEM BB1002590//ESTs//0.64:132:63//Hs.155688:AI003657
F-HEM BB1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
F-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//3.0e-152:710:98//Hs.129826:AF089749
F-HEM BB1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
F-HEM BB1002603//EST//0.10:144:63//Hs.158180:AI367945
F-HEM BB1002607//ESTs//0.024:345:62//Hs.143304:AI084058
F-HEM BB1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
F-HEM BB1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
F-HEM BB1002614//ESTs//0.0048:136:71//Hs.106280:R13901
F-HEM BB1002617//EST//0.034:320:59//Hs.41223:H89127

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- F-HEM BB1002623//ESTs//0.88:222:60//Hs.129920:AA167217
- F-HEM BB1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:100//Hs.151051:U07620
- F-HEM BB1002664//EST//0.00013:203:61//Hs.117141:AA678811
- F-HEM BB1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
- F-HEM BB1002683//ESTs//0.23:224:61//Hs.128883:AI026679
- F-HEM BB1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
- F-HEM BB1002686//EST//0.25:189:62//Hs.132431:AA909674
- F-HEM BB1002692//ESTs//0.00020:162:66//Hs.118180:N68504
- F-HEM BB1002697//EST//7.2e-17:219:74//Hs.100459:T61992
- F-HEM BB1002699//Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614
- F-HEM BB1002702//ESTs//0.26:284:61//Hs.41250:H89588
- F-HEM BB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN INSUI2-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:AI242922
- F-HEM BB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
- F-MAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990
- F-MAMMA1000019
- F-MAMMA1000020//EST//2.6e-84:431:95//Hs.143333:H51750
- F-MAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
- F-MAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
- F-MAMMA1000045//ESTs//1.7e-48:499:75//Hs.158469:AA897461
- F-MAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281
- F-MAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019
- F-MAMMA1000069//ESTs//0.58:286:60//Hs.134417:AI336840
- F-MAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067
- F-MAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB01174
- F-MAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705
- F-MAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792
- F-MAMMA1000117
- 10 F-MAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508
- F-MAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402
- F-MAMMA1000134//EST//1.2e-08:75:92//Hs.160674:AI248319
- F-MAMMA1000139//EST//5.5e-10:139:76//Hs.159121:AI383843
- F-MAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585
- F-MAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924
- F-MAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA01050
- F-MAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695
- F-MAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530
- 30 F-MAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657
- F-MAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763
- F-MAMMA1000198//ESTs//0.0092:235:62//Hs.98783:AI091739
- F-MAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035
- F-MAMMA1000227//ESTs//0.010:268:60//Hs.116412:AA506926
- 40 F-MAMMA1000241//ESTs//0.13:140:67//Hs.12328:AI377913
- F-MAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873
- F-MAMMA1000254//ESTs//0.00023:245:59//Hs.150513:AI247587
- F-MAMMA1000257//EST//4.2e-10:155:74//Hs.150409:AI03543
- F-MAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015
- 50 F-MAMMA1000266//EST//0.14:270:60//Hs.132593:AI0318

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F-MAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087

F-MAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726

F-MAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:AI347361

F-MAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505

F-MAMMA1000284

F-MAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087

F-MAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641

F-MAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243

F-MAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529

F-MAMMA1000312//EST//0.042:183:63//Hs.158928:AI379519

F-MAMMA1000313

F-MAMMA1000331

F-MAMMA1000339

F-MAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN INSTE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963

F-MAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892

F-MAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953

F-MAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-75:498:85//Hs.23094:M19503

F-MAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087

F-MAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569

F-MAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344

F-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132

F-MAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590

F-MAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frames//2.4e-58:834:68//Hs.23094:M19503

F-MAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468

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F-MAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:AI200725

F-MAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092

F-MAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C09

F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111

F-MAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:HO2532

F-MAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573

F-MAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459

F-MAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:AI377641

F-MAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546

F-MAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830

F-MAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011166

F-MAMMA1000446

F-MAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:W21827

30 F-MAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818

F-MAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830

F-MAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080

F-MAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830

F-MAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948

F-MAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482

F-MAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219

F-MAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878

F-MAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352

F-MAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497

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F-MAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352
 F-MAMMA1000565
 F-MAMMA1000567//Homo sapiens haemopoietic progenitor or homeobox HPX42B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006
 F-MAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045
 F-MAMMA1000583//ESTs//0.00099:123:70//Hs.135173:AI276780
 F-MAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622
 F-MAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744
 F-MAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886
 F-MAMMA1000605//Homo sapiens 4F5S mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519
 F-MAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494
 F-MAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
 F-MAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
 F-MAMMA1000623
 F-MAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751
 F-MAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:AF023674
 F-MAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
 F-MAMMA1000669//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.0e-30:531:64//Hs.139107:K00629
 F-MAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:AI244490
 F-MAMMA1000672//Homo sapiens CAGH32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743
 F-MAMMA1000684//Homo sapiens forkhead protein FREA C-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220
 F-MAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627
 F-MAMMA1000707//ESTs//1.4e-09:225:65//Hs.138722:N51081
 F-MAMMA1000713//Acetylcholinesterase [I4-E5 domain] [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129
 F-MAMMA1000714//Human clone 23947 mRNA, partial cd

3808

s//0.97:263:61//Hs.27414:U79275
 F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648
 F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247
 F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:AA700024
 F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513
 F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.158095:AB007953
 F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075
 F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:AF100141
 F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580
 F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:AB011147
 F-MAMMA1000746//ESTs//2.3e-42:409:76//Hs.61199:AA24494
 F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663
 F-MAMMA1000760//Myelin oligodendrocyte glycoprotein {alternative products}//6.2e-47:341:82//Hs.53217:Z48051
 F-MAMMA1000761//ESTs, Moderately similar to !!!! A LU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369
 F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288
 F-MAMMA1000776//ESTs//5.5e-43:154:84//Hs.141581:AA315361
 F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA84114
 F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137
 F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575
 F-MAMMA1000802//ESTs//3.1e-67:340:97//Hs.126081:AA459849
 F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130
 F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:AI298089
 F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e-48:241:74//Hs.155464:AF088219
 F-MAMMA1000841

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F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//Hs.82210:U47742
 F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696
 F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877
 F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022
 F-MAMMA1000855
 F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA 10 A, partial cds//0.14:320:59//Hs.71388:AF032906
 F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135
 F-MAMMA1000862//EST//1.0:92:66//Hs.157599:AI357342
 F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172
 F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812
 F-MAMMA1000867//EST//0.027:236:60//Hs.147156:AI191777
 F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459
 F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147
 F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894
 F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812
 F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465
 F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:X67055
 F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683
 F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506
 F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081
 F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628
 F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:AI125239
 F-MAMMA1000931//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.116007:S79267
 F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968
 F-MAMMA1000941//Dihydrolipoamide branched chain tr 50

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ansacylase (E2 component of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785
 F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734
 F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303
 F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714
 F-MAMMA1000957//ESTs//1.0:177:59//Hs.149864:N80474
 F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//Hs.129735:AF010144
 F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814
 F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096
 F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802
 20 F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062
 F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007
 F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:AI003724
 F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711
 F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:Y15718
 F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968
 F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HC38 mRNA, complete cds//3.6e-32:753:61//Hs.98384:AF062006
 F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857
 F-MAMMA1001038
 F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178
 40 F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:AI419882
 F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
 F-MAMMA1001067//EST//0.30:166:60//Hs.148441:AI198503
 F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585
 F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116

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F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749
 F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503
 F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420
 F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896
 F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
 F-MAMMA1001092//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:K00627
 F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045
 F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
 F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219
 F-MAMMA1001133
 F-MAMMA1001139
 F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:AI091534
 F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
 F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741
 F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147
 F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:AI014299
 F-MAMMA1001181
 F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171
 F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083
 F-MAMMA1001198
 F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
 F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974
 F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776
 F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:TO 50

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3200

F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087
 F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534
 F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587
 F-MAMMA1001244
 F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:AI220476
 F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:AI160121
 F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149
 F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561
 F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503
 F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747
 F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522
 F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832
 F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998
 F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA57426
 F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305
 F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat//1.9e-58:295:97//Hs.102336:Z83838
 F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087
 F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:745:73//Hs.93174:X57147
 F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806
 F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197
 F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267
 F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cds//0.94:89:75//Hs.109358:AB018258
 F-MAMMA1001383//Putative mismatch repair/binding p

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rotein hMSH3//7.3e-49:273:80//Hs.42674:U61981
 F-MAMMA1001388//INSULIN-LIKE GROWTH FACTOR BINDING
 PROTEIN COMPLEX ACID-LABILE CHAIN PRECURSOR//4.6e-
 09:415:58//Hs.839:M86826
 F-MAMMA1001397//Prostaglandin I2 (prostacyclin) sy
 nthase //1.3e-26:358:67//Hs.61333:D83402
 F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60
 763
 F-MAMMA1001411//Autosomal dominant polycystic kidn
 ey disease type II//1.0:176:64//Hs.82001:U50928 10
 F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partia
 l cds//4.1e-45:409:80//Hs.43681:AL022394
 F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fu
 cosyltransferase, complete cds//0.00042:125:75//H
 s.46328:D87942
 F-MAMMA1001435//Human HsLIM15 mRNA for HsLim15, co
 mplete cds//8.2e-43:543:71//Hs.37181:D64108
 F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51
 321
 F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA 20
 463590
 F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424
 040
 F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA18
 1053
 F-MAMMA1001476//Human mRNA for 5'-terminal region
 of UMK, complete cds//2.0e-24:273:72//Hs.75939:D78
 335
 F-MAMMA1001487//ESTs, Weakly similar to ORF2-like
 protein [H. sapiens]//3.2e-25:397:68//Hs.116874:AA5 30
 24909
 F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//
 Hs.2575:X04366
 F-MAMMA1001502//Human p120E4F transcription factor
 mRNA, complete cds//0.99:258:61//Hs.154196:U87269
 F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA
 420795
 F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI
 018506
 F-MAMMA1001547
 F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 pro
 tein, partial cds//7.5e-130:614:98//Hs.129937:AB00
 7931
 F-MAMMA1001575//ESTs, Weakly similar to zinc finge
 r protein C2H2-171 [H. sapiens]//0.71:181:62//Hs.11
 8866:AI017072
 F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-9
 7:529:91//Hs.150785:M61764
 F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160
 339

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F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI24
 7132
 F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA58
 3375
 F-MAMMA1001606//Human clone 23627 mRNA, complete c
 ds//0.64:336:58//Hs.23642:U79266
 F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA8
 36152
 F-MAMMA1001627//Pregnancy-associated plasma protei
 n A//0.27:379:58//Hs.158229:U28727
 F-MAMMA1001630//Human DNA sequence from clone 71L1
 6 on chromosome Xp11. Contains a probable Zinc Fing
 er protein (pseudo)gene, an unknown putative gene,
 a pseudogene with high similarity to part of anti
 gen KI-67, a putative Chondroitin 6-Sulfotransfera
 se LIKE gene and a KIAA0267 LIKE putative Na(+)/H
 (+) exchanger protein gene. Contains a predicted C
 pG island, ESTs, STSs and GSSs and genomic markers
 DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:ALO
 22165
 F-MAMMA1001633//Human zinc finger protein (LD5-1)
 mRNA, complete cds//3.6e-44:611:67//Hs.57679:U5779
 6
 F-MAMMA1001635
 F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T7
 5524
 F-MAMMA1001654//Homo sapiens retinal rod Na-Ca+K e
 xchanger (NCKX1) mRNA, complete cds//0.00069:140:68
 //Hs.59829:AB014602
 F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 pro
 tein, complete cds//0.015:135:71//Hs.27349:AB00791
 7
 F-MAMMA1001670//ESTs, Highly similar to 52 KD RO
 PROTEIN [Homo sapiens]//0.064:472:60//Hs.110819:AI
 027548
 F-MAMMA1001671
 F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA5733
 17
 F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA
 036889 40
 F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI
 138765
 F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI1885
 49
 F-MAMMA1001711//Human G protein-coupled receptor
 (STRL22) mRNA, completecds//8.0e-45:323:83//Hs.464
 68:U45984
 F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA
 936548
 F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA50 50

- 6926
F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//1.5e-111:725:84//Hs.159154:U47634
F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098
F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768
F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245
F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-67:822:69//Hs.23094:M19503
F-MAMMA1001751//Homo sapiens two P domain potassium channel subunit (H0H01) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632
F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822
F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109
F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense transcript, partial//6.6e-41:309:84//Hs.102576:AJ010230
F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072
F-MAMMA1001768//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF042832
F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-85:686:79//Hs.113283:AF018080
F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete cds//0.00071:392:60//Hs.32981:U38276
F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940
F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549
F-MAMMA1001788//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//6.7e-21:212:77//Hs.103948:K00627
F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:139:72//Hs.5158:AB007869
F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987
F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884
F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:N47096
F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582
F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA16758
- 9
F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CLF-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293
F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA992742
F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R78691
F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315, complete cds//2.0e-29:641:62//Hs.56808:D88827
F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665
F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028
F-MAMMA1001854
F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218
F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060
F-MAMMA1001868//Homo sapiens nuclear receptor corepressor N-CoR mRNA, complete cds//0.084:672:58//Hs.152455:AF044209
F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687
F-MAMMA1001878
F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944
F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576
F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078
F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521
F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874
F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529
F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859
F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:423:81//Hs.91916:AF035317
F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878
F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H. sapiens]//7.9e-09:150:72//Hs.118222:N91115
F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633
F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704

826
 F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915
 F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159
 F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.2e-54:455:70//Hs.158095:AB007953
 F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580
 F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225
 F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256
 F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305
 F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frames//8.5e-36:382:75//Hs.23094:M19503
 F-MAMMA1002078
 F-MAMMA1002082
 F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012
 F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//0.54:388:57//Hs.99423:AJ010840
 F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120
 F-MAMMA1002118//EST//0.50:202:64//Hs.126872:AA932932
 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219
 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:AI272963
 F-MAMMA1002140//ESTs//5.8e-33:212:77//Hs.141203:H52638
 F-MAMMA1002143//SERUM PROTEIN MSE55//1.9e-12:192:70//Hs.148101:M88338
 F-MAMMA1002145//EST//0.12:204:60//Hs.160983:AI392837
 F-MAMMA1002153
 F-MAMMA1002155//ESTs, Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385
 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)//0.99:310:58//Hs.87149:M35999
 F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206
 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400

F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548
 F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362
 F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120
 F-MAMMA1002219//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
 10 F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:AI024063
 F-MAMMA1002236//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:AI359536
 F-MAMMA1002243//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986
 F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903
 20 F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:AI308841
 F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172
 F-MAMMA1002269
 F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715
 F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440
 30 F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019
 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302
 F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460
 F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914
 40 F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935
 F-MAMMA1002308//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776
 F-MAMMA1002310//Homo sapiens serine protease-like protease (nes1) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481
 F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956
 50

- F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA806291
- F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
- F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536
- F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515
- F-MAMMA1002329//Homo sapiens clone 24444 RaP2 interacting protein 8 (RPIP8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026
- F-MAMMA1002332//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627
- F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254
- F-MAMMA1002339//H.sapiens mRNA for retrotransposon //3.2e-40:348:73//Hs.6940:Z48633
- F-MAMMA1002347//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591
- F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907
- F-MAMMA1002352//EST//1.7e-09:198:68//Hs.149218:AI247086
- F-MAMMA1002353//ESTs//7.4e-15:163:77//Hs.157253:AI357539
- F-MAMMA1002355//Homo sapiens KIAA0441 mRNA, complete cds//7.7e-47:307:78//Hs.32511:AB007901
- F-MAMMA1002356//ESTs//0.012:380:58//Hs.105349:AA779733
- F-MAMMA1002359//EST//1.1e-44:264:77//Hs.141095:H23818
- F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830
- F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923
- F-MAMMA1002362//EST//0.25:304:58//Hs.162427:AA576345
- F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677
- F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022
- F-MAMMA1002385//ESTs, Moderately similar to T11G6.8 [C.elegans]//8.4e-118:578:97//Hs.25516:AI086362
- F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624
- F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:AI142632
- F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W857
- 37
- F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745
- F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788
- F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030
- F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087
- F-MAMMA1002446
- 10 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809
- F-MAMMA1002461//Human diacylglycerol kinase (DACK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707
- F-MAMMA1002470
- F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779
- F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:N67059
- F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460
- F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
- F-MAMMA1002498//ESTs, Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920
- F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392
- F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214
- F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788
- F-MAMMA1002554
- F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822
- F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421
- F-MAMMA1002571//EST//0.28:115:66//Hs.156768:AI351368
- F-MAMMA1002573//ESTs//2.1e-48:265:94//Hs.155128:AI224516
- F-MAMMA1002585
- F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831
- F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:AI334107
- 50 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:

- 100//Hs. 153: X57958
 F-MAMMA1002603//EST//0.070: 99: 71//Hs. 122387: AA7892
 20
 F-MAMMA1002612//ESTs, Moderately similar to hCDC10
 protein [H. sapiens]//8.3e-18: 353: 65//Hs. 60895: AA4
 28463
 F-MAMMA1002617//B94 PROTEIN//0.0097: 229: 62//Hs. 755
 22: M92357
 F-MAMMA1002618
 F-MAMMA1002619
 F-MAMMA1002622//Homo sapiens advillin mRNA, comple
 te cds//4.7e-22: 157: 90//Hs. 47344: AF041449
 F-MAMMA1002623//EST//1.5e-33: 168: 81//Hs. 141526: N52
 300
 F-MAMMA1002625
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0507//1.1e-35: 355: 76//Hs. 158
 241: AB007976
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gen
 e, complete cds//1.9e-05: 439: 61//Hs. 91400: AB006626
 20
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47: 367: 7
 2//Hs. 117977: L04733
 F-MAMMA1002646//EST//1.2e-32: 302: 78//Hs. 112540: AA6
 01385
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08: 570: 63//Hs. 8
 2276: L09190
 F-MAMMA1002655//EST//8.8e-40: 198: 100//Hs. 159724: AI
 393335
 F-MAMMA1002662//EST//0.99: 95: 63//Hs. 144074: AI00548
 9
 F-MAMMA1002665//Lysosomal-associated membrane prot
 ein 2//1.8e-35: 722: 64//Hs. 8262: U36336
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor
 1C (p57, Kip2)//8.6e-06: 272: 64//Hs. 106070: U22398
 F-MAMMA1002673
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 pro
 tein, complete cds//1.2e-162: 752: 99//Hs. 3363: D8698
 7
 F-MAMMA1002685//ESTs//7.5e-40: 373: 78//Hs. 163937: N6
 9915
 F-MAMMA1002698//ESTs//2.5e-09: 190: 68//Hs. 138292: AI
 220397
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, comple
 te cds//4.7e-56: 398: 81//Hs. 22396: AF062085
 F-MAMMA1002701//ESTs//4.3e-10: 110: 80//Hs. 156041: AI
 274697
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2)fu
 cosytransferase, complete cds//1.1e-51: 307: 79//H
 s. 46328: D87942
 F-MAMMA1002711//EST//3.6e-38: 186: 77//Hs. 139715: N25
 50
 041
 F-MAMMA1002721//EST//3.9e-06: 110: 71//Hs. 136758: AA7
 14692
 F-MAMMA1002727//EST//0.97: 137: 63//Hs. 145153: AI1501
 65
 F-MAMMA1002728//ESTs, Highly similar to PAB-DEPEN
 DENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces c
 erevisiae]//2.6e-12: 129: 81//Hs. 154181: AA193502
 F-MAMMA1002744//ESTs//0.0026: 420: 58//Hs. 95793: AA61
 7853
 F-MAMMA1002746//ESTs//0.28: 117: 69//Hs. 12925: T66312
 F-MAMMA1002748
 F-MAMMA1002754//ESTs//1.1e-34: 340: 77//Hs. 163641: R6
 1848
 F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partia
 l cds//1.1e-27: 151: 98//Hs. 32168: AB007902
 F-MAMMA1002764//ESTs//1.7e-45: 323: 84//Hs. 155243: N7
 0293
 F-MAMMA1002765//EST//3.2e-11: 145: 73//Hs. 162551: AA5
 84782
 F-MAMMA1002769
 F-MAMMA1002775//Human ABL gene, exon 1b and intron
 1b, and putative M8604 Met protein (M8604 Met) g
 ene//7.6e-84: 417: 97//Hs. 77705: U07563
 F-MAMMA1002780//EST//0.78: 210: 63//Hs. 149413: AI2739
 88
 F-MAMMA1002782
 F-MAMMA1002796//ESTs//0.021: 122: 65//Hs. 132221: AI38
 0710
 30 F-MAMMA1002807//EST//1.0e-31: 184: 71//Hs. 161497: N66
 919
 F-MAMMA1002820//ESTs//0.21: 292: 59//Hs. 132513: AI378
 514
 F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 pro
 tein, complete cds//2.4e-57: 286: 88//Hs. 15731: AB011
 135
 F-MAMMA1002833//Human mRNA for KIAA0033 gene, part
 ial cds//9.1e-52: 583: 72//Hs. 22271: D26067
 F-MAMMA1002835
 40 F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQU
 INONE OXIDOREDUCTASE CHAIN 1 [Locusta migratoria]/
 //7.7e-38: 179: 78//Hs. 141344: H29951
 F-MAMMA1002842//ESTs//1.7e-19: 134: 89//Hs. 111583: AA
 463590
 F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 pro
 tein, partial cds//5.4e-137: 635: 99//Hs. 7531: AB0183
 53
 F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3
 [C. elegans]//1.6e-07: 329: 58//Hs. 107747: AI357868
 F-MAMMA1002858

- F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA7
67643
- F-MAMMA1002869//Human PINCH protein mRNA, complete
cds//7.0e-88:696:78//Hs.83987:U09284
- F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68
423
- F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:AI1
83632
- F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin
inhibitor, complete cds//3.8e-30:680:61//Hs.1297
32:D45027
- F-MAMMA1002886//Long (electrocardiographic) QT syn-
drome 2//0.00075:504:60//Hs.19944:U04270
- F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H916
57
- F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA61
2666
- F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R442
65
- F-MAMMA1002895//Human transcription factor ERF-1 m-
RNA, complete cds//0.00053:382:57//Hs.61796:U85658
- F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA22
4952
- F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA
176125
- F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA9237
30
- F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER
PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.1029
28:AI346344
- F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 pro-
tein, complete cds//1.6e-194:910:98//Hs.31720:AB01
4598
- F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:AI
423389
- F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:AI
313418
- F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial
cds//0.48:250:60//Hs.54697:AB007884
- F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA6
01400
- F-MAMMA1002972
- F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA
223932
- F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA6
04944
- F-MAMMA1002987//EST//0.044:254:59//Hs.135014:AI095
645
- F-MAMMA1003003//Coagulation factor III (thromboplastin,
tissue factor)//3.9e-22:185:83//Hs.62192:J02 50
- 931
- F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 spe-
cific transcript KIAA0501//1.0e-16:343:61//Hs.159
897:AB007970
- F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA5
30979
- F-MAMMA1003011//Homo sapiens histone macroH2A1.2 m-
RNA, complete cds//6.2e-51:620:69//Hs.75258:AF0541
74
- F-MAMMA1003013//Human HOX4C mRNA for a homeobox pr-
otein//0.73:347:58//Hs.74061:X59372
- F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73
062
- F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:AI37
4951
- F-MAMMA1003026//EST//1.0:136:67//Hs.9123:T50137
- F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA6
69549
- F-MAMMA1003035
- F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83
391
- F-MAMMA1003040//Homo sapiens tapasin (NCS-17) mRN-
A, complete cds//1.5e-93:339:85//Hs.5247:AF029750
- F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D1
3639
- F-MAMMA1003047//H.sapiens mRNA for F25B3.3 kinase
like protein from C.elegans//1.0:209:60//Hs.99491:
Y12336
- F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA6017
30 42
- F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R6
8518
- F-MAMMA1003056
- F-MAMMA1003057//ESTs, Moderately similar to hypoth-
etical protein MD6 [M.musculus]//1.3e-88:334:97//Hs.
96500:AI206781
- F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:AI0226
18
- F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 pro-
tein, partial cds//4.5e-51:329:71//Hs.75154:AB0145
31
- F-MAMMA1003099//Homo sapiens actin-binding protein
homolog ABP-278 mRNA, complete cds//8.5e-44:288:88
//Hs.81008:AF043045
- F-MAMMA1003104//H.sapiens mRNA for ASM-like phospho-
diesterase 3a//1.0:213:60//Hs.42945:Y08136
- F-MAMMA1003113//Homo sapiens mRNA for hair keratin
acidic 3-II//0.99:200:64//Hs.32950:X82634
- F-MAMMA1003127//Homo sapiens brush border myosin I
(BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.539

- 4: AF105424
 F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786
 F-MAMMA1003140
 F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062
 F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:AB011087
 F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632
 F-NT2RM1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204
 F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-66:385:92//Hs.82510:D31886
 F-NT2RM1000032
 F-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782
 F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:AB014590
 F-NT2RM1000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204
 F-NT2RM1000055//ESTs, Highly similar to TIP120 [R. norvegicus]//3.2e-69:353:96//Hs.154980:AA948067
 F-NT2RM1000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//Hs.46465:U45285
 F-NT2RM1000062//ESTs//0.30:368:59//Hs.131675:AA843210
 F-NT2RM1000080//Homo sapiens chromosome 9, P1 clone 11659//2.8e-102:493:97//Hs.3439:AC004472
 F-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:AB014561
 F-NT2RM1000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689
 F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:AF007155
 F-NT2RM1000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054
 F-NT2RM1000127
 F-NT2RM1000131
 F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959
 F-NT2RM1000153//Homo sapiens mRNA for MTC8-related protein MTC16a, complete cds//1.0:546:58//Hs.1100
 99: AB010419
 F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:AF007155
 F-NT2RM1000187//ESTs//3.4e-79:400:96//Hs.54971:AI424382
 F-NT2RM1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458
 F-NT2RM1000242
 F-NT2RM1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105
 F-NT2RM1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190
 F-NT2RM1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516
 F-NT2RM1000257//ESTs, Highly similar to similar to mago nashi [H. sapiens]//2.9e-98:530:93//Hs.104650:AI037879
 F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920
 F-NT2RM1000271//ESTs//0.93:224:60//Hs.91226:AA649047
 F-NT2RM1000272
 F-NT2RM1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D[Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144
 F-NT2RM1000300
 F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880
 F-NT2RM1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205
 F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976
 F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798
 F-NT2RM1000355//ESTs, Weakly similar to putative [M. musculus]//7.7e-75:387:95//Hs.108619:W28608
 F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691
 F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H. sapiens]//7.4e-91:481:95//Hs.163707:AA137181
 F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.8939:X80507
 F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353
 F-NT2RM1000399
 F-NT2RM1000421
 F-NT2RM1000430//Homo sapiens erythroblast macrophage

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ge protein EMP mRNA, complete cds//1.2e-85:418:97//
/Hs.20815:AF084928
F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 p
rotein [H.sapiens]//1.6e-38:201:97//Hs.106262:AI05
2382
F-NT2RM1000539//EST//0.070:145:62//Hs.149711:AI284
660
F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA44
9847
F-NT2RM1000555//ESTs//0.82:193:61//Hs.96944:AI3599 10
57
F-NT2RM1000563//Human plectin (PLEC1) mRNA, comple
te cds//1.0:336:58//Hs.79706:U53204
F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gen
e, partial cds//0.98:226:61//Hs.17931:AB006625
F-NT2RM1000648//ESTs, Weakly similar to similar to
M. musculus MER5 and other AHPC/TSA proteins [C.el
egans]//6.2e-51:254:98//Hs.132096:AA314601
F-NT2RM1000661//Homo sapiens translation initiatio
n factor 4e mRNA, complete cds//8.5e-55:276:97//H 20
s.19122:AF038957
F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete
cds//0.87:274:60//Hs.113936:AB005297
F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI1
88279
F-NT2RM1000672
F-NT2RM1000691//Homa sapiens mRNA for HRIHFB2060,
partial cds//7.0e-121:582:98//Hs.146282:AB015348
F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA7
15101
F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA
564706
F-NT2RM1000725//Homo sapiens mRNA for neuropathy t
arget esterase//1.5e-66:435:85//Hs.5038:AJ004832
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 pro
tein, partial cds//2.6e-127:690:92//Hs.147946:AB01
1139
F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, c
omplete cds//8.2e-68:524:83//Hs.112360:AF027208
F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA8 40
45465
F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, comple
te cds//3.3e-09:321:63//Hs.150390:AB007885
F-NT2RM1000772//Eukaryotic translation initiation
factor 3 (eIF-3). p36 subunit//0.053:271:60//Hs.139
745:U39067
F-NT2RM1000780//Human Line-1 repeat mRNA with 2 op
en reading frames//6.9e-20:128:94//Hs.23094:M19503
F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50
845

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F-NT2RM1000800
F-NT2RM1000802
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, c
omplete cds//1.2e-64:490:84//Hs.112360:AF027208
F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI3599
57
F-NT2RM1000829//Mannose-binding lectin, soluble (o
psonic defect)//0.92:283:58//Hs.2314:X15422
F-NT2RM1000833//Hydroxysteroid (11-beta) dehydroge
nase 2//0.022:178:67//Hs.1376:U26726
F-NT2RM1000850//Human protein tyrosine kinase rela
ted mRNA sequence//3.8e-06:384:59//Hs.90314:L05148
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependen
t RNA helicase, partial//3.0e-149:726:97//Hs.9942
3:AJ010840
F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447
643
F-NT2RM1000867//ESTs, Highly similar to signal pep
tidase:SUBUNIT//5.3e-54:277:96//Hs.11125:AI015619
F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442
239
F-NT2RM1000882//Homo sapiens chromosome 11, BAC CI
T-HSP-311e8 (BC269730) containing the hFEN1 gene//
4.0e-155:750:97//Hs.132898:AC004770
F-NT2RM1000883//Homo sapiens I-1 receptor candidat
e protein mRNA, complete cds//8.8e-158:762:97//Hs.
26285:AF082516
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 pro
tein, complete cds//6.3e-19:310:67//Hs.65238:AB014
561
F-NT2RM1000894
F-NT2RM1000898
F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI26
8701
F-NT2RM1000924//HOMEBOX PROTEIN HOX-A5//0.00051:4
58:59//Hs.37034:M26679
F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 pro
tein, partial cds//0.084:386:58//Hs.101474:AB01835
0
F-NT2RM1000962//Human mRNA for KIAA0252 gene, part
ial cds//0.98:299:59//Hs.83419:D87440
F-NT2RM1000978
F-NT2RM1001003//Homo sapiens alpha-catenin related
protein (ACRP) mRNA, complete cds//1.3e-161:760:98
//Hs.58488:U97067
F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI
025200
F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395
F-NT2RM1001044//ESTs, Weakly similar to C43E11.9
50 [C.elegans]//3.0e-98:491:96//Hs.102173:AA045270

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F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:533:57//Hs.79706:U53204
 F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:A1380703
 F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//0.69:586:56//Hs.62354:M83822
 F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846
 F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198
 F-NT2RM1001085
 F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.74107:X59244
 F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331
 F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:U10564
 F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495
 F-NT2RM1001115
 F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074
 F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113
 F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:640:59//Hs.148027:X63563
 F-NT2RM2000030
 F-NT2RM2000032//ESTs//7.1e-18:138:68//Hs.114031:AA700958
 F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243
 F-NT2RM2000092
 F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085
 F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428
 F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//5.8e-46:287:88//Hs.77271:X07767
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//3.0e-139:566:97//Hs.18953:AF067223
 F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999
 F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-93:489:95//Hs.143499:R72672
 F-nnnnnnnnnnnn//ESTs//1.0e-70:269:97//Hs.156175:AI334328
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.0e-129:615:98//Hs.111862:ABO11162

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F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520
 F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500
 F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981
 F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54434:U51127
 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds//2.8e-176:805:99//Hs.129952:ABO11132
 F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds//3.7e-96:599:86//Hs.75871:U48251
 F-NT2RM2000371
 F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866
 20 F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L13698
 F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.28757:U81006
 F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582
 F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053
 F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transporter, serotonin), member 4//1.5e-06:260:61//Hs.553:L05568
 30 F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379
 F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.4e-16:386:63//Hs.8309:ABO18290
 F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA, complete cds//0.99:272:61//Hs.76669:U08021
 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//1.6e-172:824:97//Hs.4812:AF061243
 F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.18:313:60//Hs.129725:AF047487
 F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.7e-41:231:94//Hs.7049:AI141736
 F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220
 50

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F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs. 74369:AF032108
 F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs. 89631:U48508
 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs. 158277:HO9128
 F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs. 55609:W37993
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs. 3363:D86987
 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs. 136990:AA769220
 F-NT2RM2000594
 F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs. 102402:AF040963
 F-NT2RM2000609//ESTs//1.0:220:59//Hs. 110155:AA007313
 F-NT2RM2000612//ESTs//0.97:208:59//Hs. 73217:AA846548
 F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs. 6150:AB011093
 F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs. 145904:AA203258
 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs. 19542:AB018272
 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs. 7278:AB014558
 F-NT2RM2000639//ESTs//0.98:144:65//Hs. 154364:AI189702
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs. 115763:AB014576
 F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs. 156342:AI337371
 F-NT2RM2000691//Homo sapiens actin-related protein 40 Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs. 5321:AF006083
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs. 7938:D86984
 F-NT2RM2000718//Homo sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs. 136058:AB015342
 F-NT2RM2000735//Zinc finger protein 43 (HTF6)//2.7e-112:756:82//Hs. 74107:X59244
 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASEIN ALC7-ENP1 INTERGENIC REGIO

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N [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs. 161551:W24286
 F-NT2RM2000795//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.0e-82:640:81//Hs. 5247:AF029750
 F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:679:59//Hs. 105919:AB002338
 F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs. 101514:AI346701
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs. 137580:AB015046
 F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs. 59075:AI023761
 F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:351:62//Hs. 84753:D87433
 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs. 36049:AA436831
 F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs. 17035:AI080471
 F-NT2RM2001065
 F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs. 75111:D87258
 F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs. 102732:U88153
 F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs. 82276:L09190
 F-NT2RM2001141
 F-NT2RM2001152//ESTs//0.53:333:58//Hs. 153087:AA649042
 F-NT2RM2001177
 F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs. 10618:AI288739
 F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs. 59628:W91959
 F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs. 155291:D13630
 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs. 24279:AB018349
 F-NT2RM2001238//EST//6.8e-67:420:89//Hs. 130586:AI004766
 F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs. 75889:U65928
 F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs. 132206:AF039694
 F-NT2RM2001256
 F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs. 10267:W27

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F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601

F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615

F-NT2RM2001319//ESTs, Weakly similar to No definitive line found [C.elegans]//5.2e-30:277:77//Hs.25347:AI138605

F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567

F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706

F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905

F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:224:61//Hs.82925:U70322

F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382

F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378

F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-97:453:99//Hs.155218:AJ007509

F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303

F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903

F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969

F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459

F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262

F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//6.9e-28:582:64//Hs.1042:M62800

F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077

F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902

F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:AI391729

F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:749:75//Hs.76272:S66431

F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:AI393918

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F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518

F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:AI276952

F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725

F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073

F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301

F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287

F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195

F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907

F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129

F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:AI365356

F-NT2RM2001675

F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305

F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211

F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA35216

F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937

F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:AI277415

F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:AI003817

F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826

F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788

F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650

F-NT2RM2001718

F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:163:95//Hs.12457:AF052123

50 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 pro

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tein, partial cds//2.0e-112:530:98//Hs.129937:AB007931
 F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132
 F-NT2RM2001743
 F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399
 F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.131840:AI016073
 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:AI222742
 F-NT2RM2001771//Zinc finger protein 10 (KIX 1)//1.1e-66:669:71//Hs.2479:X78933
 F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698
 F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:AI193595
 F-NT2RM2001785//Homo sapiens chromosome 11, BAC ClonT-HSP-311e8 (BC269730)containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770
 F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-66:481:72//Hs.70617:D31763
 F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, complete cds//0.49:142:66//Hs.78202:U29175
 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195
 F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341
 F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068
 F-NT2RM2001823//H. sapiens mRNA for 218kD Mi-2 protein//9.7e-21:554:60//Hs.74441:X86691
 F-NT2RM2001839//Homo sapiens calumecin (Calu) mRNA, complete cds//1.2e-132:738:90//Hs.7753:AF013759
 F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8e-58:329:86//Hs.113283:AF018080
 F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:M57567
 F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C. elegans]//3.0e-28:421:66//Hs.8763:W30741
 F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723
 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds//6.1e-189:866:97//Hs.4198:AB014610
 F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and

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IMAGE 45355 and LLNLc110113307 (RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892
 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds//9.4e-178:859:97//Hs.129937:AB007931
 F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete cds//4.2e-08:481:59//Hs.27621:U52840
 F-NT2RM2001935//ESTs, Highly similar to MULTIDrug RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U66688
 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequence//2.2e-139:653:98//Hs.21811:AF091080
 F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392
 F-NT2RM2001982
 F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, partial cds//1.2e-21:123:98//Hs.6454:AF089816
 F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//Hs.104135:AJ006778
 F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538
 F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H. sapiens]//0.99:271:60//Hs.63888:AA203398
 F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cds//3.5e-37:509:65//Hs.6214:AB018274
 F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//0.79:429:58//Hs.79090:D89729
 F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-89:822:73//Hs.1674:M90516
 F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427
 F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154
 F-NT2RM2002088//ESTs//6.1e-75:302:96//Hs.153471:AI198377
 F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//Hs.89631:U48508
 F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.5e-165:776:98//Hs.99423:AJ010840
 F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435
 F-NT2RM2002128
 F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274
 F-NT2RM2002145//Homo sapiens erythroblast macrophage

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ge protein EMP mRNA, complete cds//1.4e-144:800:92
//Hs.20815:AF084928

F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 pro
tein, partial cds//1.7e-165:787:97//Hs.11147:AB007
936

F-NT2RM2002580//Keratin 10 (epidermolytic hyperker
atosis; keratosis palmaris et plantaris)//0.064:29
1:61//Hs.99936:X14487

F-NT2RM4000024//RNA polymerase II polypeptide B (1
40 kD)//8.0e-10:610:59//Hs.148027:X63563

F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93
074

F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI3914
64

F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI
094674

F-NT2RM4000061//ESTs//0.89:207:60//Hs.98445:AI0385
11

F-NT2RM4000085//ESTs, Weakly similar to The KIAA01
34 gene product is related to human RNA helicase
A. [H.sapiens]//1.6e-30:369:70//Hs.114623:AI204280
F-NT2RM4000086

F-NT2RM4000104//Homo sapiens chromosome 16 zinc fi
nger protein ZNF210 (ZNF210) mRNA, complete cds//
1.3e-24:345:69//Hs.13128:AF060865

F-NT2RM4000139

F-NT2RM4000155

F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:A
A573632

F-NT2RM4000167//Homo sapiens kinesin family member
protein KIF3A mRNA, complete cds//9.8e-30:676:61/
/Hs.159228:AF041853

F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA
497044

F-NT2RM4000191//TRICHOHYALIN//0.011:324:60//Hs.822
76:L09190

F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W2
7744

F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU S
UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.13:32
2:61//Hs.145088:AI221147

F-NT2RM4000200

F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gen
e, complete cds//0.0027:424:60//Hs.91400:AB006626

F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 pro
tein, complete cds//4.4e-184:856:98//Hs.111138:AB0
18255

F-NT2RM4000215//SET translocation (myeloid leukem
ia-associated)//0.0013:358:60//Hs.75055:M93651

F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 pro 50

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tein, complete cds//0.65:572:60//Hs.47061:AF045458
F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T3
3582

F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA5734
39

F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTE
IN [Schizosaccharomyces pombe]//1.1e-16:112:92//H
s.93841:AA442297

F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fu
cosyltransferase, complete cds//1.8e-48:229:83//H
s.46328:D87942

F-NT2RM4000290//Human transducin-like enhancer pro
tein (TLE3) mRNA, complete cds//2.5e-154:609:93//H
s.31305:M99438

F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-r
eceptor, complete cds//0.070:460:59//Hs.5372:AB000
712

F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:AI24
0707

F-NT2RM4000344//ESTs, Highly similar to YME1 PROT
EIN [Saccharomyces cerevisiae]//2.7e-83:432:95//H
s.12796:W27884

F-NT2RM4000349//Human mRNA for KIAA0005 gene, comp
lete cds//5.2e-53:666:68//Hs.155291:D13630

F-NT2RM4000354//ESTs, Weakly similar to lethal (2)d
enticleless [D.melanogaster]//0.0078:55:92//Hs.590
75:AI023761

F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:AI4184
25

F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 pro
tein, partial cds//5.3e-135:628:99//Hs.8152:AB0145
42

F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA
662745

F-NT2RM4000386//Human DNA sequence from clone 1052
M9 on chromosome Xq25. Contains the SH2D1A gene for
SH2 domain protein 1A, Duncan's disease (lymphopr
oliferative syndrome) (DSHP), part of a 60S Acidic
Ribosomal protein 1 (RPLP1) LIKE gene and part of
a mouse DOC4 LIKE gene. Contains ESTs and
GSSs//2.0e-72:843:68//Hs.
23796:AL022718

F-NT2RM4000395//Nitric ox
ide synthase 2A (inducibl
e, hepatocytes)//0.63:16
6:65//Hs.946:X73029

F-NT2RM4000414//Homo sapi
ens XYLB mRNA for xylulok
inase, complete cds//4.9e
-17:114:94//Hs.137580:AB0

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15046

F-NT2RM4000421

F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.1e-42:432:74//Hs. 154872:AB011166

F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)//0.023:543:58//Hs. 2175:M59820

F-NT2RM4000457

F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRNA, complete cds//0.060:178:63//Hs. 66369:U95040

F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs. 160685:AF280004

F-NT2RM4000496//ESTs//0.069:252:61//Hs. 155958:AA573632

F-NT2RM4000511//EST//0.92:191:58//Hs. 61517:AA028915

F-NT2RM4000514

F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs. 120975:AA034409

F-NT2RM4000520//ESTs//0.13:183:65//Hs. 144828:AI221305

F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.8e-153:756:96//Hs. 125870:AI364967

F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs. 105665:H78987

F-NT2RM4000534

F-NT2RM4000585

F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete cds//1.2e-19:593:62//Hs. 7764:AB007938

F-NT2RM4000595//ESTs, Highly similar to HYPOTHETI

CAL 54.9 KD PROTEIN C02F 5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:532:96//Hs. 6092:T75227

F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-15:305:68//Hs. 40100:AB002390

F-NT2RM4000611//EST//0.76:268:58//Hs. 150031:AI292068

10 F-NT2RM4000616

F-NT2RM4000674

F-NT2RM4000689

F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs. 76260:M12529

F-NT2RM4000700

F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs. 42400:AF022789

20 F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771:97//Hs. 6823:W18181

F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs. 957:M84605

F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-159:743:98//Hs. 137168:AB018303

F-NT2RM4000741

30 F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs. 112361:R99396

F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs. 24739:H67815

F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs. 99838:AA204731

F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//1.8e-173:810:98//Hs. 18586:AB007920

F-NT2RM4000787//EST//0.011:182:65//Hs. 159928:AA969186

40 F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-156:736:98//Hs. 25817:AC005306

F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PRECURSOR [Homo sapiens]//6.7e-19:160:80//Hs. 124902:AI337820

F-NT2RM4000796//Human K⁺ channel subunit gene, complete cds//0.96:292:62//Hs. 124212:M64676

F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs. 128203:AA972301

F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete

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cds//0.052:238:64//Hs.113265:AF032387
 F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H1656
 8
 F-NT2RM4000833
 F-NT2RM4000848//Human mRNA for KIAA0324 gene, part
 ial cds//0.97:374:61//Hs.7841:AB002322
 F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA71893
 4
 F-NT2RM4000855//ESTs, Highly similar to RAS-RELAT
 ED C3 BOTULINUM TOXINSUBSTRATE 2 [Homo sapiens]// 10
 4.4e-29:164:95//Hs.115095:AI392943
 F-NT2RM4000887
 F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N
 -acetylglucosamine pyrophosphorylase, complete cds
 //6.8e-22:407:64//Hs.21293:AB011004
 F-NT2RM4000950
 F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:A
 I014546
 F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, comple
 te cds//3.7e-63:571:77//Hs.7289:AB007875 20
 F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7
 e-34:381:67//Hs.2481:X78926
 F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 pro
 tein, partial cds//1.6e-171:803:98//Hs.19542:AB018
 272
 F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 pro
 tein, partial cds//1.1e-126:584:99//Hs.15711:AB014
 539
 F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 pro
 tein, complete cds//4.8e-05:469:58//Hs.5333:AB0182 30
 54
 F-NT2RM4001047//ESTs, Moderately similar to M025 P
 ROTEIN [M.musculus]//7.0e-56:340:92//Hs.87310:AI24
 7543
 F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA
 FC RECEPTOR I "A FORM" PRECURSOR//0.79:142:69//H
 s.77424:M63835
 F-NT2RM4001084
 F-NT2RM4001092//Human mRNA for KIAA0050 gene, comp
 lete cds//0.045:235:62//Hs.108947:D30758 40
 F-NT2RM4001116
 F-NT2RM4001140//Human engrailed protein (EN2) gen
 e, 5' end//0.00029:225:61//Hs.134989:L12701
 F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA
 443730
 F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:AI
 004145
 F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA6773
 51
 F-NT2RM4001187

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F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18
 220
 F-NT2RM4001200//Zinc finger protein 10 (K0X 1)//4.
 0e-68:799:69//Hs.2479:X78933
 F-NT2RM4001203//Homo sapiens rab3-GAP regulatory d
 omain mRNA, complete cds//1.4e-153:707:99//Hs.1493
 4:AF004828
 F-NT2RM4001204//ESTs, Moderately similar to HYPOT
 HETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III
 [Caenorhabditis elegans]//0.19:291:62//Hs.31582:AA
 877205
 F-NT2RM4001217//Homo sapiens nuclear matrix protei
 n NRP/B (NRPB) mRNA, complete cds//7.0e-63:715:70/
 /Hs.104925:AF059611
 F-NT2RM4001256//ESTs, Weakly similar to probable C
 BP3 protein homolog [C.elegans]//1.1e-67:208:96//H
 s.26676:AA033997
 F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 pro
 tein, complete cds//0.0019:435:59//Hs.6360:AB00795
 20 0
 F-NT2RM4001309//Human Chromosome 16 BAC clone CIT9
 87SK-254P9//0.019:356:59//Hs.26971:AC003003
 F-NT2RM4001313//H.sapiens mRNA for phosphatidylinos
 itol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973
 F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA
 258335
 F-NT2RM4001320//Human mRNA for Neuroblastoma, comp
 lete cds//3.6e-43:642:66//Hs.87435:D89016
 F-NT2RM4001340//EST//0.40:135:70//Hs.161198:AI4189
 88
 F-NT2RM4001344//ESTs, Highly similar to HYPOTHETI
 CAL GTP-BINDING PROTEIN IN PMI40-PAC2 INTERGENIC R
 EGION [Saccharomyces cerevisiae]//0.0096:284:58//H
 s.120997:R56714
 F-NT2RM4001347//ESTs, Weakly similar to weakly sim
 ilar to ANK repeat region of Fowlpox virus BamHI-o
 rf7 protein [C.elegans]//3.7e-52:252:100//Hs.1530
 1:AA167818
 F-NT2RM4001371//EST//0.52:262:59//Hs.145991:AI2776
 40 56
 F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRN
 A, complete cds//7.2e-169:790:98//Hs.5151:AF098799
 F-NT2RM4001384
 F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA1
 60575
 F-NT2RM4001411//Homo sapiens mRNA for APS, complet
 e cds//2.5e-23:475:64//Hs.105052:AB000520
 F-NT2RM4001412
 F-NT2RM4001414//ESTs, Moderately similar to F18547
 50 _1 [H.sapiens]//5.2e-18:133:87//Hs.28209:AI073817

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F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-42:611:70//Hs.154326:D42087

F-NT2RM4001444

F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658

F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914

F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784

F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//3.9e-157:724:99//Hs.153121:AB014585

F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619

F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.cerevisiae]//1.3e-114:536:99//Hs.88820:AA456247

F-NT2RM4001557

F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487

F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453

F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:AI198859

F-NT2RM4001582

F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566

F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0072:484:60//Hs.129892:AB011094

F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2.3e-72:387:95//Hs.114722:AA448077

F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//1.1e-163:750:99//Hs.23255:AB018334

F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e-05:91:79//Hs.24647:W19739

F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEMBRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:AI147946

F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:328:60//Hs.101761:AB002339

F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-83:449:93//Hs.153685:AB002320

F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323

F-NT2RM4001682//EST//0.027:145:70//Hs.133253:AI052638

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F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384

F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-86:748:74//Hs.80712:D86957

F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:AI332905

F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M13903

10 F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-80:737:73//Hs.150443:AB002318

F-NT2RM4001746//H.sapiens NF-H gene, exon 1 (and joined CDS)//2.1e-07:418:61//Hs.75735:X15306

F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719

F-NT2RM4001758//H.sapiens mRNA for serine/threonine protein kinase EMK//2.1e-86:729:75//Hs.157199:X97630

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//7.4e-175:803:99//Hs.39871:AB018270

F-NT2RM4001783//ESTs, Weakly similar to T12D8.1 [C.elegans]//3.1e-71:376:95//Hs.108396:AA160677

F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105

F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:249:70//Hs.146312:AF070547

F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712

F-NT2RM4001823//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.3e-40:252:90//Hs.119294:AI379442

F-NT2RM4001828//Zinc finger protein 157 (HZF22)//1.8e-75:688:72//Hs.89897:U28687

F-NT2RM4001836//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824

F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:AI214204

40 F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814

F-NT2RM4001856

F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//2.3e-150:704:98//Hs.61628:Y17711

50 F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984

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- F-NT2RM4001880
 F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:AI204212
 F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:AI312633
 F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875
 F-NT2RM4001938
 F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162
 F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087
 F-NT2RM4001965//ESTs, Weakly similar to KIAA0157 gene product is novel. [H.sapiens]//1.8e-65:337:96//Hs.130135:AA905493
 F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:AI312862
 F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341
 F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082
 F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936
 F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:AI302271
 F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601
 F-NT2RM4002034
 F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048
 F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912
 F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540
 F-NT2RM4002062//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:AI126802
 F-NT2RM4002063
 F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309
 F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040
 F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302
 F-NT2RM4002075//Homo sapiens actin binding protein 50
 MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569
 F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) {alternative products}//9.2e-34:532:65//Hs.146459:X66975
 F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743
 F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542
 F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877
 F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158
 F-NT2RM4002146//ESTs, Highly similar to similar to mago nashi [H.sapiens]//1.6e-135:646:97//Hs.104650:AI037879
 F-NT2RM4002161//Homo sapiens laforin (EPW2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535
 F-NT2RM4002174
 F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998
 F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276
 F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454
 F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182
 F-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984
 F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966
 F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:AI205764
 F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118
 F-NT2RM4002278//EST//0.33:138:63//Hs.144096:AI032180
 F-NT2RM4002281
 F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
 F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457
 F-NT2RM4002301
 F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:AI343331
 F-NT2RM4002339
 F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA9064

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F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549
F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263
F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293
F-NT2RM4002390
F-NT2RM4002398
F-NT2RM4002409
F-NT2RM4002438//ESTs, Weakly similar to probable C BP3 protein homolog [C.elegans]//1.1e-55:282:96//Hs.26676:AA033997
F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151
F-NT2RM4002452
F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783
F-NT2RM4002460//EST//1.0:142:65//Hs.145370:AI252780
F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, completecds//8.9e-165:777:98//Hs.8765:AF083255
F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591
F-NT2RM4002493
F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347
F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219
F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, completecds//0.99:290:60//Hs.154968:U02020
F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075
F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176
F-NT2RM4002558//Homo sapiens amphipysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004
F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273
F-NT2RM4002567//ESTs, Weakly similar to C17G10.1 [C.elegans]//3.3e-88:484:93//Hs.105837:AA536054
F-NT2RM4002571//ESTs, Weakly similar to UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase [H.sapiens]//0.059:121:70//Hs.155413:AA429394
F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275
F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587
F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449
F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
F-NT2RP1000101//Homo sapiens hook2 protein (H00K2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924
F-NT2RP1000111
F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:AI084025
F-NT2RP1000130//ESTs, Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H.sapiens]//1.4e-71:382:94//Hs.127842:W38901
F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792
F-NT2RP1000170//EST//0.68:130:63//Hs.146994:AI184430
F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535
F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
F-NT2RP1000202//H.sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703
F-NT2RP1000243
F-NT2RP1000259
F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.4214:AF067730
F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661

- F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551
- F-NT2RP1000333//Homo sapiens monocyte/macrophage I g-related receptor MIR-10 (MIR cl-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231
- F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204
- F-NT2RP1000357
- F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07 10 807
- F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014 538
- F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96 //Hs.120360:AF064594
- F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA 828031
- F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 pro 20 tein, complete cds//3.0e-179:710:98//Hs.21862:AB01 1159
- F-NT2RP1000416//ESTs, Highly similar to BONE MORP HOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e -177:857:97//Hs.6823:W18181
- F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNN3)mRNA, complete cds//0.46:22 2:60//Hs.89230:AF031815
- F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA1016 03
- F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862
- F-NT2RP1000460
- F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R27090, genomic sequence//3.7e-134:665: 96//Hs.143187:AC002985
- F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//H s.159154:U47634
- F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA5 40 35102
- F-NT2RP1000493
- F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA 480977
- F-NT2RP1000522//Homo sapiens clone DT1P1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992
- F-NT2RP1000547//H.sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098
- F-NT2RP1000574//Homo sapiens homeobox protein MEIS 2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.10 50 90
- 4105:AF017418
- F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213
- F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR// 1.6e-33:223:89//Hs.110802:X04385
- F-NT2RP1000609//Homo sapiens chromosome 11, BAC CI T-HSP-311e8 (BC269730)containing the hFEN1 gene// 2.2e-49:506:73//Hs.132898:AC004770
- F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, completecds//3.6e-19:556:62//Hs.1529 36:D63475
- F-NT2RP1000630
- F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:389:59//Hs.3844:U245 76
- F-NT2RP1000688//ESTs, Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
- F-NT2RP1000695//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:AI 141736
- F-NT2RP1000701//Myogenic factor 3//0.81:186:63//H s.2834:AF027148
- F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D3061 2
- F-NT2RP1000730//ESTs, Weakly similar to putative p 150 [H.sapiens]//6.2e-40:297:84//Hs.18122:AI338045
- F-NT2RP1000733//G1 to S phase transition 1//1.4e-3 1:286:78//Hs.2707:X17644
- 30 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds //2.6e-123:604:96//Hs.21771:AF101434
- F-NT2RP1000746
- F-NT2RP1000767
- F-NT2RP1000782//Human globin gene//3.6e-21:140:91/ /Hs.100090:M69023
- F-NT2RP1000796//H.sapiens mRNA for ROX protein//0. 17:404:57//Hs.25497:X96401
- F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTP ase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:91//Hs.102336:Z83838
- F-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96// Hs.18953:AF067223
- F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:AI332 903
- F-NT2RP1000836//EST//0.60:103:66//Hs.145708:AI2679 90

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F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:AI28838
 F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875
 F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094
 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:AI218683
 F-NT2RP1000915//ESTs//8.8e-11:102:81//Hs.163740:AI248847
 F-NT2RP1000916//ESTs, Weakly similar to coded for by *C. elegans* cDNA cm04e9 [*C. elegans*]//2.2e-27:159:94//Hs.122153:AA780270
 F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248
 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400
 F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U39317
 F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803
 F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:AI248847
 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885
 F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M60858
 F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:N28866
 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435
 F-NT2RP1001011
 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:AI089163
 F-NT2RP1001014
 F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764
 F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901
 F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:AI360531
 F-NT2RP1001080//Homo sapiens forkhead protein (FKHL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886
 F-NT2RP1001113//ESTs, Weakly similar to coded for by *C. elegans* cDNA CEESB82F [*C. elegans*]//1.4e-65:293:95//Hs.32751:H38087

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F-NT2RP1001173
 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174
 F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524
 F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:AI022150
 F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523
 F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:AI337094
 F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231
 F-NT2RP1001286//H.sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724
 F-NT2RP1001294
 F-NT2RP1001302
 F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341
 F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:H67815
 F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770
 F-NT2RP1001361//ESTs, Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [*Bos taurus*]//6.8e-101:480:94//Hs.75017:AA166853
 F-NT2RP1001385//EST//0.86:127:65//Hs.156304:AI336859
 F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673
 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081
 F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700
 F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149
 F-NT2RP1001457//H.sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
 F-NT2RP1001466
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
 F-NT2RP1001482
 F-NT2RP1001494
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:AI

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F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277

F-NT2RP1001569

F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, partial cds//2.5e-41:496:74//Hs.12956:U90913

F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420

F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA 10 A, complete sequence//4.7e-137:685:96//Hs.93677:AF091081

F-NT2RP2000006//ESTs, Weakly similar to B0035.14 [C.elegans]//8.2e-47:300:89//Hs.6473:AA853955

F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390

F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763

F-NT2RP2000027//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-2 20 6:214:82//Hs.140385:AA773359

F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:AI038867

F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290

F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749

F-NT2RP2000054//HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1/ 30 /1.0:110:70//Hs.74095:L20433

F-NT2RP2000056//Human HPTP epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134

F-NT2RP2000067//Human DNA sequence from clone 1052 M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs// 40 8.1e-41:767:61//Hs.23796:AL022718

F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203013 (LBNL H155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609

F-NT2RP2000076//H. sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887

F-NT2RP2000077//Homo sapi 50

ens. growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078

F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:AI279879

F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338

F-NT2RP2000091

F-NT2RP2000097

F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:AI371963

F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390

F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356

F-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670

F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA A, complete cds//1.4e-120:607:96//Hs.159273:AF054177

F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195

F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475

F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910

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F-NT2RP2000157//ESTs//0.5
 3:75:81//Hs. 24885:R49291
 F-NT2RP2000161//ESTs//2.6
 e-06:89:84//Hs. 21738:AI18
 8190
 F-NT2RP2000173
 F-NT2RP2000175
 F-NT2RP2000183//Homo sapiens mRNA for dihydropyrim
 idinase related protein 4, complete cds//0.0018:32
 4:58//Hs. 100058:AB006713
 F-NT2RP2000195//ESTs, Weakly similar to C37E2.2
 [C.elegans]//3.6e-37:233:90//Hs. 56750:AI148761
 F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs. 49559:AA
 01050
 F-NT2RP2000208
 F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL
 receptor related protein 105, complete cds//0.007
 1:243:61//Hs. 143641:AB009462
 F-NT2RP2000232//EST//0.0087:187:62//Hs. 151024:Z399
 90
 F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA,
 complete cds//0.17:342:59//Hs. 8546:U97669
 F-NT2RP2000239//Human mRNA for KIAA0380 gene, comp
 lete cds//1.0:227:60//Hs. 47822:AB002378
 F-NT2RP2000248//EST//0.49:117:70//Hs. 61016:AA01971
 9
 F-NT2RP2000257//Macrophage stimulating 1 (hepatocy
 te growth factor-like)//0.51:227:60//Hs. 30223:X908
 46
 F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs. 128230:AA
 972691
 F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs. 140329:AA
 714011
 F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs. 47646:AA
 307599
 F-NT2RP2000283//EST//1.0:139:63//Hs. 128256:AA97291
 0
 F-NT2RP2000288
 F-NT2RP2000289
 F-NT2RP2000297//Human repressor transcriptional fa
 ctor (ZNF85) mRNA, complete cds//4.2e-60:744:70//H
 s. 37138:U35376
 F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs. 159490:AI
 123467
 F-NT2RP2000310//Human proline dehydrogenase/prolin
 e oxidase (PRODH) mRNA, complete cds//4.3e-13:140:
 80//Hs. 58218:U82381
 F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs. 126212:AI
 417006
 F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs. 127336:AI

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332905
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHO
 NDRIAL//6.6e-41:607:66//Hs. 101642:X60673
 F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRN
 A, complete cds//0.96:126:69//Hs. 153706:AF026547
 F-NT2RP2000346//Homo sapiens apoptosis associated
 protein (GADD34) mRNA, complete cds//1.2e-130:627:9
 7//Hs. 76556:U83981
 F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 pro
 tein, partial cds//0.56:464:57//Hs. 12259:AB014530
 F-NT2RP2000412//ESTs//1.0:214:60//Hs. 91226:AA64904
 7
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA,
 complete cds//1.6e-67:375:93//Hs. 808:L28010
 F-NT2RP2000420//ESTs, Moderately similar to zinc f
 inger protein [H.sapiens]//3.9e-75:413:92//Hs. 3677
 9:AA626790
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-p
 hosphate mutase mRNA, complete cds//6.7e-128:609:96
 20 //Hs. 5819:AF102265
 F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs. 156532:AA9
 13381
 F-NT2RP2000448//EST//1.1e-24:136:98//Hs. 160402:AI3
 93918
 F-NT2RP2000459//H.sapiens mRNA for imogen 38//1.9e
 -22:158:87//Hs. 154655:Z68747
 F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs. 155243:N7
 0293
 F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs. 62751:AA
 765702
 F-NT2RP2000510
 F-NT2RP2000516
 F-NT2RP2000523//ESTs, Highly similar to APOLIPOR
 TEIN B mRNA EDITING PROTEIN [Rattus norvegicus]//
 3.2e-15:167:75//Hs. 10984:AA806768
 F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 pro
 tein, partial cds//5.6e-38:196:98//Hs. 14409:AB0111
 44
 F-NT2RP2000617//Myosin, heavy polypeptide 6, cardi
 ac muscle, alpha (cardiomyopathy, hypertrophic 1)/
 /1.0:242:57//Hs. 114001:Z20656
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 pro
 tein, partial cds//4.2e-151:732:97//Hs. 7314:AB0145
 14
 F-NT2RP2000644//ESTs//0.035:276:60//Hs. 43660:N3317
 4
 F-NT2RP2000656
 F-NT2RP2000658//ESTs//0.032:281:59//Hs. 124853:AA42
 0602
 F-NT2RP2000668

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F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:AI093453
 F-NT2RP2000704//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442
 F-NT2RP2000710
 F-NT2RP2000715
 F-NT2RP2000731
 F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA5 10 73242
 F-NT2RP2000764//ESTs, Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739
 F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101
 F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880
 F-NT2RP2000814
 F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 pro 20 tein, partial cds//1.0:311:61//Hs.118087:AB011182
 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292
 F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.75794:U80811
 F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:AI336850
 F-NT2RP2000863//ESTs, Highly similar to HYPOTHETI 30 CAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:AI081880
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:AB018284
 F-NT2RP2000892//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H. sapiens]//0.50:189:65//Hs.46146:AA418097
 F-NT2RP2000931//MATRIN 3//1.1e-130:610:98//Hs.7882 40 5:AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21//5.5e-66:326:97//Hs.15144:AC005014
 F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:AB018298
 F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494

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F-NT2RP2000970
 F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN INSIS2-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3e-76:385:96//Hs.21875:AA243700
 F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944
 F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292
 F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.67619:AB007957
 F-NT2RP2001065
 F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313
 F-NT2RP2001081
 F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:AI356560
 F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219
 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191
 F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITORALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:AI336362
 F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582
 F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:AI091361
 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949
 F-NT2RP2001174//H. sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011
 F-NT2RP2001196
 F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598
 F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053
 F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:656:70//Hs.69740:U09367
 F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353
 F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277
 50 F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, comp

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lete cds//1.8e-62:527:76//Hs.75848:U39412
 F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA
 810287
 F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:AI1463
 87
 F-NT2RP2001327//Human B12 protein mRNA, complete c
 ds//1.9e-30:359:71//Hs.76090:M80783
 F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA
 628522
 F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:H41 10
 883
 F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5
 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244
 F-NT2RP2001378
 F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:AI377
 558
 F-NT2RP2001392//Homo sapiens chromosome 5, BAC clo
 ne 203o13 (LBNL H155), complete sequence//0.28:225:
 62//Hs.159402:AC005609
 F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:AI 20
 189767
 F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA63
 3088
 F-NT2RP2001420
 F-NT2RP2001423//ESTs, Weakly similar to hypothetic
 al protein [H.sapiens]//0.030:443:59//Hs.140506:AA
 308018
 F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:AI0
 32875
 F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA9729 30
 66
 F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptopha
 n 5-monooxygenase activation protein, eta polypept
 ide//9.8e-56:603:72//Hs.75544:Z82248
 F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA
 504218
 F-NT2RP2001449
 F-NT2RP2001450
 F-NT2RP2001467
 F-NT2RP2001506
 F-NT2RP2001511//ESTs, Weakly similar to F48F7.1
 [C.elegans]//3.2e-83:409:98//Hs.156161:AI333779
 F-NT2RP2001520//Homo sapiens mRNA for mitochondria
 l carrier protein ARALAR1//6.4e-138:657:97//Hs.427
 7:Y14494
 F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA43713
 4
 F-NT2RP2001536//Homo sapiens X-ray repair cross-co
 mplementing protein 3(XRCC3) mRNA, complete cds//
 5.2e-105:384:94//Hs.99742:AF035586

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F-NT2RP2001560
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0488//1.4e-124:590:98//Hs.67
 619:AB007957
 F-NT2RP2001576//Erythrocyte membrane protein band
 4.9 (dematin)//0.046:521:60//Hs.75936:U28389
 F-NT2RP2001581//EST//1.0:28:96//Hs.148002:AI264876
 F-NT2RP2001597//Casein kinase 2, alpha prime polyp
 eptide//0.069:165:65//Hs.82201:M55268
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 pro
 tein, partial cds//2.3e-138:647:98//Hs.27197:AB018
 340
 F-NT2RP2001613
 F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:AI
 082229
 F-NT2RP2001634//Homo sapiens alpha-catenin related
 protein (ACRP) mRNA, complete cds//4.9e-124:604:96
 //Hs.58488:U97067
 F-NT2RP2001660//Homo sapiens putative 13 S Golgi t
 ransport complex 90kDsubunit brain-specific isoform
 mRNA, complete cds//1.3e-145:687:97//Hs.159558:A
 F058718
 F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74
 //Hs.675:M14328
 F-NT2RP2001675//X-LINKED HELICASE II//0.040:454:58
 //Hs.96264:U72936
 F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 pro
 tein, partial cds//0.028:285:63//Hs.6162:AB018314
 F-NT2RP2001678//Homo sapiens semaphorin F homolog
 mRNA, complete cds//1.7e-34:328:76//Hs.27621:U5284
 0
 F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA8890
 91
 F-NT2RP2001720//ESTs, Highly similar to Rap2 inter
 acting protein 8 [M.musculus]//1.0:173:62//Hs.1073
 61:AI197870
 F-NT2RP2001721
 F-NT2RP2001740//Homo sapiens Rlgui (RIGUI) mRNA, c
 omplete cds//0.58:403:57//Hs.8114:AF022991
 40 F-NT2RP2001748//Farnesyl diphosphate synthase (far
 nesyl pyrophosphate synthetase, dimethylallyltrans
 ferase, geranyltranstransferase)//1.2e-19:15
 1:86//Hs.77393:D14697
 F-NT2RP2001762//Homo sapiens exonuclease 1a (EX01
 a) mRNA, complete cds//5.2e-34:191:96//Hs.47504:AF
 091754
 F-NT2RP2001813//EST//0.46:183:57//Hs.144096:AI0321
 80
 F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:AI05
 2250

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F-NT2RP2001861//Homo sapiens mRNA for paraplegin//
 0.068:146:71//Hs.78497:Y16610
 F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202)
 mRNA, complete cds//0.0013:174:62//Hs.9443:AF0272
 19
 F-NT2RP2001876//Allograft inflammatory factor 1//
 2.2e-08:162:67//Hs.76364:Y14768
 F-NT2RP2001883
 F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE
 5-PHOSPHATASE PRECURSOR//3.0e-113:633:90//Hs.1421 10
 89:M74161
 F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA9
 02650
 F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3,
 long form [H.sapiens]//0.37:263:62//Hs.106377:H29
 757
 F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:AI
 393754
 F-NT2RP2001936
 F-NT2RP2001943
 F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
 F-NT2RP2001947
 F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W444
 89
 F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, comple
 te cds//0.20:238:63//Hs.155174:AB007892
 F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 pro
 tein, partial cds//7.4e-05:235:62//Hs.129943:AB011
 117
 F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA57 30
 9196
 F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 pro
 tein, partial cds//3.2e-62:314:97//Hs.116604:AB018
 299
 F-NT2RP2002032
 F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:AI0
 03543
 F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939
 336
 F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R5 40
 1509
 F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:AI284
 198
 F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 pro
 tein, complete cds//0.96:137:71//Hs.3615:AB018284
 F-NT2RP2002066//Homo sapiens transmembrane recepto
 r UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66/
 /Hs.44553:AF055634
 F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R842
 41

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F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequ
 ence//3.4e-129:643:96//Hs.11039:AF052183
 F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
 F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:AI
 313156
 F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-as
 sociated protein//3.2e-112:533:97//Hs.155218:AJ007
 509
 F-NT2RP2002105//Homo sapiens serine threonine kina
 se 11 (STK11) mRNA, complete cds//6.1e-07:408:60//
 Hs.122755:AF032986
 F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA
 224286
 F-NT2RP2002137//ATPase, Ca++ transporting, plasma
 membrane 4//0.0032:319:59//Hs.995:M83363
 F-NT2RP2002154//Homo sapiens mRNA for C17orf1 prot
 ein//1.0:149:65//Hs.100217:AJ008112
 F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:AI0
 85314
 20 F-NT2RP2002185//ESTs, Weakly similar to ubiquitin
 S6(1) [D.melanogaster]//6.8e-61:354:91//Hs.109966:
 C06057
 F-NT2RP2002192//Human 75-kD autoantigen (PM-Sc1) m
 RNA, complete cds//3.7e-37:194:97//Hs.91728:M58460
 F-NT2RP2002193//Homo sapiens protein inhibitor of
 activated STAT protein PIASx-alpha mRNA, complete c
 ds//6.8e-15:228:67//Hs.111323:AF077954
 F-NT2RP2002208
 F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA15
 1628
 F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:AI394
 318
 F-NT2RP2002235//H.sapiens mRNA for PHAPI2b protein
 //0.86:67:82//Hs.84264:U70439
 F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 pro
 tein, partial cds//0.79:264:59//Hs.129748:AB011099
 F-NT2RP2002256//Homo sapiens retinoic acid hydroxy
 lase mRNA, complete cds//2.1e-51:315:89//Hs.15059
 5:AF005418
 F-NT2RP2002259//Human L-myc protein gene, complete
 cds//1.2e-26:343:71//Hs.92137:M19720
 F-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTE
 IN [H.sapiens]//1.3e-31:206:88//Hs.4029:Z78373
 F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:H23
 079
 F-NT2RP2002312//Homo sapiens CDP-diacylglycerol sy
 nthase 2 (CDS2) mRNA, partial cds//5.0e-95:467:96//
 Hs.24812:AF069532
 F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805
 445

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F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds//1.3e-124:640:95//Hs. 31034:AB015594
 F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:257:60//Hs. 75516:X54637
 F-NT2RP2002373
 F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//3.1e-139:673:97//Hs. 109051:AF038958
 F-NT2RP2002394//Human clone 23695 mRNA sequence// 10 0.16:456:59//Hs. 90798:U79289
 F-NT2RP2002408//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65//Hs. 74095:L20433
 F-NT2RP2002426//EST//4.3e-33:271:79//Hs. 145743:AI269098
 F-NT2RP2002439//ESTs//0.0041:129:68//Hs. 146064:AA714326
 F-NT2RP2002442//ESTs, Weakly similar to similar to molybdoterin biosynthesis MOEB proteins [C.elegans]//5.6e-26:169:89//Hs. 25198:AA904265
 F-NT2RP2002457//ESTs//0.00031:121:71//Hs. 134860:AI091436
 F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.0013:207:63//Hs. 1560:D42045
 F-NT2RP2002475//ESTs//1.0:85:75//Hs. 155371:AI139929
 F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds//7.6e-125:607:96//Hs. 125856:AB005289
 F-NT2RP2002498
 F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete cds//2.2e-89:314:87//Hs. 102681:U95044
 F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//3.8e-159:761:97//Hs. 23255:AB018334
 F-NT2RP2002520//RAB6, member RAS oncogene family//0.99:216:59//Hs. 107563:M28212
 F-NT2RP2002537
 F-NT2RP2002546//EST//0.81:161:65//Hs. 120562:AA7410 40 96
 F-NT2RP2002549//ESTs//0.76:228:61//Hs. 146313:AA594979
 F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete cds//2.9e-33:285:78//Hs. 159277:AB018341
 F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs. 2522:Z35309
 F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frames//6.4e-24:144:95//Hs. 23094:M19503 50

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F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1) mRNA, complete cds//1.0:120:68//Hs. 334:U02082
 F-NT2RP2002618//H. sapiens mRNA for arginine methyltransferase, splice variant, 1262 bp//4.3e-28:460:63//Hs. 20521:Y10805
 F-NT2RP2002621
 F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0022:210:64//Hs. 155302:U57317
 F-NT2RP2002672//ESTs//7.4e-30:226:84//Hs. 94694:W52493
 F-NT2RP2002701//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:278:97//Hs. 109857:AA088385
 F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs. 662:M58583
 F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds//8.0e-42:631:65//Hs. 6336:AB014572
 F-NT2RP2002727
 F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs. 86583:AA761217
 F-NT2RP2002740//EST//1.0e-70:352:97//Hs. 145168:AI150297
 F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-30:628:62//Hs. 87435:D89016
 F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-29:285:75//Hs. 146395:AB002329
 F-NT2RP2002752//EST//2.2e-06:126:74//Hs. 159913:AA862709
 F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs. 133478:T79705
 F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:507:57//Hs. 79706:U53204
 F-NT2RP2002778//EST//1.6e-57:319:93//Hs. 147519:AI216407
 F-NT2RP2002800
 F-NT2RP2002839//ESTs//0.075:177:62//Hs. 132445:AA921763
 F-NT2RP2002857//ESTs//0.99:88:69//Hs. 132104:AI382142
 F-NT2RP2002862
 F-NT2RP2002880
 F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cds//1.0:237:62//Hs. 106487:AB014573
 F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs. 16808:W22606
 F-NT2RP2002928//Homo sapiens pre-mRNA splicing fac

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- tor (PRP17) mRNA, complete cds//3.9e-136:623:99//Hs.116674:AF038392
- F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.24:158:65//Hs.108447:AJ000517
- F-NT2RP2002939
- F-NT2RP2002954
- F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317
- F-NT2RP2002979
- F-NT2RP2002980
- F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.8e-11:272:61//Hs.122967:AF059569
- F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:AI04740
- F-NT2RP2002993
- F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:81//Hs.155464:AF088219
- F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741
- F-NT2RP2003073//Human clone 230971 defective mariner transposon Hsmar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019
- F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190
- F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:67//Hs.153704:U11050
- F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633
- F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:AI291379
- F-NT2RP2003125//Serum response factor (c-fos serum response element-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161
- F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544
- F-NT2RP2003137
- F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cds//0.40:227:61//Hs.105958:AB014520
- F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds//5.7e-113:581:93//Hs.9736:D67025
- F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:AI424170
- F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944
- F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-39:342:79//Hs.153014:AB002353
- F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:N911
- 23
- F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:AI393223
- F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594
- F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794
- F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947
- 10 F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//Hs.108966:U48696
- F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153
- F-NT2RP2003265F-NT2RP2003272//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//5.8e-57:313:93//Hs.109966:C06057
- F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.9e-147:714:96//Hs.154919:AB014525
- F-NT2RP2003280
- F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete cds//0.0097:243:65//Hs.21862:AB011159
- F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:AI269334
- F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 mei-50 dating protein, complete cds//2.0e-86:416:97//Hs.7943:AB006572
- F-NT2RP2003297//EST//0.99:240:60//Hs.133228:AI052312
- F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA42752
- F-NT2RP2003308
- F-NT2RP2003329//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:532:95//Hs.6092:T75227
- 40 F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:AI346765
- F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963
- F-NT2RP2003367//Human HsLIM15 mRNA for HsLim15, complete cds//0.99:243:60//Hs.37181:D64108
- F-NT2RP2003391
- F-NT2RP2003393
- F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023

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F-NT2RP2003401
 F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800
 F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893
 F-NT2RP2003446//Prostaglandin receptor, epl subtype//0.81:273:61//Hs.159360:L22647
 F-NT2RP2003456//EST//0.17:95:65//Hs.147190:AI193320
 F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730)containing the hFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770
 F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106
 F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136
 F-NT2RP2003506
 F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803
 F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270
 F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simiansarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783F-NT2RP2003522//Zinc finger protein 148 (pHZ-52)//1.1e-17:512:60//Hs.112180:AF039019
 F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:AI138765
 F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010
 F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:AI356513
 F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800
 F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931
 F-NT2RP2003581//EST//1.0:59:76//Hs.158575:AI368947
 F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:AA126463
 F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067
 F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166
 F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252

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F-NT2RP2003668//Homo sapiens haemopoietic progenitor or homeobox HPX42B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006
 F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:AI032875
 F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247
 F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561
 10 F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271
 F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097
 F-NT2RP2003713
 F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180
 F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879
 20 F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbcH5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318
 F-NT2RP2003751
 F-NT2RP2003760
 F-NT2RP2003764
 F-NT2RP2003769
 F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677
 30 F-NT2RP2003777
 F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689
 F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955
 F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742
 F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HSJ1//0.95:300:59//Hs.77768:X63368
 F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425
 40 F-NT2RP2003859
 F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780
 F-NT2RP2003885
 F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA[Emmericella nidulans]//2.2e-113:632:92//Hs.50072:AI378221
 F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.156920:AA489296
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F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//6.8e-30:165:96//Hs.35086:AB014458
 F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916
 F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347
 F-NT2RP2003984
 F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:AI050036
 F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
 F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//Hs.111081:AI380378
 F-NT2RP2004014
 F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
 F-NT2RP2004042
 F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573
 F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:AI217942
 F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2)mRNA, complete cds//0.15:199:60//Hs.104315:AF054828
 F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
 F-NT2RP2004142
 F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
 F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
 F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:AI419966
 F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:AI343501
 F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H. sapiens]//1.7e-16:276:67//Hs.36779:AA626790
 F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317
 F-NT2RP2004196
 F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
 F-NT2RP2004226//ESTs, Weakly similar to teg292 pro

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tein [M. musculus]//1.8e-80:386:98//Hs.68791:AA527270
 F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
 F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
 F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
 F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
 F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C. elegans]//8.2e-51:474:74//Hs.108990:N25951
 F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:490:60//Hs.112432:AC005263
 F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4, 5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544
 F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416
 F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
 F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
 F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
 F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA56202
 F-NT2RP2004365
 F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986
 F-NT2RP2004373
 F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916
 F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
 F-NT2RP2004396//Homo sapiens BAC clone RC135C18 from 7q21//1.4e-174:875:95//Hs.152759:AC005164
 F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C. elegans]//1.2e-92:519:91//Hs.13275:AI341468
 F-NT2RP2004400//EST//0.018:150:65//Hs.158739:AI375367
 F-NT2RP2004412
 F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944
 F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15

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F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823

F-NT2RP2004490

F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:AI091203

F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.3e-29:270:79//Hs.73614:U83460

F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds//4.6e-139:687:96//Hs.129908:AB011163

F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:AI346891

F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//8.8e-06:291:61//Hs.132206:AF039694

F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:82//Hs.155464:AF088219

F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete cds//0.98:136:64//Hs.28020:AB018309

F-NT2RP2004594//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//1.0:104:68//Hs.125729:N99898

F-NT2RP2004600//Homo sapiens mRNA for Hrs, complete cds//0.20:260:60//Hs.24756:U43895

F-NT2RP2004602//ESTs, Weakly similar to HUMAN ALU SUBFAMILY J WARNING ENTRY [H. sapiens]//3.0e-59:273:93//Hs.12845:N28835

F-NT2RP2004614//EST//0.99:103:68//Hs.148738:AI224908

F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-104:496:98//Hs.5198:AJ006291

F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds//5.2e-155:728:98//Hs.29956:AB007929

F-NT2RP2004675//EST//0.65:151:62//Hs.130504:AI003839

F-NT2RP2004681

F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds//4.1e-61:327:94//Hs.154919:AB014525

F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942

F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780

F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds//2.1e-118:582:96//Hs.4236:AB007947

F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609250

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F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183

F-NT2RP2004768//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASEPAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504

F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p54 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451

10 F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, complete cds//0.99:121:64//Hs.2864:L40157

F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF058953

F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043

F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//6.8e-103:495:97//Hs.67052:AF054179

20 F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83//Hs.84775:M23161

F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:AI290258

F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111

F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.5e-84:418:95//Hs.25619:AB007144

F-NT2RP2004936

30 F-NT2RP2004959

F-NT2RP2004961//Human mRNA for KIAA0065 gene, partial cds//7.2e-26:456:66//Hs.70617:D31763

F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:AI149478

F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:AI239735

F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete cds//1.0:218:61//Hs.7414:AB007927

F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.13:260:60//Hs.41723:U37426

F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-22:431:65//Hs.8127:D63478

F-NT2RP2004999

F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164

F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//1.9e-160:782:97//Hs.155972:AB014515

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F-NT2RP2005003//H.sapiens Staf50 mRNA//9.9e-44:43
 O:75//Hs.68054:X82200
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, c
 omplete cds//4.5e-100:501:96//Hs.31575:AF100141
 F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:2
 32:58//Hs.89499:J03600
 F-NT2RP2005020//ESTs//1.2e-06:61:100//Hs.106160:AA
 527433
 F-NT2RP2005022//Eukaryotic translation initiation
 factor 3 (eIF-3) p36 subunit//0.095:271:60//Hs.139 10
 745:U39067
 F-NT2RP2005031//Homo sapiens mRNA for SCP-1, compl
 ete cds//0.99:338:61//Hs.112743:D67035
 F-NT2RP2005037//Homo sapiens mRNA for repressor pr
 otein, partial cds//0.098:217:60//Hs.58167:D30612
 F-NT2RP2005038//Homo sapiens protease-activated re
 ceptor 4 mRNA, complete cds//0.22:498:59//Hs.13757
 4:AF055917
 F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657
 838
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 pro
 tein, partial cds//6.4e-105:495:98//Hs.22616:AB014
 564
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (M
 yc-regulated dead boxprotein)//9.2e-29:157:98//Hs.
 100555:X98743
 F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W4
 2803
 F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA5349
 47
 F-NT2RP2005144//Homo sapiens tubby like protein 3
 (TULP3) mRNA, completecds//8.3e-91:447:96//Hs.1322
 26:AF045583
 F-NT2RP2005147
 F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:AI
 357582
 F-NT2RP2005162//ESTs, Weakly similar to Y53C12A.3
 [C.elegans]//0.97:80:73//Hs.107747:AI357868
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-as
 sociated protein//4.4e-127:633:96//Hs.155218:AJ007 40
 509
 F-NT2RP2005204//H.sapiens 5T4 gene for 5T4 Oncofet
 al antigen//0.0034:187:66//Hs.82128:AJ012159
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 f
 rom 7p12-p14//1.3e-66:340:95//Hs.8173:AC005189
 F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA9
 94783
 F-NT2RP2005254//H.sapiens mRNA for PHAPI2b protein
 //1.0:101:71//Hs.84264:U70439
 F-NT2RP2005270//Homo sapiens creatine transporter 50

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mRNA, complete cds//0.56:114:68//Hs.154503:U36341
 F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4
 (ACS4) mRNA, completecds//1.2e-40:594:65//Hs.8145
 2:AF030555
 F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:AI
 383932
 F-NT2RP2005288//Homo sapiens RCC1-like G exchangein
 g factor RLG mRNA, complete cds//2.3e-123:604:96//
 Hs.27007:AF060219
 F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein
 //1.3e-141:670:98//Hs.44766:AJ007590
 F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA5
 05833
 F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 pro
 tein, partial cds//3.6e-97:483:96//Hs.115763:AB014
 576
 F-NT2RP2005325//Human LIM-homeobox domain protein
 (hLH-2) mRNA, completecds//2.6e-23:166:90//Hs.156
 9:U11701
 20 F-NT2RP2005336//Homo sapiens snRNA activating prot
 ein complex 190kD subunit (SNAP190) mRNA, complete
 cds//0.016:353:62//Hs.113265:AF032387
 F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 pro
 tein, partial cds//2.8e-30:456:66//Hs.44697:AB0111
 38
 F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA7089
 58
 F-NT2RP2005358//Homo sapiens methyl-CpG binding pr
 otein MBD3 (MBD3) mRNA, complete cds//1.4e-100:48
 9:96//Hs.107254:AC005943
 30 F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA
 700122
 F-NT2RP2005393//Homo sapiens CTC26 alternate open
 reading frame mRNA, complete cds//0.87:244:59//Hs.
 113252:U80761
 F-NT2RP2005407
 F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 pro
 tein, partial cds//0.28:338:57//Hs.6189:AB011133
 F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA78
 0068
 F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:AI
 091164
 F-NT2RP2005457//ESTs, Highly similar to NADH-UBIQ
 UINONE OXIDOREDUCTASESUBUNIT B14.5B [Bos taurus]//
 8.5e-48:295:90//Hs.75017:AA166853
 F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA80
 8243
 F-NT2RP2005465//V-crk avian sarcoma virus CT10 onc
 ogene homolog//0.032:176:64//Hs.16:D10656
 F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:AI

- 378412
F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete cds//9.9e-48:432:77//Hs.15519:AB018315
F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
F-NT2RP2005491
F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:AI084164
F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-48:621:68//Hs.6833:AB002324
F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, completecds//1.6e-63:503:78//Hs.7688:M64930
F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.56:139:66//Hs.8546:U97669
F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546
F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//1.2e-82:444:92//Hs.119023:AF092563
F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds//2.2e-19:112:99//Hs.6232:AB018307
F-NT2RP2005531//ESTs, Weakly similar to erythrocyte membrane protein 4.1[H.sapiens]//3.5e-50:366:83//Hs.61833:AA036735
F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//9.4e-155:747:97//Hs.159597:AJ012449
F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:AB007963
F-NT2RP2005549//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407
F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822
F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839
F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436
F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627
F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071
F-NT2RP2005620//Homo sapiens epsin 2b mRNA, complete cds//3.1e-92:447:97//Hs.22396:AF062085
F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523 50
- 702
F-NT2RP2005635
F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905
F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145
F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440
F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.143065:M86917
F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:AB006626
F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239
F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//Hs.25664:AF089814
F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702
F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:M77836
F-NT2RP2005694
F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (PP2A) mRNA, complete cds//0.15:496:55//Hs.79326:L76703
F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:AB018342
F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527
F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367
F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017
F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191
F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086
F-NT2RP2005741//Homo sapiens chondroadherin gene, 5' flanking region and//0.80:362:58//Hs.97220:U96769
F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688
F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868
F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516
F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LI

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- KE NUK-34//2.3e-05:425:56//Hs.79768:D21853
 F-NT2RP2005767//Homolog 2 of Drosophila large disc
 s//0.085:262:61//Hs.23205:X82895
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE/
 /2.0e-16:153:82//Hs.79217:W77836
 F-NT2RP2005775//Human thimet oligopeptidase (THOP
 1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z5
 0115
 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI3
 78556
 F-NT2RP2005784//Inhibitor of DNA binding 4, domina
 nt negative helix-loop-helix protein//2.9e-06:201:
 67//Hs.34853:U28368
 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA8
 83820
 F-NT2RP2005812
 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI
 193595
 F-NT2RP2005835
 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca+K e 20
 xchanger (NCKX1) mRNA, complete cds//0.94:148:65//H
 s.59829:AB014602
 F-NT2RP2005853
 F-NT2RP2005857//Homo sapiens chromosome-associated
 protein-C (hCAP-C) mRNA, partial cds//5.4e-176:82
 9:98//Hs.50758:AF092564
 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W2
 2567
 F-NT2RP2005868
 F-NT2RP2005886//Human putative M phase phosphoprot 30
 ein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.24
 0:L16782
 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA
 279943
 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360
 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA
 521399
 F-NT2RP2005933//ESTs, Highly similar to nucleopori
 n p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:AA
 292186
 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67
 //Hs.49007:X76770
 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA
 883339
 F-NT2RP2006023
 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA
 418382
 F-NT2RP2006043//Human novel homeobox mRNA for a DN
 A binding protein//0.51:271:59//Hs.37035:U07664
 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA 50
 663093
 F-NT2RP2006069//Human mRNA for KIAA0279 gene, part
 ial cds//0.0082:770:58//Hs.57652:D87469
 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI
 337416
 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA4059
 70
 F-NT2RP2006100
 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA
 883135
 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA
 315349
 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA
 649240
 F-NT2RP2006166
 F-NT2RP2006184//H.sapiens p63 mRNA for transmembra
 ne protein//1.0:94:73//Hs.74368:X69910
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 pro
 tein, partial cds//2.5e-114:567:96//Hs.109299:AB01
 4554
 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 pro
 tein, complete cds//2.0e-23:187:85//Hs.15519:AB018
 315
 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI2055
 03
 F-NT2RP2006219//H.sapiens mRNA for DGC6 protein//
 4.4e-118:618:93//Hs.153910:X96484
 F-NT2RP2006237
 F-NT2RP2006238
 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI2
 69970
 F-NT2RP2006261//H.sapiens mRNA for serine/threonin
 e protein kinase EMK//0.019:111:71//Hs.157199:X976
 30
 F-NT2RP2006275//Homo sapiens mRNA for serin protea
 se with IGF-binding motif, complete cds//2.4e-05:3
 88:60//Hs.75111:D87258
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, c
 omplete cds//2.1e-121:598:97//Hs.3404:AF035262
 40 F-NT2RP2006320//ESTs, Moderately similar to matern
 al transcript Maid [M.musculus]//1.9e-29:151:100//
 Hs.36794:AI038407
 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09
 371
 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, comp
 lete cds//4.7e-06:170:70//Hs.87202:D82344
 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP)
 mRNA, complete cds//0.11:43:100//Hs.6892:AF076974
 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 pro
 tein, partial cds//3.1e-05:233:65//Hs.37656:AB0111

- 74
F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AAO58501
F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341
F-NT2RP2006436//Human homeodomain-containing protein (HANF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734
F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934
F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509
F-NT2RP2006456
F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs.72160:AJ006266
F-NT2RP2006467
F-NT2RP2006472
F-NT2RP2006534//ESTs//5.6e-05:192:66//Hs.135750:AA160048
F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134
F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966
F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U22029
F-NT2RP2006573
F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223
F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180
F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JW21)//1.9e-137:637:98//Hs.6764:AJ011972
F-NT2RP3000046//Homo sapiens TTF-I interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560
F-NT2RP3000047
F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376
F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961
F-NT2RP3000068
F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769
F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670
F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:665:60//Hs.80741:X14608
- F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140
F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595
F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//5.0e-94:438:100//Hs.8173:AC005189
F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164
10 F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frames//4.1e-20:133:94//Hs.23094:M19503
F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961
F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779
F-NT2RP3000207
F-NT2RP3000220
F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569
F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-111:691:86//Hs.75863:D86972
F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
F-NT2RP3000252
F-NT2RP3000255
30 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568
F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821
F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863
F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153
F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:AI091242
F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097
F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390
F-NT2RP3000348
F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754
F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673
- 50

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F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921
 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [*Lymanaea stagnalis*]//4.0e-116:596:95//Hs.21094:AI337016
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185
 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-33:610:65//Hs.23094:M19503
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487
 F-NT2RP3000441
 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:AI051562
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705
 F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:AI289822
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:AI084058
 F-NT2RP3000512//Homeo box B3//3.1e-18:109:97//Hs.49931:X16667
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA86412
 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723
 F-NT2RP3000578
 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277
 F-NT2RP3000584
 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914

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F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811
 F-NT2RP3000599//ESTs, Weakly similar to T19B10.6 [*C.elegans*]//9.3e-61:355:92//Hs.114622:AA693492
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:59//Hs.79170:D86980
 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:AI421203
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162
 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:AI017333
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904
 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219
 F-NT2RP3000661
 F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789
 F-NT2RP3000685
 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001
 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884
 F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854
 F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:AI369426
 F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937
 F-NT2RP3000815
 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:N45132
 F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476
 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012
 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630
 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)

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S)//2.0e-49:323:86//Hs.155464:AF088219
 F-NT2RP3000852
 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699
 918
 F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA8114
 76
 F-NT2RP3000868//Human ovarian cancer downregulated
 myosin heavy chain homolog (Doc1) mRNA, complete
 cds//6.4e-31:766:60//Hs.15432:U53445
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, comple 10
 te cds//1.1e-13:701:60//Hs.79706:U53204
 F-NT2RP3000875
 F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99
 101
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:AI
 348374
 F-NT2RP3000917
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:34
 0:60//Hs.109895:X68277
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-4 20
 4:351:83//Hs.2953:X84407
 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:AI2
 04212
 F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:A
 A918411
 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N9
 2198
 F-NT2RP3001007
 F-NT2RP3001055//ESTs, Weakly similar to weak simil
 arity to procollagen alpha chain 1(V) chain [C.ele 30
 gans]//2.9e-121:588:98//Hs.128781:AA160707
 F-NT2RP3001057//ESTs, Highly similar to ZINC FING
 ER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.3
 0303:AI244662
 F-NT2RP3001081//Homo sapiens RCC1-like G exchangin
 g factor RLC mRNA, complete cds//2.7e-51:534:74//H
 s.27007:AF060219
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 pro
 tein, partial cds//3.7e-16:474:60//Hs.21264:AB0183
 25
 F-NT2RP3001096//Homo sapiens mRNA for cartilage-as
 sociated protein (CASP)//4.4e-16:428:60//Hs.15548
 1:AJ006470
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, comp
 lete cds//2.8e-34:712:64//Hs.82292:D86969
 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:AI
 337050
 F-NT2RP3001111
 F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA6
 09088

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F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA
 688023
 F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W747
 79
 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, co
 mplete cds//0.96:258:61//Hs.12107:AF042384
 F-NT2RP3001120//Zinc finger protein 136 (clone pHZ
 -20)//2.4e-77:687:75//Hs.69740:U09367
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 pro
 tein, complete cds//0.00018:341:60//Hs.94790:AB018
 318
 F-NT2RP3001133//Homeo box A4//0.00011:484:59//Hs.7
 7637:W74297
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 pro
 tein, partial cds//1.1e-180:851:98//Hs.5378:AB0183
 05
 F-NT2RP3001147
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.9
 7:257:59//Hs.957:W84605
 F-NT2RP3001155//Homo sapiens mRNA for AND-1 protei
 n//1.7e-191:891:98//Hs.72160:AJ006266
 F-NT2RP3001176
 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:AI4178
 59
 F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W1
 9981
 F-NT2RP3001221//ESTs, Weakly similar to M05D6.7
 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866
 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA59
 4010
 F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:AI
 362756
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B/
 /1.7e-20:501:62//Hs.103042:L06237
 F-NT2RP3001245//ESTs//7.1e-80:434:93//Hs.22587:AA7
 43132
 F-NT2RP3001253//Human prepromulimerin mRNA, compl
 ete cds//0.99:293:60//Hs.32934:U27109
 F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 pro
 tein, complete cds//1.2e-48:761:64//Hs.107809:AB01
 8269
 F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-
 associated box (KRAB) domain polypeptide)//1.2e-42:
 454:72//Hs.41728:L75847
 F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA1
 02566
 F-NT2RP3001274
 F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA
 836811
 50 F-NT2RP3001297//Human mRNA for KIAA0281 gene, comp

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lete cds//2.4e-48:544:69//Hs.31463:D87457
 F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete cds//0.72:151:68//Hs.159437:U44060
 F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glu canotransferase (glycogen debranching enzyme, glyc ogen storage disease type III)//0.012:522:56//Hs.9 04:U84010
 F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA2 04731
 F-NT2RP3001338//Human mRNA for KIAA0211 gene, comp 10 lete cds//1.6e-30:345:73//Hs.79347:D86966
 F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 pro tein, complete cds//6.3e-67:559:80//Hs.18586:AB007 920
 F-NT2RP3001340//Homo sapiens hyperpolarization-act ivated channel 1 (IH1)mRNA, partial cds//0.00019:4 73:61//Hs.124161:AF065164
 F-NT2RP3001355//ESTs, Weakly similar to ADP,ATP CA RRIER PROTEIN, LIVER ISOFORM T2 [H.sapiens]//1.1e- 81:421:96//Hs.32508:H29831
 F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, co mplete cds//0.15:313:60//Hs.129725:AF047487
 F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873 022
 F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:65//Hs.30965:AB001451
 F-NT2RP3001384//Homa sapiens mRNA for HRIHFB2018, partial cds//2.1e-158:743:98//Hs.146214:AB015332
 F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514 595
 F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10 783
 F-NT2RP3001398//Zinc finger protein 45 (a Kruppel- associated box (KRAB) domain polypeptide)//1.0e-05: 189:66//Hs.41728:L75847
 F-NT2RP3001399//Homo sapiens mitochondrial citrate transport protein (CTP) mRNA, 3' end//0.77:132:66 //Hs.111024:L77567
 F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658
 F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA64904 40 7
 F-NT2RP3001426
 F-NT2RP3001427
 F-NT2RP3001428//Neurotrophic tyrosine kinase, rece ptor, type 1//1.8e-73:431:91//Hs.85844:X66397
 F-NT2RP3001432//ESTs, Moderately similar to !!!! A LU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//6. 9e-05:195:65//Hs.115868:AA568393
 F-NT2RP3001447
 F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCL 50

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E//0.00033:187:68//Hs.89631:U48508
 F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203 212
 F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA9 88323
 F-NT2RP3001459
 F-NT2RP3001472//Homo sapiens Sox-like transcriptio nal factor mRNA, complete cds//4.2e-10:168:70//Hs. 32317:AF072836
 F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA 250877
 F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA 970231
 F-NT2RP3001497//Homo sapiens multiple membrane spa nning receptor TRC8 (TRC8) mRNA, complete cds//2.8 e-172:804:98//Hs.28285:AF064801
 F-NT2RP3001527//Human lymphoid-specific SP100 homo log (LYSP100-B) mRNA, complete cds//9.4e-139:743:91 //Hs.85283:U36500
 20 F-NT2RP3001529//ESTs, Moderately similar to topois omerase I C-terminal fragment [H.sapiens]//0.28:22 4:65//Hs.105912:AI431328
 F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI 198074
 F-NT2RP3001554//Microtubule-associated protein 1A/ /9.8e-16:327:64//Hs.147918:U38291
 F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
 F-NT2RP3001587//Guanine nucleotide binding protein (G protein), alpha 11(Gq class)//0.049:185:65//H s.1686:M69013
 30 F-NT2RP3001589//Human mRNA for tryptophan hydroxyl ase (EC 1.14.16.4)//9.6e-51:345:82//Hs.144563:AF05 7280
 F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22 688
 F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI0 91349
 F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:A A306435
 F-NT2RP3001629
 F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, c omplete cds//1.4e-62:276:97//Hs.9899:AF099149
 F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173
 F-NT2RP3001646
 F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.1e-172:816:98//Hs.159597:AJ012 449
 F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T6 9027

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F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [*Pseudomonas fluorescens*]/9.0e-53:375:85//Hs.41127:AA555184
 F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:321:65//Hs.79077:D87071
 F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [*Caenorhabditis elegans*]/4.0e-111:518:99//Hs.20364:AI420022
 F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:230:63//Hs.7486:D83198
 F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
 F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
 F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR [*D.melanogaster*]/1.4e-31:191:94//Hs.131279:AA486291
 F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds//0.41:259:59//Hs.58435:AF001862
 F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [*Mus musculus*]/7.6e-159:747:98//Hs.6823:W18181
 F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177
 F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME III [*Caenorhabditis elegans*]/3.5e-116:554:98//Hs.144332:AA046836
 F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-105:811:78//Hs.90998:D50918
 F-NT2RP3001739
 F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:80//Hs.116549:AL009172
 F-NT2RP3001753//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.22138:U49250
 F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete cds//2.4e-47:725:64//Hs.41688:U27193
 F-NT2RP3001777//Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525
 F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//9.1e-153:710:98//Hs.28169:AB007928
 F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:69//Hs.79024:L03532
 F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI0

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91361
 F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.53563:L41162
 F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-II//0.90:379:58//Hs.32950:X82634
 F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
 F-NT2RP3001855//Human homeobox-containing protein mRNA, complete cds//7.8e-35:481:67//Hs.158225:U68727
 F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
 F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [*C.elegans*]/2.9e-94:452:98//Hs.54952:AA872675
 F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin 1a//0.65:245:61//Hs.6139:AL022326
 F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA723896
 F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
 F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
 F-NT2RP3001931
 F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//0.0022:268:61//Hs.106070:U22398
 F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds//5.8e-167:815:96//Hs.15869:AB014575
 F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335
 F-NT2RP3001969
 F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180
 F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:83//Hs.155464:AF088219
 F-NT2RP3002004//H. sapiens mRNA for FAST kinase//5.2e-28:104:100//Hs.75087:X86779
 F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
 F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
 F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:175:67//Hs.147189:D88153
 F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [*M.musculus*]/3.8e-48:353:81//Hs.127507:AA993745
 F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [*H.sapiens*]/3.0e-25:212:83//Hs.71622:AA195155
 F-NT2RP3002056//ESTs, Highly similar to RETINOBLA

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- STOMA BINDING PROTEIN1 [Homo sapiens]//4.2e-82:40
7:97//Hs.131888:AI091806
- F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frames//3.7e-21:168:85//Hs.23094:M19503
- F-NT2RP3002062//EST//0.46:198:62//Hs.157711:AI359710
- F-NT2RP3002063//Membrane metallo-endorpeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779
- F-NT2RP3002081
- F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.073:297:61//Hs.102732:U88153
- F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256
- F-NT2RP3002108
- F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018
- F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260
- F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009
- F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644
- F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985
- F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140
- F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046
- F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915
- F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA306435
- F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656
- F-NT2RP3002248
- F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261
- F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.110637:AC004080
- F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA25139
- F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA989386
- F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910
- F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871
- 10 F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383
- F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396
- F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//4.2e-166:770:98//Hs.6483:Y16355
- F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200
- 20 F-NT2RP3002399
- F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274
- F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:AB014578
- F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:AI291310
- F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108
- 30 F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935
- F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.57738:U35246
- F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:AB018272
- F-NT2RP3002549//ESTs, Weakly similar to POLYPOSIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.96759:AA469984
- F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706
- F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054
- F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:AI187919
- F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508
- F-NT2RP3002603
- 50 F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, compl

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- ete cds//1.5e-05:264:61//Hs.3845:AB014888
 F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial
 cds//0.97:320:58//Hs.121287:AF029900
 F-NT2RP3002650//Homo sapiens mRNA for cartilage-as
 sociated protein (CASP)//2.6e-13:441:63//Hs.15548
 1:AJ006470
 F-NT2RP3002659//Human TAR RNA loop binding protein
 (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.
 151518:U38847
 F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:A 10
 A584308
 F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL
 -BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//H
 s.41086:AI337400
 F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:AI
 421991
 F-NT2RP3002682//ESTs, Weakly similar to F17C11.8
 [C.elegans]//1.6e-61:294:100//Hs.128750:AI367584
 F-NT2RP3002687
 F-NT2RP3002688//EST//1.0:312:58//Hs.156800:AI35220 20
 0
 F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:AI39
 3657
 F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:AI279
 514
 F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W8
 6291
 F-NT2RP3002770//Homo sapiens G protein-coupled rec
 eptor kinase 6 (GRK6) gene, partial cds//0.91:161:6
 2//Hs.129736:AF040753
 F-NT2RP3002785
 F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA1
 48713
 F-NT2RP3002810//ESTs, Weakly similar to KIAA0062
 [H.sapiens]//1.4e-76:423:93//Hs.41068:AA844350
 F-NT2RP3002818//Homo sapiens jerky gene product ho
 molog mRNA, complete cds//2.2e-55:615:70//Hs.10594
 0:AF004715
 F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA
 524070
 F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T3
 3582
 F-NT2RP3002876//Homo sapiens mRNA for B120, comple
 te cds//2.7e-90:557:88//Hs.123090:AB001895
 F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA
 626040
 F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 pro
 tein, partial cds//1.8e-181:853:98//Hs.6162:AB0183
 14
 F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:AI 50
 138765
 F-NT2RP3002948//ESTs, Highly similar to RING CANA
 L PROTEIN [Drosophila melanogaster]//1.4e-133:645:9
 7//Hs.3826:U69560
 F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 pro
 tein, complete cds//5.2e-13:594:57//Hs.74599:AB011
 160
 F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 pro
 tein, complete cds//0.76:412:57//Hs.21198:AB018262
 F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA5
 63870
 F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 fr
 om 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
 F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:AI
 287703
 F-NT2RP3002985//Human TFIIIB related factor hBRF (H
 BRF) mRNA, complete cds//0.071:550:58//Hs.32935:U2
 8838
 F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:AI21
 8308
 F-NT2RP3003008//Human DNA-binding protein (HRC1) m
 RNA, complete cds//0.59:201:63//Hs.72925:M91083
 F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C0
 6446
 F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA8
 97749
 F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:6
 33:59//Hs.1242:X16609
 F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA77
 7928
 F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56
 079
 F-NT2RP3003078
 F-NT2RP3003101
 F-NT2RP3003121//EST, Moderately similar to !!!! AL
 U SUBFAMILY SC WARNINGENTRY !!!! [H.sapiens]//0.9
 8:88:68//Hs.99715:AA292700
 F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:AI0
 90740
 F-NT2RP3003138//Homo sapiens vasopressin-activated
 calcium mobilizing putative receptor protein (VAC
 M-1) mRNA, complete cds//0.013:438:57//Hs.101299:A
 F017061
 F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W8897
 5
 F-NT2RP3003145//Homo sapiens aortic carboxypeptida
 se-like protein ACLP mRNA, complete cds//2.2e-20:4
 30:63//Hs.118397:AF053944
 F-NT2RP3003150
 F-NT2RP3003157//Human repressor transcriptional fa

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ctor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
 F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
 F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933
 F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
 F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
 F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
 F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
 F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
 F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460
 F-NT2RP3003251//H. sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
 F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225
 F-NT2RP3003278//Homo sapiens hook2 protein (H00K2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924
 F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2e-133:694:93//Hs.11702:L36983
 F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953
 F-NT2RP3003301//EST//1.0:58:74//Hs.158575:AI368947
 F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frames//3.1e-91:681:80//Hs.23094:M19503
 F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947
 F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:AI084058
 F-NT2RP3003327//H. sapiens Staf50 mRNA//8.0e-31:253:67//Hs.68054:X82200
 F-NT2RP3003330
 F-NT2RP3003344
 F-NT2RP3003346//H. sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//1.2e-42:644:66//Hs.2638:Z28339
 F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.66746:L78833

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F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:416:60//Hs.148090:D83542
 F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791
 F-NT2RP3003385//ESTs, Highly similar to SKD3 [M. musculus]//7.0e-74:384:96//Hs.21263:H16363
 F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA63850
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653
 F-NT2RP3003411//Human metallothionein-1e gene (hMT-1e)//0.99:116:62//Hs.74170:M10942
 F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:AI422830
 F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12//1.0:243:61//Hs.62:M93425
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.7e-182:853:98//Hs.14934:AF004828
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//5.2e-175:826:98//Hs.26450:AB018268
 F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.90821:X98330
 F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302
 F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, complete cds//0.64:626:58//Hs.150828:AF038169
 F-NT2RP3003552
 F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:AI418322
 F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365
 F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311
 F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.123109:X56741
 F-NT2RP3003621//HEPATOCTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0e-09:564:61//Hs.104:D14012
 F-NT2RP3003625
 F-NT2RP3003656
 F-NT2RP3003659
 F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586
 F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184
 F-NT2RP3003680//Human Bcl2, p53 binding protein Bb

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p/53BP2 (BBP/53BP2) mRNA, complete cds//0.013:190:63//Hs.44585:U58334
 F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds//0.69:246:62//Hs.118463:AF055000
 F-NT2RP3003701//EST//0.93:79:69//Hs.145285:AI249848
 F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24:478:61//Hs.48998:AB007865
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//7.4e-150:700:98//Hs.48513:AB018300
 F-NT2RP3003746
 F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230
 F-NT2RP3003799
 F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog//4.7e-41:432:73//Hs.1422:M19722
 F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656
 F-NT2RP3003809//Human transcription factor, forkhead related activator 4 (FREAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF042832
 F-NT2RP3003819//Human ring zinc-finger protein (ZN F127-Xp) gene and 5' flanking sequence//0.84:171:63//Hs.102877:U41315
 F-NT2RP3003825
 F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:AI346481
 F-NT2RP3003831
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//2.6e-48:242:98//Hs.25300:AF070611
 F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds//1.3e-37:335:68//Hs.26450:AB018268
 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds//1.3e-175:805:99//Hs.118738:AB018343
 F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R. norvegicus]//6.8e-39:243:90//Hs.124832:AA846576
 F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D. melanogaster]//1.1e-107:499:99//Hs.105794:AA701659
 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358
 F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396 50

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F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:AI359006
 F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498
 F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H. sapiens]//2.8e-127:617:97//Hs.142151:AA984061
 F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//0.0086:283:62//Hs.155302:U57317
 F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234
 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-63:774:67//Hs.26441:AB002317
 F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:AI032875
 F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA classII expression)//5.3e-90:520:90//Hs.100007:X76091
 F-NT2RP3004093
 F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:69//Hs.81281:U79258
 F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-20:211:77//Hs.40100:AB002390
 F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEIN XLCOF7.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:AI096509
 F-NT2RP3004145
 F-NT2RP3004148
 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds//2.1e-121:578:98//Hs.157113:AF032900
 F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706
 F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
 F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)//0.095:281:62//Hs.101047:M31523
 F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:AI221835
 F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361
 F-NT2RP3004242
 F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240
 F-NT2RP3004253//ESTs//1.2e-36:204:96//Hs.143588:AI149140
 F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2e-07:369:59//Hs.71346:Y00067

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F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds//1.0e-154:733:98//Hs.158471:AF088982

F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4.2e-26:597:61//Hs.19261:AF007871

F-NT2RP3004332

F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285

F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426

F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA30999

F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:337:83//Hs.141429:AA631915

F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procollagen alpha chain 1(V) chain [C.elegans]//4.3e-125:608:98//Hs.128781:AA160707

F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein1//2.3e-141:804:90//Hs.123122:X97249

F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-122:609:96//Hs.20132:AA203113

F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:60//Hs.153638:AF010403

F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016

F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//2.0e-124:583:99//Hs.27349:AB007917

F-NT2RP3004466//Homo sapiens mRNA for KIAA0664 protein, partial cds//0.48:399:58//Hs.22616:AB014564

F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219

F-NT2RP3004472

F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.8e-152:715:98//Hs.5003:AB007925

F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851

F-NT2RP3004498//ESTs, Moderately similar to ROSA26 AS [M.musculus]//3.5e-89:425:99//Hs.126082:AI077718

F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256

F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 pro 50

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tein, partial cds//1.0:370:59//Hs.158244:AB007948

F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046

F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110

F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571

F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:AB014532

F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:AB011126

F-NT2RP3004566//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.125870:AI364967

F-NT2RP3004569

F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445

F-NT2RP3004578//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923

F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266

F-NT2RP3004617//ESTs, Weakly similar to estrogen-responsive finger protein, efp [H.sapiens]//6.4e-13:356:64//Hs.124138:AI266336

F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232

F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204

F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13436

F-NT2RP4000008//ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919

F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668

F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495

F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761

F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470

F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.0e-151:720:97//Hs.159597:AJ012449

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3900

F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
 F-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
 F-NT2RP4000111
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952
 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:D26069
 F-NT2RP4000150
 F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
 F-NT2RP4000159
 F-NT2RP4000167
 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600
 F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA22006
 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA51731
 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, completecds//6.2e-34:425:71//Hs.46468:U45984
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470
 F-NT2RP4000246//ESTs, Highly similar to NPC DERIVED PROLINE RICH PROTEIN1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092
 F-NT2RP4000263
 F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
 F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732
 F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
 F-NT2RP4000355
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107479:AB018281

F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195
 F-NT2RP4000370//ESTs, Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678
 10 F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965
 F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368
 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, completecds//2.0e-34:431:73//Hs.46468:U45984
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087
 F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:Z72499
 30 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535
 F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, completecds//0.94:133:69//Hs.159234:U89995
 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904
 F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840
 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372
 50 F-NT2RP4000524

- F-NT2RP4000528
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154
 F-NT2RP4000556//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730
 F-NT2RP4000638//Fibroblast growth factor 2 (basic) //1.0:226:61//Hs.56066:J04513
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907
 F-NT2RP4000704//Homo sapiens mRNA expressed in 19 week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783
 F-NT2RP4000724//ESTs, Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440
 F-NT2RP4000739//DESMOPLAKIN I AND II//0.99:192:63//Hs.74316:AL031058
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162
 F-NT2RP4000787//Human mRNA for ESP1/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:W27603
 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.750
 5875:U49278
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
 F-NT2RP4000907//Homo sapiens BAC clone RC118D07 from 7q31//4.5e-52:933:61//Hs.3781:AC004142
 10 F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901
 F-NT2RP4000918
 F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865
 F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:AI341503
 F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532
 20 F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:AI281371
 F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542
 F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888
 F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:AI084058
 F-NT2RP4000979
 F-NT2RP4000984
 30 F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913
 F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068
 F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204
 F-NT2RP4001004
 F-NT2RP4001006//ESTs, Moderately similar to ROSA26 AS [M.musculus]//7.4e-90:425:99//Hs.126082:AI077718
 F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204
 F-NT2RP4001029//Human transcription factor LSF mRNA A, complete cds//9.6e-84:778:74//Hs.154970:U03494
 F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:L40157
 F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157

- F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.15548
1:AJ006470
- F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA
702497
- F-NT2RP4001079//Homo sapiens mRNA for putative Ca2
+-transporting ATPase, partial//1.4e-131:634:98//H
s.106778:AJ010953
- F-NT2RP4001080//Polypyrimidine tract binding prote
in (hnRNP I) {alternative products}//0.025:166:66/ 10
/Hs.146459:X66975
- F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 pro
tein, partial cds//1.5e-85:604:86//Hs.13273:AB0111
64
- F-NT2RP4001095
- F-NT2RP4001100//ESTs, Weakly similar to C17G10.1
[C.elegans]//1.4e-93:448:98//Hs.105837:AA536054
- F-NT2RP4001117//ESTs, Highly similar to PROTEIN T
RANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familia
ris]//2.2e-26:171:92//Hs.14038:R06800 20 0
- F-NT2RP4001122//Human mRNA for histone H1x, comple
te cds//0.99:185:66//Hs.109804:D64142
- F-NT2RP4001126//ESTs, Moderately similar to The KI
AA0138 gene product is novel. [H.sapiens]//5.8e-37:
185:100//Hs.126925:AA931237
- F-NT2RP4001138//ESTs//3.4e-09:125:77//Hs.143382:AA
476266
- F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:AI3582
61
- F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992 30
207
- F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16
171
- F-NT2RP4001150//AXONIN-1 PRECURSOR//7.7e-07:562:59
//Hs.2998:X67734
- F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA3773
24
- F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:A
A884264
- F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA3773 40
24
- F-NT2RP4001207
- F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:AI0
17636
- F-NT2RP4001213//KRAB zinc finger protein {alternat
ive products}//1.1e-45:187:74//Hs.22556:U37251
- F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA
936262
- F-NT2RP4001228//Homo sapiens actin binding protein
MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.1229 50
67:AF059569
- F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, comple
te cds//1.0:257:59//Hs.106387:AF029778
- F-NT2RP4001256//Human mRNA for KIAA0273 gene, comp
lete cds//0.96:247:62//Hs.75899:D87463
- F-NT2RP4001260//Syntrophin, alpha (dystrophin-asso
ciated protein A1, 59kD, acidic component)//0.015:
246:62//Hs.31121:U40571
- F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequ
ence//1.2e-06:259:64//Hs.71168:AF070578
- F-NT2RP4001276//Homo sapiens CAGF9 mRNA, partial c
ds//7.6e-06:266:62//Hs.110826:U80736
- F-NT2RP4001313//Homo sapiens mitochondrial outer m
embrane protein (TOM40) mRNA, nuclear gene encodin
g mitochondrial protein, complete cds//2.3e-31:53
5:65//Hs.30928:AF043250
- F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:AI3
75917
- F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA60311
- F-NT2RP4001339
- F-NT2RP4001343
- F-NT2RP4001345//Lecithin-cholesterol acyltransfera
se//8.0e-39:686:64//Hs.112125:M12625
- F-NT2RP4001351//Human ovarian cancer downregulated
myosin heavy chain homolog (Doc1) mRNA, complete
cds//2.0e-31:784:62//Hs.15432:U53445
- F-NT2RP4001353//Homo sapiens chromosome 7q22 seque
nce//0.0034:497:57//Hs.125742:AF053356
- F-NT2RP4001372
- F-NT2RP4001373//Homo sapiens clone DtlP1b11 mRNA,
CAG repeat region//0.43:290:58//Hs.82101:Z50194
- F-NT2RP4001375
- F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.8
2276:L09190
- F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:AI3
93918
- F-NT2RP4001407//Homo sapiens mRNA for RGS5, comple
te cds//0.93:218:58//Hs.24950:AB008109
- F-NT2RP4001414//Human mRNA for KIAA0202 gene, part
ial cds//6.3e-78:818:71//Hs.80712:D86957
- F-NT2RP4001433//Zinc finger protein 10 (K0X 1)//1.
1e-88:839:73//Hs.2479:X78933
- F-NT2RP4001442
- F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 pro
tein, complete cds//0.0075:218:63//Hs.41153:AB0183
26
- F-NT2RP4001474//ESTs, Weakly similar to probable C
BP3 protein homolog [C.elegans]//2.1e-90:460:96//H
s.26676:AA033997

3905

3906

- F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523
- F-NT2RP4001498//ESTs, Weakly similar to CA BINDING PROTEIN BETA-2 CHAIN[H.sapiens]//0.25:216:60//Hs.63220:AA522707
- F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:N40395
- F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260
- F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]//9.4e-30:173:94//Hs.5570:AI377863
- F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494
- F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:U13220
- F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534
- F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174
- F-NT2RP4001567
- F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN INMET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]//1.1e-54:252:83//Hs.158208:AA167836
- F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
- F-NT2RP4001574
- F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228
- F-NT2RP4001592
- F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
- F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:AI343952
- F-NT2RP4001634
- F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN INFKH1-STH1 INTERGENIC REGION [S.cerevisiae]//8.6e-57:287:97//Hs.117439:C18436
- F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409
- F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.0:311:59//Hs.57969:AA203629
- F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376
- F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080
- F-NT2RP4001696
- F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
- F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302
- F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
- F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
- F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
- F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522
- F-NT2RP4001803//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L36069
- F-NT2RP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
- F-NT2RP4001823//Human faciogenital dysplasia (FGD1) mRNA, complete cds//3.1e-07:509:59//Hs.1572:U11690
- F-NT2RP4001828
- F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-55:555:73//Hs.78398:D31888
- F-NT2RP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
- F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-57:813:65//Hs.6336:AB014572
- F-NT2RP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170
- F-NT2RP4001889
- F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-108:535:97//Hs.15144:AC005014
- F-NT2RP4001896
- F-NT2RP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
- F-NT2RP4001927
- F-NT2RP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//2.8e-54:375:84//Hs.119294:AI379442
- F-NT2RP4001946//EST//0.050:268:60//Hs.148341:AA921894
- F-NT2RP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
- F-NT2RP4001953//ESTs//0.018:206:65//Hs.130105:AA904868
- F-NT2RP4001966//Human DNA sequence from clone 1052

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M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022718

F-NT2RP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, complete cds//0.0019:279:65//Hs.159439:AF092047

F-NT2RP4002018//ESTs, Highly similar to RING CANA L PROTEIN [Drosophila melanogaster]//0.58:463:55//Hs.3826:U69560

F-NT2RP4002047//EST//2.5e-13:102:90//Hs.148997:AI243139

F-NT2RP4002052

F-NT2RP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873

F-NT2RP4002071//Homo sapiens TTAGGG repeat binding factor 2 (hTRF2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999

F-NT2RP4002075

F-NT2RP4002078//ESTs, Moderately similar to zinc finger protein [H. sapiens]//1.0e-38:243:90//Hs.139115:AA325104

F-NT2RP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M55654

F-NT2RP4002083//H. sapiens Pur (pur-alpha) mRNA, complete cds//0.0015:152:70//Hs.25180:M96684

F-NT2RP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cds//8.0e-10:401:59//Hs.89616:M55284

F-NT2RP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204

F-NT2RP4002888

F-NT2RP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960

F-NT2RP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:193:96//Hs.74456:U34995

F-NT2RP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071

F-NT2RP5003477//Eukaryotic translation initiation factor 3 (eIF-3) p36 subunit//0.18:271:60//Hs.139745:U39067

F-NT2RP5003492

F-NT2RP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotransferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179

F-NT2RP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//5.1e-14:348:62//Hs.154050:AC004131

F-NT2RP5003512//Homo sapiens mRNA for KIAA0642 pro

3908

tein, partial cds//0.94:202:63//Hs.8152:AB014542
F-NT2RP5003522

F-NT2RP5003524//ESTs//8.7e-08:340:62//Hs.152730:AI308943

F-NT2RP5003534

F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.0e-69:373:94//Hs.108258:AB007934

F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:AI391729

F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina moschata]//4.4e-75:355:99//Hs.36727:AI051983

F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304

F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-171:815:98//Hs.81449:AF058922

F-OVARC1000017//Homo sapiens mRNA for NTAK, complete cds//0.50:482:58//Hs.113264:AB005060

20 F-OVARC1000035//Homo sapiens GA17 protein mRNA, complete cds//2.2e-37:238:89//Hs.69469:AF064603

F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA03549

F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor [H. sapiens]//6.7e-60:305:97//Hs.31696:H50008

F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798

F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543

F-OVARC1000085

F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442

F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017:414:59//Hs.106387:AF029778

F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600

F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C. elegans]//2.9e-73:406:92//Hs.109463:AI205174

F-OVARC1000109

F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250

F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete cds//3.4e-43:532:72//Hs.118401:AB011134

F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:AI384010

F-OVARC1000139

F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA29

- 1293
F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
F-OVARC1000151
F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)//0.10:504:59//Hs.154083:U70136
F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:AI249131
F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379
F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:466:68//Hs.8136:U81984
F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.00084:170:65//Hs.107747:AI357868
F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA55306
F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN BINDING PROTEIN PRECURSOR [Feliscatus]//0.51:193:66//Hs.6194:AI378579
F-OVARC1000321
F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946
F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
F-OVARC1000347
F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-06:353:62//Hs.121895:AF001450
F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:231:64//Hs.156016:D50930
F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:231:58//Hs.156016:D50930
F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7e-25:190:84//Hs.139513:AA259082
- F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93:281:60//Hs.76279:X53416
F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:116:99//Hs.83987:U09284
F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:AI377423
F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.2e-140:566:99//Hs.12334:AB014583
F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:AI024524
F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58//Hs.108112:AF070640
F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
F-OVARC1000479
F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:AI023327
F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-115:539:99//Hs.111285:AF051850
F-OVARC1000526//ESTs//2.9e-08:368:61//Hs.42771:N26740
F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475
F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA, complete cds//0.87:135:66//Hs.85302:U76421
F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358
F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200
F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729
F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725
F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722
F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:AI281881

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F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:ABO11162
 F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:AI277106
 F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279
 F-OVARC1000681//EST//0.017:315:61//Hs.147799:AI221639
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds//4.8e-153:549:99//Hs.125315:AF027156
 F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306
 F-OVARC1000700
 F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:AI284320
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661
 F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:AI141736
 F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411
 F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196
 F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-2 [H.sapiens]//1.2e-38:194:99//Hs.157059:W28130
 F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793
 F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835
 F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584
 F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032
 F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:ABO14543
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584

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F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155
 F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.159234:U89995
 F-OVARC1000883//ESTs//0.44:154:63//Hs.98183:AA417143
 F-OVARC1000885//EST//0.91:152:63//Hs.160765:AI313323
 F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:AI025777
 F-OVARC1000890
 F-OVARC1000891
 F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818
 F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:AI376601
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691
 F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456
 F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:M11119
 F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078
 F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.136243:AA307843
 F-OVARC1000948
 F-OVARC1000959//EST//0.65:293:55//Hs.134725:AI088986
 F-OVARC1000960//Ley I-L//1.4e-41:425:72//Hs.37062:AC005952
 F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288
 F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:AI283069
 F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661
 F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U57317
 F-OVARC1000999//Homo sapiens mRNA for chemokine LE C precursor, complete cds//0.0056:209:62//Hs.10458:AF088219
 F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114

- F-OVARC1001004
F-OVARC1001010
F-OVARC1001011//ESTs, Moderately similar to Tera
[*M. musculus*]//3.8e-47:234:99//Hs.110327:AA205866
F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE
I ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75
063:ALO23584
F-OVARC1001034//ESTs, Highly similar to mitogen-in
duced [*M. musculus*]//3.9e-97:578:89//Hs.111974:AI05
0735
F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, c
omplete cds//8.6e-152:733:97//Hs.9899:AF099149
F-OVARC1001040//ESTs//2.2e-38:204:96//Hs.128927:AI
168074
F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017
385
F-OVARC1001051
F-OVARC1001055//Human pre-B cell enhancing factor
(PBEF) mRNA, completecds//1.1e-46:381:81//Hs.15496
8:U02020
F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:AI31
2873
F-OVARC1001065//ESTs, Weakly similar to C50F4.12
[*C. elegans*]//1.4e-21:183:84//Hs.46680:AA809451
F-OVARC1001068//Homo sapiens Era GTPase A protein
(HERA-A) mRNA, partialcds//6.6e-132:620:98//Hs.342
6:AF082657
F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA
709013
F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001
937
F-OVARC1001085//H. sapiens mRNA for sortilin//0.99:
142:67//Hs.104247:X98248
F-OVARC1001092//Homo sapiens mRNA for JM5 protein,
complete CDS (clone IMAGE 53337, LLNLc110F1857Q7
(RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//
1.3e-75:289:95//Hs.21753:AJ005897
F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete
cds//1.2e-73:351:86//Hs.12912:AF015913
F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) 40
mRNA, complete cds//2.1e-151:710:98//Hs.26584:AF05
1782
F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA
813102
F-OVARC1001118
F-OVARC1001129
F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.7545
1:AF055008
F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA
621725
- F-OVARC1001162
F-OVARC1001167
F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:AI0782
79
F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA
813287
F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA
226159
F-OVARC1001173//ESTs, Moderately similar to GLUTA
10 MATE DEHYDROGENASE 1 PRECURSOR [*Homo sapiens*]//1.8
e-11:192:69//Hs.130020:AA887581
F-OVARC1001176//Homo sapiens chromosome 19, cosmid
R26529//0.61:387:58//Hs.91103:AC005551
F-OVARC1001180//ESTs, Weakly similar to ubiquitin
S6(1) [*D. melanogaster*]//1.5e-13:199:71//Hs.109966:
C06057
F-OVARC1001188//ESTs, Weakly similar to HYPOTHETIC
AL 27.8 KD PROTEIN INVMA7-RPS31A INTERGENIC REGION
[*S. cerevisiae*]//1.4e-52:324:90//Hs.114673:W72675
20 F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA
883889
F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X5
1688
F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745
676
F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:AI424
825
F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.
75243:D42040
30 F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:AI3
77837
F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576
821
F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625
224
F-OVARC1001271//Homo sapiens mRNA for KIAA0643 pro
tein, partial cds//6.8e-144:644:96//Hs.155995:AB01
4543
F-OVARC1001282//ESTs, Weakly similar to Ydr438wp
[*S. cerevisiae*]//0.11:355:60//Hs.108812:AA044835
F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78
172
F-OVARC1001306//Homo sapiens nuclear receptor co-r
epressor N-CoR mRNA, complete cds//0.20:188:64//H
s.152455:AF044209
F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA
884264
F-OVARC1001330
F-OVARC1001339//Solute carrier family 4, anion exc
50 hanger, member 2 (erythrocyte membrane protein ban

- d 3-like 1)/0.021:232:62//Hs.79410:U62531
 F-OVARC1001341//ESTs, Weakly similar to C17G10.1
 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054
 F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA89749
 3
 F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67
 251
 F-OVARC1001357//Homo sapiens jerky gene product ho
 molog mRNA, complete cds//0.64:198:61//Hs.105940:A
 F004715
 F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:AI
 264633
 F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:AI
 025777
 F-OVARC1001372//Homo sapiens mRNA for KIAA0654 pro
 tein, partial cds//1.4e-69:533:74//Hs.109299:AB014
 554
 F-OVARC1001376//Homo sapiens neuronal thread prote
 in AD7c-NTP mRNA, complete cds//2.5e-49:365:73//H
 s.129735:AF010144
 F-OVARC1001381//Homo sapiens mRNA for candidate tu
 mor suppressor involved in B-CLL//4.1e-149:683:99/
 /Hs.151428:AJ224819
 F-OVARC1001391//Homo sapiens methyl-CpG binding pr
 otein MBD2 (MBD2) mRNA, complete cds//0.097:235:65
 //Hs.25674:AF072242
 F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28
 225
 F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete
 cds//1.3e-150:707:98//Hs.21586:AB006651
 F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, com
 plete cds//1.6e-49:586:69//Hs.74597:U52426
 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T8
 3651
 F-OVARC1001436
 F-OVARC1001442
 F-OVARC1001453
 F-OVARC1001476//ESTs, Weakly similar to HYPOTHETIC
 AL 38.6 KD PROTEIN INTIF4631-KRE11 INTERGENIC REGI
 ON [S.cerevisiae]//1.9e-125:581:99//Hs.110950:AI04
 1823
 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584
 568
 F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA
 897343
 F-OVARC1001496//Homo sapiens C-terminal binding pr
 otein 2 mRNA, completecds//2.6e-86:479:92//Hs.653
 4:AF016507
 F-OVARC1001506//Polycystic kidney disease 1 (autos
 omal dominant)//1.1e-97:538:92//Hs.75813:L33243
- F-OVARC1001525
 F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:
 U53786
 F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N9059
 5
 F-OVARC1001555
 F-OVARC1001577//Homo sapiens SRp46 splicing factor
 retropseudogene mRNA//6.8e-57:275:98//Hs.155160:A
 F031166
 10 F-OVARC1001600//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:
 271:60//Hs.108465:AI144299
 F-OVARC1001610//ESTs, Weakly similar to F22E10.5
 [C.elegans]//1.4e-43:216:99//Hs.120002:AI038398
 F-OVARC1001611
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA9935
 00
 F-OVARC1001668//Homo sapiens mRNA for KIAA0572 pro
 tein, partial cds//3.3e-37:217:94//Hs.14409:AB0111
 20 44
 F-OVARC1001702//Homo sapiens mRNA for hSOX20 prote
 in, complete cds//5.9e-49:393:81//Hs.95582:AB00686
 7
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA7
 57229
 F-OVARC1001711//Fms-related tyrosine kinase 3 liga
 nd//0.049:353:61//Hs.428:U03858
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA
 621807
 30 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA
 236863
 F-OVARC1001731//Tropomyosin beta chain (skeletal m
 uscle)//1.7e-83:617:80//Hs.155652:X06825
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:AI1485
 88
 F-OVARC1001762
 F-OVARC1001766//Homo sapiens eukaryotic translatio
 n initiation factor eIF3, p35 subunit mRNA, comple
 te cds//1.4e-150:706:98//Hs.155377:U97670
 40 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 pro
 tein, complete cds//9.8e-117:580:96//Hs.15869:AB01
 4575
 F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:AI218
 697
 F-OVARC1001791
 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA06283
 0
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:AI0
 05102
 50 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 pro

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tein, complete cds//0.77:362:58//Hs.116753:AB018287

F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172

F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825

F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453

F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567

F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537

F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973

F-OVARC1001861

F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611

F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709

F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127

F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953

F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749

F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:AI263834

F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261

F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263

F-OVARC1001928

F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204

F-OVARC1001943//ESTs, Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794

F-OVARC1001949//KRAB zinc finger protein {alternative products}//1.8e-17:294:67//Hs.22556:U37251

F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:AI051228

F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639

F-OVARC1001989//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-2

3918

3:213:78//Hs.105292:AA504776

F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417

F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934

F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:AI375865

F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063

F-OVARC1002107

F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174

F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913

F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022

F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795

20 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097

F-OVARC1002158//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:AI357868

F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568

F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517

F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230

F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:AI378928

F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789

F-PLACE1000014

F-PLACE1000031

F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088

F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494

F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:AI076755

F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499

F-PLACE1000066//ESTs, Weakly similar to coded for by C. elegans cDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:AI356771

F-PLACE1000078//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-

- 15:203:70//Hs.157422:R85366
 F-PLACE1000081//Human transporter protein (g17) mRNA, complete cds//0.30:324:60//Hs.76460:U49082
 F-PLACE1000094
 F-PLACE1000133//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:AI380378
 F-PLACE1000142//ESTs, Weakly similar to enoyl-CoA hydratase [H. sapiens]//7.7e-27:205:85//Hs.9670:AA632135
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291
 F-PLACE1000185
 F-PLACE1000213
 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:AI167255
 F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
 F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:W22022
 F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:AI278202
 F-PLACE1000308//EST//0.0024:253:62//Hs.144238:W52294
 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
 F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
 F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197
 F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153
 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
 F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516
 F-PLACE1000406//ESTs, Highly similar to PTB-ASSOCIATED SPLICING FACTOR[Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260
 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
 F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053
 F-PLACE1000424
 F-PLACE1000435//Homo sapiens mRNA for XPR2 protein 50
- //0.58:674:55//Hs.44766:AJ007590
 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531
 F-PLACE1000453//Human mRNA for MTC8a protein, complete cds//0.026:240:60//Hs.31551:D43638
 F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878
 F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:302:60//Hs.153014:AB002353
 F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573
 F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds//0.0046:223:65//Hs.75578:M85289
 F-PLACE1000562
 F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538
 F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:525:72//Hs.21838:AF038179
 F-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kD//2.3e-85:503:88//Hs.62661:M55542
 F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//1.2e-165:798:97//Hs.159597:AJ012449
 F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751
 F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.98:215:60//Hs.8152:AB014542
 F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986
 F-PLACE1000636
 F-PLACE1000653//Homo sapiens N-acetylglucosamine-6-phosphate mutase mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265
 F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F185707 (RZPD Berlin))//7.5e-158:775:97//Hs.29595:AJ005896
 F-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1)mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353
 F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949
 F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-38:426:70//Hs.47313:D87447
 F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288
 F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene,

3921

3922

- complete cds//0.72:331:57//Hs.37110:U10694
 F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.7911
 O:M60858
 F-PLACE1000769
 F-PLACE1000785//Homo sapiens mRNA for KIAA0648 pro
 tein, partial cds//1.1e-139:663:98//Hs.31921:AB014
 548
 F-PLACE1000786//Myosin, heavy polypeptide 9, non-m
 uscle//8.5e-06:362:59//Hs.44782:Z82215
 F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56 10
 079
 F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N3
 2189
 F-PLACE1000841//EST//0.47:143:61//Hs.144096:AI0321
 80
 F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial c
 ds//1.6e-06:266:63//Hs.110826:U80736
 F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA4
 70000
 F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA7 20
 77428
 F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906
 455
 F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA
 195201
 F-PLACE1000948
 F-PLACE1000972//Homo sapiens enhancer of filamen
 ta tion (HEF1) mRNA, complete cds//7.9e-10:294:66//H
 s.80261:L43821
 F-PLACE1000977//ESTs, Weakly similar to coded for 30
 by C. elegans cDNA yk28h2.5 [C.elegans]//9.3e-45:3
 09:88//Hs.13531:R61789
 F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF1
 O)//0.0034:229:62//Hs.8597:L11672
 F-PLACE1000987//Homo sapiens mRNA for KIAA0724 pro
 tein, complete cds//2.6e-141:694:96//Hs.158497:AB0
 18267
 F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39
 913
 F-PLACE1001007//Guanylate cyclase 2D, membrane (re 40
 tina-specific)//0.050:338:61//Hs.1974:M92432
 F-PLACE1001010//H.sapiens mRNA for retrotransposon
 //1.6e-45:371:80//Hs.6940:Z48633
 F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA2
 56876
 F-PLACE1001024
 F-PLACE1001036//EST//1.0:133:65//Hs.161424:AI42474
 1
 F-PLACE1001054//Human plectin (PLEC1) mRNA, comple
 te cds//0.98:284:59//Hs.79706:U53204 50
- F-PLACE1001062
 F-PLACE1001076//EST//0.84:223:59//Hs.161147:AI4178
 59
 F-PLACE1001088
 F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA,
 complete cds//1.0e-96:489:96//Hs.95448:AF065485
 F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595
 817
 F-PLACE1001118//Homo sapiens KRAB domain zinc fing
 er protein (ZFP37) mRNA, complete cds//8.2e-66:67
 6:71//Hs.150406:AF022158
 F-PLACE1001136//Amphiregulin (schwannoma-derived g
 rowth factor)//1.5e-16:122:91//Hs.1257:M30704
 F-PLACE1001168
 F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R9
 5135
 F-PLACE1001185//ESTs, Weakly similar to ZK792.1
 [C.elegans]//1.6e-28:421:66//Hs.8763:W30741
 F-PLACE1001238
 F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R4
 9494
 F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA
 913929
 F-PLACE1001272//COATOMER BETA' SUBUNIT//0.012:50:9
 6//Hs.75724:X70476
 F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:N5128
 3
 F-PLACE1001280//Homo sapiens hyperpolarization-act
 ivated channel 1 (IH1)mRNA, partial cds//1.2e-08:5
 86:58//Hs.124161:AF065164
 F-PLACE1001294//Homo sapiens mRNA for myosin phosph
 atase target subunit1 (MYPT1)//0.91:221:61//Hs.16
 533:D87930
 F-PLACE1001304//Human zinc finger protein mRNA, co
 mplete cds//8.6e-08:370:60//Hs.42672:AF016052
 F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z7
 8385
 F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA
 699591
 F-PLACE1001351
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 pro
 tein, partial cds//2.8e-26:155:95//Hs.61638:AB0183
 42
 F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA,
 complete cds//3.4e-44:393:79//Hs.152005:AF009615
 F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA9737
 48
 F-PLACE1001384//Homo sapiens multi PDZ domain prot
 ein MUPP1 (MUPP1) mRNA, complete cds//2.6e-09:117:
 84//Hs.21301:AF093419

- F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 [H.sapiens]//0.00083:187:64//Hs.5399:N30646
- F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransferase, complete CDS//0.0038:496:57//Hs.97681:AJ223333
- F-PLACE1001399//Human melanoma antigen recognized by T-cells (MART-1) mRNA//7.0e-45:456:75//Hs.154069:U06452
- F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//6.5e-71:365:96//Hs.110404:AF091087
- F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232
- F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987
- F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510
- F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:AI379455
- F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:H52716
- F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529
- F-PLACE1001503
- F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914
- F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753
- F-PLACE1001545
- F-PLACE1001551
- F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835
- F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete cds//0.013:159:66//Hs.266:U06233
- F-PLACE1001603//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//1.1e-10:133:77//Hs.146406:AF069987
- F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:AI342230
- F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
- F-PLACE1001611//Human faciogenital dysplasia (FGD1) mRNA, complete cds//0.96:141:66//Hs.1572:U11690
- F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.4e-76:702:75//Hs.159277:AB018341
- F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:AI276198
- F-PLACE1001640
- F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
- F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
- F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//Hs.24309:AI125696
- F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, complete cds//6.0e-30:347:76//Hs.101555:U93869
- F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-69:369:73//Hs.12413:D83776
- F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:AI391686
- F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cds//0.0084:484:60//Hs.129892:AB011094
- F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:64//Hs.1480:M60052
- F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
- F-PLACE1001745
- F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361
- F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//2.8e-160:773:97//Hs.4812:AF061243
- F-PLACE1001756//Homo sapiens tapasin (NCS-17) mRNA, complete cds//2.7e-35:269:83//Hs.5247:AF029750
- F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283
- F-PLACE1001771//Human putative calcium influx channel (htrp3) mRNA, complete cds//3.4e-52:548:72//Hs.150981:U47050
- F-PLACE1001781
- F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115
- F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138
- F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953
- F-PLACE1001821
- F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494
- F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214
- F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906
- F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:AI343

- 257
F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R182
20
F-PLACE1001920//Homo sapiens TNF-induced protein G
G2-1 mRNA, complete cds//4.0e-153:685:95//Hs.1783
9:AF099936
F-PLACE1001928//H.sapiens HUMM9 mRNA//0.063:196:66
//Hs.2750:X74837
F-PLACE1001983//Homo sapiens Jagged 2 mRNA, comple
te cds//9.8e-06:431:58//Hs.106387:AF029778
F-PLACE1001989
F-PLACE1002004
F-PLACE1002046
F-PLACE1002052//Human mRNA for phospholipase C, co
mplete cds//0.0092:465:58//Hs.153322:D42108
F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA9085
55
F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 pro
tein, partial cds//4.2e-39:635:64//Hs.38176:AB0111
78
F-PLACE1002090//Homo sapiens signal recognition pa
rticle 72 (SRP72) mRNA, complete cds//4.3e-83:388:
99//Hs.5171:AF069765
F-PLACE1002115//EST//0.18:215:62//Hs.135747:AI0026
37
F-PLACE1002119//Human transcription factor ETR101
mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831
F-PLACE1002140//EST, Moderately similar to ALPHA-
1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75
//Hs.144290:T61747
F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA1156
31
F-PLACE1002157//Human mRNA for KIAA0392 gene, part
ial cds//2.8e-51:440:79//Hs.40100:AB002390
F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:AI366
891
F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90
627
F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H6
6674
F-PLACE1002205//Human clone 23695 mRNA sequence//
0.00080:472:60//Hs.90798:U79289
F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA39
9989
F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:AI
024442
F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA
970935
F-PLACE1002259//Human Line-1 repeat mRNA with 2 op 50
en reading frames//2.3e-75:434:83//Hs.23094:M19503
F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA0366
75
F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA2802
79
F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA03
4291
F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA43
6710
10 F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA
421067
F-PLACE1002437//Human ATP binding cassette transpo
rter (ABCR) mRNA, complete cds//2.6e-23:458:66//H
s.40993:AF000148
F-PLACE1002438//EST//0.81:48:77//Hs.158575:AI36894
7
F-PLACE1002450//Homo sapiens KRAB domain zinc fing
er protein (ZFP37) mRNA, complete cds//7.1e-07:27
0:66//Hs.150406:AF022158
20 F-PLACE1002465
F-PLACE1002474//Homo sapiens mRNA for matrilin-4,
partial//1.3e-14:369:63//Hs.129361:AJ007581
F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA
343523
F-PLACE1002493
F-PLACE1002499
F-PLACE1002500//Human putative zinc transporter Zn
T-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//H
s.111967:U76010
30 F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA1
26482
F-PLACE1002529//Homo sapiens mRNA for KIAA0713 pro
tein, partial cds//2.9e-144:583:95//Hs.88756:AB018
256
F-PLACE1002532//Homo sapiens BAC clone RG300E22 fr
om 7q21-q31.1//3.1e-115:566:96//Hs.99348:AC004774
F-PLACE1002537//Thiopurine S-methyltransferase//1.
9e-28:198:86//Hs.51124:AF019369
F-PLACE1002571//Homo sapiens mRNA for TP55, comple
te cds//0.99:274:59//Hs.138202:AF027866
F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90
627
F-PLACE1002583//EST//0.0028:348:61//Hs.160396:AI39
3725
F-PLACE1002591//Human mRNA for actin binding prote
in p57, complete cds//2.8e-27:279:74//Hs.109606:D4
4497
F-PLACE1002598//EST//0.011:209:62//Hs.131470:AI024
187
50 F-PLACE1002604//EST//0.47:220:61//Hs.145434:AI1989

- 15
F-PLACE1002625
F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-3
6:693:62//Hs. 80562: X04412
F-PLACE1002665//EST//0.15:156:65//Hs. 161793: AA3807
06
F-PLACE1002685//Homo sapiens B cell linker protein
BLNK mRNA, alternatively spliced, complete cds//
1.1e-187:804:97//Hs. 124903: AF068180
F-PLACE1002714//Human involucrin mRNA//3.6e-08:50
9:60//Hs. 157091: M13903
F-PLACE1002722//Human protease-activated receptor
3 (PAR3) mRNA, complete cds//0.34:230:58//Hs. 15919
6: U92971
F-PLACE1002768//EST//0.37:126:69//Hs. 125353: AA8770
80
F-PLACE1002772//ESTs//0.0017:147:69//Hs. 132439: AA9
23728
F-PLACE1002775//EST//5.5e-09:129:75//Hs. 135336: AI0
49827
F-PLACE1002782//Homo sapiens I-1 receptor candidat
e protein mRNA, complete cds//0.0031:298:62//Hs. 26
285: AF082516
F-PLACE1002794//ESTs//0.71:125:66//Hs. 97441: AI3689
26
F-PLACE1002811//Human mRNA for KIAA0172 gene, part
ial cds//5.8e-46:567:70//Hs. 77546: D79994
F-PLACE1002815
F-PLACE1002816//Homo sapiens mRNA for KIAA0600 pro
tein, partial cds//4.3e-70:687:73//Hs. 9028: AF03969
1
F-PLACE1002834//ESTs//2.6e-41:393:74//Hs. 120206: AI
089163
F-PLACE1002839//ESTs//0.26:177:63//Hs. 149013: AI334
167
F-PLACE1002851//EST//0.0034:102:72//Hs. 129630: AI00
0405
F-PLACE1002853//ESTs//1.1e-20:136:90//Hs. 125895: AA
889024
F-PLACE1002881//Interleukin 10//1.1e-41:454:72//H
s. 2180: M57627
F-PLACE1002908//ESTs//3.8e-48:325:88//Hs. 54702: AI0
40029
F-PLACE1002941//ESTs//5.0e-18:128:88//Hs. 17376: AA8
55056
F-PLACE1002962
F-PLACE1002968//ESTs, Highly similar to trg gene p
roduct [R. norvegicus]//0.031:372:59//Hs. 8021: AI041
815
F-PLACE1002991
F-PLACE1002993
F-PLACE1002996//ESTs, Weakly similar to T20D3.3
[C. elegans]//1.3e-12:104:86//Hs. 124808: T86959
F-PLACE1003025//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0510//0.99:192:64//Hs. 92660:
AB007979
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 pro
tein, partial cds//2.0e-131:632:97//Hs. 129872: AB01
1088
10 F-PLACE1003044//Homo sapiens mRNA for KIAA0667 pro
tein, partial cds//2.7e-14:555:58//Hs. 154740: AB014
567
F-PLACE1003045
F-PLACE1003092//ESTs//1.1e-108:506:99//Hs. 22119: AA
885491
F-PLACE1003100//Human Hep27 protein mRNA, complete
cds//2.9e-66:650:73//Hs. 102137: U31875
F-PLACE1003108//EST//0.016:181:65//Hs. 119762: AA703
419
20 F-PLACE1003136
F-PLACE1003145
F-PLACE1003153//ESTs//3.1e-09:209:65//Hs. 111583: AA
463590
F-PLACE1003174//ESTs//0.073:97:69//Hs. 12992: W01997
F-PLACE1003176//ESTs//3.3e-60:296:90//Hs. 58239: AA2
15797
F-PLACE1003190//Homo sapiens C19steroid specific U
DP-glucuronosyltransferase mRNA, complete cds//0.9
8:221:60//Hs. 139756: U59209
30 F-PLACE1003200//EST//0.0021:309:60//Hs. 140561: AA76
5532
F-PLACE1003205//EST//1.2e-07:204:65//Hs. 147372: AI2
08770
F-PLACE1003238//ESTs//7.4e-62:343:94//Hs. 121302: AA
758208
F-PLACE1003249//Insulin-like growth factor 1 (soma
tomedia C)//0.99:175:62//Hs. 85112: X57025
F-PLACE1003256
F-PLACE1003258//H. sapiens mRNA for ZYG homologue//
0.00020:217:64//Hs. 29285: X99802
F-PLACE1003296//ESTs//2.6e-14:80:86//Hs. 155441: AA5
33106
F-PLACE1003302//Human repressor transcriptional fa
ctor (ZNF85) mRNA, complete cds//4.3e-51:700:67//H
s. 37138: U35376
F-PLACE1003334
F-PLACE1003342//ESTs//0.94:310:57//Hs. 131502: AI023
308
F-PLACE1003343//EST//1.2e-09:114:77//Hs. 103418: AA0
35568
50

3929

3930

- F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715
- F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277
- F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575
- F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858
- F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:AI343009
- F-PLACE1003375//EST//0.75:119:68//Hs.160270:AI149069
- F-PLACE1003383
- F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-14 [Rattus norvegicus]//8.9e-113:590:94//Hs.125175:AI142546
- F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178
- F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846
- F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912
- F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874
- F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635
- F-PLACE1003516//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627
- F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145
- F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:Z48633
- F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248
- F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428
- F-PLACE1003553
- F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
- F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367
- F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932
- F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
- F-PLACE1003592//ESTs, Moderately similar to !!!! A 50
- LU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620
- F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
- F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961
- F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:D83200
- F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104
- F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
- F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503
- F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
- F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
- F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413
- F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299
- F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:669:95//Hs.98658:AF053305
- F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
- F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553
- F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344
- F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
- F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983
- F-PLACE1003768//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629
- F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
- F-PLACE1003783
- F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308
- F-PLACE1003795//Human homologue of yeast sec7 mRNA A, complete cds//0.85:314:60//Hs.1050:M85169
- F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786

- F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI2
54165
- F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI1681
24
- F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370
359
- F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI0
91257
- F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72
//Hs.49007:X76770
- F-PLACE1003886
- F-PLACE1003888//Human mRNA for phospholipase C, co
mplete cds//8.4e-55:702:67//Hs.153322:D42108
- F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24
050
- F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI0
04944
- F-PLACE1003903//CTP synthetase//1.6e-49:528:71//H
s.84112:X52142
- F-PLACE1003915//ESTs, Highly similar to ARGINYL-T 20
RNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharom
yces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
- F-PLACE1003923//Interferon, alpha 16//0.48:278:60/
/Hs.56303:M28585
- F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA7
07537
- F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123
536
- F-PLACE1003968//Human 5'-AMP-activated protein kin
ase, gamma-1 subunit mRNA, complete cds//2.0e-47:5 30
22:71//Hs.3136:U42412
- F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI0
26812
- F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA5069
40
- F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA1
48516
- F-PLACE1004118//Spleen focus forming virus (SFFV)
proviral integration oncogene sp1//0.85:164:64//H
s.153045:X52056
- F-PLACE1004128//Guanine nucleotide binding protein
(G protein), beta polypeptide 1//3.1e-41:422:74//
Hs.3620:X04526
- F-PLACE1004149//ESTs, Weakly similar to F48F7.1
[C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
- F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053
552
- F-PLACE1004161//Human mRNA for KIAA0200 gene, comp
lete cds//0.85:269:64//Hs.76986:D83785
- F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI3 50
- 43666
- F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA2
92201
- F-PLACE1004203//Homo sapiens GPI-anchored membrane
protein CDw108 precursor, mRNA, complete cds//1.3
e-145:695:98//Hs.24640:AF069493
- F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699
722
- F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789
273
- F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608
689
- F-PLACE1004258//ESTs, Weakly similar to vanilloid
receptor subtype 1 [R.norvegicus]//1.1e-98:479:97/
/Hs.31718:N29128
- F-PLACE1004270//Homo sapiens CACF9 mRNA, partial c
ds//0.00010:369:63//Hs.110826:U80736
- F-PLACE1004274//Homo sapiens mRNA for KIAA0445 pro
tein, complete cds//0.085:573:56//Hs.154139:AB0079
14
- F-PLACE1004277//Homo sapiens two pore domain K+ ch
annel (TASK-2) mRNA, complete cds//2.0e-157:756:97
//Hs.127007:AF084830
- F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI
271884
- F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA5
86576
- F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.0
32:513:59//Hs.83363:M34677
- F-PLACE1004316//H.sapiens mRNA for apoptosis speci
fic protein//9.3e-152:797:94//Hs.11171:Y11588
- F-PLACE1004336
- F-PLACE1004358//Homo sapiens connector enhancer of
KSR-like protein CNK1mRNA, complete cds//1.9e-14
0:688:97//Hs.16232:AF100153
- F-PLACE1004376//ESTs, Weakly similar to F27D4.4
[C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
- F-PLACE1004384//Human HsLIM15 mRNA for HsLim15, co
mplete cds//2.0e-49:466:76//Hs.37181:D64108
- F-PLACE1004388
- F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217
871
- F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03
579
- F-PLACE1004428//H.sapiens mRNA for Branched chain
Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
- F-PLACE1004437//Human NAD+-specific isocitrate deh
ydrogenase beta subunit precursor, mRNA, nuclear g
ene encoding mitochondrial protein, completecds//
9.9e-131:536:99//Hs.155410:U49283

- F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI 348867
 F-PLACE1004460
 F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA 824363
 F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA6 44085
 F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA7244 16
 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA39 8163
 F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.5 4457:M33680
 F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//2.5e-147:69 9:97//Hs.122752:AF026445
 F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:N24 150
 F-PLACE1004518
 F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA46131 20 4
 F-PLACE1004550//ESTs, Weakly similar to No definit ion line found [C.elegans]//4.0e-120:627:94//Hs.10 7387:AA058854
 F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
 F-PLACE1004629//Centromere protein B (80kd)//0.001 5:242:64//Hs.85004:X05299
 F-PLACE1004645
 F-PLACE1004646//Retinal pigment epithelium-specifi c protein (65kd)//1.4e-12:386:63//Hs.2133:U18991 30
 F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA2915 90
 F-PLACE1004664
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) g ene//1.5e-66:357:95//Hs.77705:U07563
 F-PLACE1004674//Homo sapiens calcium binding prote in (ALG-2) mRNA, complete cds//1.4e-110:625:91//H s.80019:AF035606
 F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI2 40 81589
 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA 704561
 F-PLACE1004691//Homo sapiens clone 23963 mRNA sequ ence//0.54:242:61//Hs.48483:AF007131
 F-PLACE1004693//ESTs, Weakly similar to pot. ORF I II [H.sapiens]//0.56:96:71//Hs.125740:AA884845
 F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI 306542
 F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA 50 485891
 F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA 700148
 F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA9 10680
 F-PLACE1004743
 F-PLACE1004751//ESTs, Highly similar to CMP-N-ACE TYLNEURAMINATE-BETA-1,4-GALACTOSIDE ALPHA-2,3-SIAL YLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90/ /Hs.6863:W52470
 F-PLACE1004773//Homo sapiens inversin protein mRN A, complete cds//1.7e-172:828:97//Hs.104715:AF0843 67
 F-PLACE1004777//Human myosin-IXb mRNA, complete cd s//1.0e-29:556:63//Hs.159629:U42391
 F-PLACE1004793
 F-PLACE1004804
 F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI3 10340
 F-PLACE1004814//ESTs, Weakly similar to U1 SMALL N UCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]// 2.4e-78:415:95//Hs.80965:AA493284
 F-PLACE1004815//Human mRNA for KIAA0364 gene, comp lete cds//4.3e-14:294:69//Hs.22111:AB002362
 F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA9 34047
 F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943
 F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669
 F-PLACE1004838
 F-PLACE1004840//Protein phosphatase 1, catalytic s ubunit, beta isoform//0.89:200:66//Hs.21537:X80910
 F-PLACE1004868
 F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633 772
 F-PLACE1004900
 F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI4 24382
 F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA90 4929
 F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complet e cds//4.1e-24:402:64//Hs.118910:U82130
 F-PLACE1004930//Homo sapiens TNF-induced protein G G2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839: AF099936
 F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA 628592
 F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
 F-PLACE1004969

3935

F-PLACE1004972//Human retinoic acid- and interfero
n-inducible 58K protein RI58 mRNA, complete cds//
0.031:235:60//Hs.27610:U34605

F-PLACE1004979//Homo sapiens mRNA for KIAA0575 pro
tein, complete cds//4.9e-43:331:83//Hs.153468:AB01
1147

F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI21
8520

F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA2
42831

F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA
351459

F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15
159

F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI
308943

F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA8
13594

F-PLACE1005055//Homo sapiens mRNA for KIAA0576 pro
tein, partial cds//6.2e-161:761:98//Hs.14687:AB011
148

F-PLACE1005066//Homo sapiens actin binding protein
MAYVEN mRNA, completecds//3.0e-11:757:56//Hs.1229
67:AF059569

F-PLACE1005077//EST//0.79:283:59//Hs.89276:AA28389
9

F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA
324740

F-PLACE1005086//Homo sapiens mRNA for KIAA0575 pro
tein, complete cds//1.9e-49:401:80//Hs.153468:AB01
1147

F-PLACE1005101//Homo sapiens (clone zap128) mRNA,
3' end of cds//8.2e-20:194:80//Hs.75437:L40401

F-PLACE1005102//Homo sapiens HIV-1 inducer of shor
t transcripts bindingprotein (FBI1). mRNA, complete
cds//8.9e-18:538:62//Hs.104640:AF000561

F-PLACE1005108//Treacher Collins syndrome suscepti
bility protein//0.73:405:57//Hs.73166:U76366

F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N9322
7

F-PLACE1005128//Breakpoint cluster region protein
BCR//5.6e-08:291:63//Hs.2557:Y00661

F-PLACE1005146//ESTs, Weakly similar to hypothetic
al protein II [H.sapiens]//4.8e-12:360:63//Hs.1421
77:H11741

F-PLACE1005162//Human mRNA for KIAA0118 gene, part
ial cds//3.9e-49:563:72//Hs.154326:D42087

F-PLACE1005176//Homo sapiens mRNA for KIAA0641 pro
tein, complete cds//0.82:259:60//Hs.128316:AB01454
1

3936

F-PLACE1005181//ESTs, Weakly similar to No definit
ion line found [C.elegans]//4.4e-126:583:99//Hs.25
347:AI138605

F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N7
0417

F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767
009

F-PLACE1005232//ESTs, Weakly similar to synapse-as
sociated protein sap47-1 [D.melanogaster]//0.56:19
2:60//Hs.47334:W72370

F-PLACE1005243

F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e
-06:484:60//Hs.89591:M97252

F-PLACE1005277//Homo sapiens mRNA for KIAA0610 pro
tein, partial cds//5.1e-150:706:98//Hs.118087:AB01
1182

F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:A
A447947

20 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHO
NDRIAL//4.4e-37:597:66//Hs.101642:X60673

F-PLACE1005308//High-mobility group (nonhistone ch
romosomal) protein 2//0.83:239:62//Hs.80684:X62534

F-PLACE1005313

F-PLACE1005327//ESTs, Weakly similar to No definit
ion line found [C.elegans]//6.0e-81:459:91//Hs.146
177:R51650

F-PLACE1005331//Homo sapiens chromosome 19, cosmid
F20569//3.7e-66:412:88//Hs.134031:AC004794

30 F-PLACE1005335//Homo sapiens mRNA for KIAA0754 pro
tein, partial cds//0.96:510:56//Hs.159183:AB018297

F-PLACE1005373

F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI
141348

F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA
856751

F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087
951

40 F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1/
/0.0043:148:67//Hs.74095:L20433

F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:N66
925

F-PLACE1005477//Human Line-1 repeat mRNA with 2 op
en reading frames//3.5e-126:744:87//Hs.23094:M1950
3

F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:N3
9323

F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA7079
73

50 F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA

- 633029
F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
F-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:W81261
F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
F-PLACE1005611//ESTs, Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:N48234
F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255
F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917
F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI04944
F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258
F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
F-PLACE1005763//ESTs, Highly similar to S-ACYL FA
TTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696
F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
F-PLACE1005802
F-PLACE1005803
F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156
F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482
F-PLACE1005828//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.1e-42:327:81//Hs.138404:R70986
F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870
F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497
F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905
F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242
F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487
F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552
F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300
F-PLACE1005898
F-PLACE1005921
F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504
F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:AI288274
F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:M18391
F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142
F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978
F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357
F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468
F-PLACE1005955//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:AI357868
F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:U13948
F-PLACE1005968

F-PLACE1005990

F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981

F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256

F-PLACE1006011

F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743

F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:AB018332

F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906

F-PLACE1006076//EST//0.29:92:64//Hs.161536:N80395

F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:AF039023

F-PLACE1006129

F-PLACE1006139

F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353

F-PLACE1006157//ESTs, Weakly similar to ETX1 [alternatively spliced] [H.sapiens]//2.9e-12:119:84//Hs.23153:R92857

F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868

F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721

F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239

F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:AI074005

F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433

F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:N49608

F-PLACE1006196//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719

F-PLACE1006205

F-PLACE1006223//ESTs, Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:AI279486

F-PLACE1006225

F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668

F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185

F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:AI085802

F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.31921:AB014548

F-PLACE1006262

F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625

F-PLACE1006318

F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:AI246503

F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:AI361492

F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249

F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481

F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581

F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715

F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693

F-PLACE1006385//Homo sapiens epsin 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085

F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296

F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735

30 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129

F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866

F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470

40 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194

F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511

F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493

F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584

F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706

3941

F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA
699358
F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:AI35
6219
F-PLACE1006540//Homo sapiens mRNA for cadherin-6,
complete cds//0.96:383:58//Hs.32963:D31784
F-PLACE1006552//Human (clone N5-4) protein p84 mRNA
A, complete cds//0.058:464:57//Hs.1540:L36529
F-PLACE1006598//Homo sapiens mRNA for KIAA0737 pro
tein, complete cds//4.1e-17:372:65//Hs.17630:AB018 10
280
F-PLACE1006615//Homo sapiens eukaryotic translatio
n initiation factor eIF3, p35 subunit mRNA, comple
te cds//2.2e-168:781:99//Hs.155377:U97670
F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99
088
F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.7911
0:M60858
F-PLACE1006629//Homo sapiens (clone s22i71) mRNA f
ragment//0.097:229:63//Hs.26956:L403 20
96
F-PLACE1006640//ESTs//0.0
0019:380:59//Hs.13672:AI1
31473
F-PLACE1006673//ESTs, Wea
kly similar to T14B4.2 ge
ne product [C.elegans]//
1.6e-12:113:83//Hs.3385:N
25917
F-PLACE1006678 30
F-PLACE1006704//Homo sapi
ens ALR mRNA, complete cd
s//0.16:284:60//Hs.15363
8:AF010403
F-PLACE1006731//Homo sapi
ens SOX22 protein (SOX22)
mRNA, complete cds//1.6e
-05:382:63//Hs.43627:U356
12
F-PLACE1006754//Biliary g 40
lycoprotein//8.9e-27:305:
72//Hs.50964:X16354
F-PLACE1006760//ESTs//0.1
0:207:62//Hs.152589:AA954
152
F-PLACE1006779//Kallmann
syndrome 1 sequence//0.00
025:251:64//Hs.89591:M972
52
F-PLACE1006782//ESTs//1.2 50

3942

e-90:423:100//Hs.132826:A
I075783
F-PLACE1006792//ESTs//1.5
e-10:439:58//Hs.138501:AI
051228
F-PLACE1006795//TYROSINE-
PROTEIN KINASE RECEPTOR E
TK1 PRECURSOR//4.5e-10:8
4:95//Hs.123642:M83941
F-PLACE1006800//ESTs//0.0
0068:360:61//Hs.157876:AI
422017
F-PLACE1006805//ESTs//4.6
e-103:491:98//Hs.140465:A
A769892
F-PLACE1006815//Homo sapi
ens mRNA for KIAA0618 pro
tein, complete cds//0.47:
403:56//Hs.15832:AB014518
F-PLACE1006819//Human Lin
e-1 repeat mRNA with 2 op
en reading frames//3.7e-1
03:619:87//Hs.23094:M1950
3
F-PLACE1006829//ESTs//1.5
e-22:141:94//Hs.142988:AA
142876
F-PLACE1006860//EST//0.00
62:206:65//Hs.158793:AI37
6773
F-PLACE1006867//ESTs//0.0
68:218:62//Hs.91166:AA551
273
F-PLACE1006878//Homo sapi
ens mRNA for KIAA0711 pro
tein, complete cds//1.0:2
68:58//Hs.5333:AB018254
F-PLACE1006883//ESTs//1.6
e-75:398:94//Hs.119544:T9
5601
F-PLACE1006901//ESTs//1.9e-13:87:96//Hs.134737:AI0
89187
F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
F-PLACE1006917
F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:AI423
913
F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:
L14565
F-PLACE1006958//Heat shock 70kD protein 4//6.4e-4

- O: 456: 70//Hs. 127: L12723
 F-PLACE1006961//ESTs, Highly similar to RSP5 PROT
 EIN [Saccharomyces cerevisiae]//3.2e-07: 67: 98//Hs.
 21806: AA630312
 F-PLACE1006962//H. sapiens irlB mRNA//2.3e-16: 202: 7
 1//Hs. 135202: X63417
 F-PLACE1006966//Homo sapiens syntaxin 4 binding pr
 otein UNC-18c (UNC-18c) mRNA, complete cds//0.14: 1
 91: 67//Hs. 8813: AF032922
 F-PLACE1006989//Cyclin B1//0.99: 224: 59//Hs. 23960: M 10
 25753
 F-PLACE1007014//Homo sapiens NBMPR-insensitive nuc
 leoside transporter ei (ENT2) mRNA, complete cds//
 3.1e-05: 594: 58//Hs. 32951: AF034102
 F-PLACE1007021//ESTs//7.2e-89: 446: 96//Hs. 7111: U559
 71
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 op
 en reading frames//1.0e-117: 775: 84//Hs. 23094: M1950
 3
 F-PLACE1007053//Homo sapiens mRNA for ARN03 protei 20
 n//0.35: 63: 82//Hs. 129811: AJ223957
 F-PLACE1007068//Polycystic kidney disease 1 (autos
 omal dominant)//0.22: 361: 60//Hs. 75813: L33243
 F-PLACE1007097//ESTs//2.9e-25: 197: 83//Hs. 105665: H7
 8987
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glu
 canotransferase (glycogen debranching enzyme, glyc
 ogen storage disease type III)//0.18: 268: 63//Hs. 90
 4: U84010
 F-PLACE1007111//EST//0.0066: 260: 60//Hs. 147903: AI22 30
 3385
 F-PLACE1007112
 F-PLACE1007132//ESTs//3.1e-30: 195: 76//Hs. 46158: AI1
 60121
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-
 II//0.13: 302: 60//Hs. 78869: M81601
 F-PLACE1007178//ESTs//9.6e-54: 289: 95//Hs. 12251: H12
 965
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA,
 complete cds//0.00090: 412: 59//Hs. 8546: U97669 40
 F-PLACE1007238//Human plectin (PLEC1) mRNA, comple
 te cds//1.4e-07: 492: 64//Hs. 79706: U53204
 F-PLACE1007239//Human mRNA for transcription elong
 ation factor S-II, hS-II-T1, complete cds//2.0e-5
 8: 405: 87//Hs. 80598: D50495
 F-PLACE1007242//EST//0.014: 55: 89//Hs. 88432: AA26214
 1
 F-PLACE1007243//ESTs//2.0e-43: 227: 97//Hs. 124775: AA
 648467
 F-PLACE1007257//Homo sapiens mRNA for dia-156 prot 50
 ein//3.7e-144: 677: 98//Hs. 121556: Y15909
 F-PLACE1007274
 F-PLACE1007276//ATPase, Cu++ transporting, alpha p
 olypeptide (Menkes syndrome)//0.94: 167: 64//Hs. 606:
 L06133
 F-PLACE1007282
 F-PLACE1007286//ESTs//1.0e-25: 333: 71//Hs. 134860: AI
 091436
 F-PLACE1007301//EST//0.78: 171: 61//Hs. 160990: H52412
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydr
 oxylase (CYP7b1) mRNA, complete cds//0.88: 298: 58//H
 s. 144877: AF029403
 F-PLACE1007342
 F-PLACE1007346//Homo sapiens estrogen-responsive B
 box protein (EBBP) mRNA, complete cds//1.7e-121: 5
 67: 98//Hs. 76596: AF096870
 F-PLACE1007367//H. sapiens mRNA for MACH-alpha-2 pr
 otein//2.2e-55: 532: 77//Hs. 19949: X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00066: 61: 91//Hs. 149318: AI2
 48642
 F-PLACE1007402//EST//1.7e-06: 193: 65//Hs. 132124: AI0
 41287
 F-PLACE1007409//Homo sapiens mitoxantrone resistan
 ce protein 1 mRNA, partial sequence//3.8e-18: 128: 9
 2//Hs. 14387: AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36: 194: 97//Hs. 22359: AI0
 24436
 F-PLACE1007452//EST//1.8e-34: 197: 94//Hs. 134795: AI0
 90359
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fra
 gment//2.6e-53: 317: 93//Hs. 6445: L40391
 F-PLACE1007460//ESTs//0.0012: 168: 64//Hs. 151708: AA5
 54714
 F-PLACE1007478//ESTs//1.0e-42: 440: 74//Hs. 141722: AA
 769103
 F-PLACE1007484//ESTs//7.1e-18: 127: 91//Hs. 100251: AA
 535975
 F-PLACE1007488
 F-PLACE1007507//ESTs//1.2e-99: 274: 98//Hs. 123462: AA
 903385
 F-PLACE1007511//Keratin 19//4.2e-31: 586: 64//Hs. 237
 61: Y00503
 F-PLACE1007524//ESTs//6.8e-71: 356: 97//Hs. 163067: AA
 897296
 F-PLACE1007525//ESTs//0.073: 242: 59//Hs. 128711: AA85
 6979
 F-PLACE1007537//Homo sapiens PYRIN (MEFV) mRNA, co
 mplete cds//0.93: 468: 57//Hs. 113283: AF018080

3945

3946

- F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:AI
076755
- F-PLACE1007547//Homo sapiens mRNA for KIAA0661 pro
tein, complete cds//1.0e-70:733:71//Hs.65238:AB014
561
- F-PLACE1007557//EST//0.58:80:72//Hs.130267:AI00186
3
- F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA
584257
- F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:AI 10
089163
- F-PLACE1007618//Homo sapiens mRNA for KIAA0633 pro
tein, partial cds//7.2e-12:778:56//Hs.33010:AB0145
33
- F-PLACE1007621
- F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA
781867
- F-PLACE1007645
- F-PLACE1007649
- F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA 20
476266
- F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:AI
027055
- F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:AI3
48503
- F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR//0.99:216:63//Hs.1103:X02812
- F-PLACE1007705//Human mRNA for RTP, complete cds//
4.8e-58:637:70//Hs.75789:D87953
- F-PLACE1007706//Homo sapiens metalloprotease 1 (MP 30
1) mRNA, complete cds//4.1e-149:709:97//Hs.4812:AF
061243
- F-PLACE1007725//ESTs, Weakly similar to No definit
ion line found [C.elegans]//4.5e-36:233:89//Hs.108
797:AA476815
- F-PLACE1007729//ESTs, Moderately similar to RETROV
IRUS-RELATED PROTEASE[H.sapiens]//0.00033:270:64//
Hs.104129:AA923278
- F-PLACE1007730//Homo sapiens mRNA for KIAA0685 pro
tein, complete cds//2.6e-156:728:98//Hs.153121:ABO 40
14585
- F-PLACE1007737//Coagulation factor II (thrombin) r
eceptor//1.1e-18:364:68//Hs.159347:M62424
- F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA45
7030
- F-PLACE1007746//ESTs//6.7e-55:330:89//Hs.153392:AI
089469
- F-PLACE1007791//EST//0.39:261:62//Hs.145991:AI2776
56
- F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA 50
- 640504
- F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA
533107
- F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA8838
41
- F-PLACE1007843//EST//0.020:307:59//Hs.145535:AI261
635
- F-PLACE1007846//Human Line-1 repeat mRNA with 2 op
en reading frames//6.3e-38:396:77//Hs.23094:M19503
- F-PLACE1007852
- F-PLACE1007858//Homo sapiens mRNA for KIAA0766 pro
tein, complete cds//1.3e-190:894:98//Hs.28020:AB01
8309
- F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:AI0
38387
- F-PLACE1007877
- F-PLACE1007897//EST//1.0:59:72//Hs.138770:N70943
- F-PLACE1007908//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0487//7.3e-156:755:97//Hs.92
381:AB007956
- F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:N24
002
- F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA05
6538
- F-PLACE1007955//Homo sapiens cyclin-D binding Myb-
like protein mRNA, complete cds//8.9e-173:813:98//
Hs.5671:AF084530
- F-PLACE1007958//Homo sapiens cAMP-specific phospho
diesterase 8B (PDE8B)mRNA, partial cds//8.2e-155:7
30:98//Hs.78106:AF079529
- F-PLACE1007969//ESTs, Weakly similar to hnRNA-bind
ing protein M4 [H.sapiens]//5.1e-45:264:92//Hs.422
22:W28567
- F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:A
I097043
- F-PLACE1008000//Homo sapiens veli 1 mRNA, complete
cds//5.7e-63:578:74//Hs.150380:AF087693
- F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603
031
- F-PLACE1008044
- F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60
382
- F-PLACE1008080//Human homeodomain protein (Prox 1)
mRNA, complete cds//0.00037:151:71//Hs.159437:U44
060
- F-PLACE1008095//Human hybrid receptor gp250 precu
sor mRNA, complete cds//1.0:461:58//Hs.155494:U609
75
- F-PLACE1008111//Homo sapiens B lymphocyte chemoatt
ractant BLC mRNA, complete cds//0.034:497:58//Hs.1

- 00431: AF044197
 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N2876
 9
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA
 778874
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:AI2
 18683
 F-PLACE1008177//ESTs, Moderately similar to melosi
 s-specific nuclear structural protein 1 [M.musculu
 s]//5.1e-20:124:95//Hs.146238:AI263135 10
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281
 427
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA6
 43524
 F-PLACE1008201
 F-PLACE1008209
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:AI001
 856
 F-PLACE1008244//Miller-Dieker syndrome chromosome
 region//0.22:247:61//Hs.77318:L13385 20
 F-PLACE1008273
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:AI27511
 3
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0501//2.6e-25:389:70//Hs.159
 897:AB007970
 F-PLACE1008309//Homo sapiens serine phosphatase FC
 Pla (FCP1) mRNA, complete cds//0.16:263:63//Hs.407
 6:AF081287
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R820 30
 71
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 pro
 tein, partial cds//1.5e-45:291:83//Hs.101414:AB011
 129
 F-PLACE1008331//ESTs, Weakly similar to ORF2-like
 protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA
 96362
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 pro
 tein, partial cds//3.4e-139:659:98//Hs.5734:AB0145
 79
 F-PLACE1008368//Homo sapiens actin binding protein
 MAYVEN mRNA, completecds//0.011:355:60//Hs.12296
 7:AF059569
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA
 526911
 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:AI2
 89171
 F-PLACE1008398
 F-PLACE1008401//Homo sapiens methyl-CpG binding pr
 otein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461: 50
 62//Hs.25674:AF072242
 F-PLACE1008402//Homo sapiens mRNA for p115, comple
 te cds//1.4e-149:711:98//Hs.7763:D86326
 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:A
 A628943
 F-PLACE1008424//Human DNA sequence from clone 753P
 9 on chromosome Xq25-26.1. Contains the gene codin
 g for Aminopeptidase P (EC 3.4.11.9, XAA-Pro/X-Pro
 /Proline/Aminoacylproline Aminopeptidase) and a no
 vel gene. Contains ESTs, STSs, GSSs and a gaaa rep
 eat polymorphism//0.98:113:67//Hs.57922:AL023653
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28
 499
 F-PLACE1008429//Orf1 5' to PD-ECCF/TP...orf2 5' to
 PD-ECCF/TP [human, epidermoid carcinoma cell line
 A431, mRNA, 3 genes, 1718 nt]//0.019:530:58//Hs.7
 2248:S72487
 F-PLACE1008437
 F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782
 335
 F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA0
 53901
 F-PLACE1008465//Human mRNA for KIAA0383 gene, part
 ial cds//0.0084:210:63//Hs.27590:AB002381
 F-PLACE1008488//Human density enhanced phosphatase
 -1 mRNA, complete cds//6.8e-07:469:60//Hs.1177:U10
 886
 F-PLACE1008524//Homo sapiens TWIK-related acid-sen
 sitive K+ channel (TASK) mRNA, complete cds//1.0:3
 04:60//Hs.24040:AF006823
 F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:AI
 274697
 F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:2
 31:71//Hs.89887:D38081
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 fr
 om 22q12.1-qter//1.1e-45:507:71//Hs.8003:AC004997
 F-PLACE1008568//Homo sapiens mRNA for neuronatin a
 lpha, complete cds//1.0:95:71//Hs.117546:U31767
 F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:AI
 283069
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 pro
 tein, complete cds//3.9e-175:812:98//Hs.23255:AB01
 8334
 F-PLACE1008621//ESTs, Weakly similar to reverse tr
 ansriptase [H.sapiens]//1.2e-15:350:66//Hs.15108
 7:AA649326
 F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:N26794
 F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560
 F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H8
 2458

- F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211
- F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394
- F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D38535
- F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333
- F-PLACE1008693//EST//0.19:36:94//Hs.138817:N93728
- F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondria l protein, complete cds//8.3e-25:137:97//Hs.90443:AF038406
- F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs.119534:AJ224741
- F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080
- F-PLACE1008757//ESTs, Weakly similar to unknown protein [R.norvegicus]//4.3e-17:285:69//Hs.35460:H65503
- F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds//1.4e-121:503:97//Hs.6458:AF060543
- F-PLACE1008798//ESTs, Weakly similar to putative p150 [H.sapiens]//0.30:127:68//Hs.111380:AA258772
- F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542
- F-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//6.7e-104:376:98//Hs.7179:AF011905
- F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318:61//Hs.75668:M81883
- F-PLACE1008851//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2HOMOLOG [Plasmodium falciparum (isolate kl / thailand)]//0.73:354:59//Hs.26322:AA156858
- F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:AI052728
- F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:AI221563
- F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frames//5.5e-51:701:68//Hs.23094:M19503
- F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323
- F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.1e-159:753:98//Hs.62318:AB018308
- F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:W847
- 71
- F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:AI394026
- F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937
- F-PLACE1008947//Human TBP-associated factor (hTAFI1130) mRNA, partial cds//2.4e-13:625:58//Hs.24644:U75308
- F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:AI024950
- F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:96//Hs.34780:AJ003112
- F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762
- F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689
- F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e-16:93:100//Hs.119689:S70585
- F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:AI239698
- F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:AI090525
- F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800
- F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:AI093091
- F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:AI337031
- F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:X68011
- F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:AI040890
- F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
- F-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3(XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF035586
- F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-24:718:59//Hs.35804:D25215
- F-PLACE1009150//Human HsLIM15 mRNA for HsLim15, complete cds//1.7e-50:440:78//Hs.37181:D64108
- F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.0e-46:440:69//Hs.158095:AB007953
- F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.28:245:61//Hs.92614:M62302
- F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
- F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:N22770

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F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:AI282821
 F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
 F-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396
 F-PLACE1009190//EST//0.046:95:70//Hs.131646:AI025689
 F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
 F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77//Hs.146403:M29540
 F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
 F-PLACE1009298//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735
 F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
 F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192
 F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-91:594:86//Hs.23094:M19503
 F-PLACE1009335//EST//0.037:169:63//Hs.148875:AI240767
 F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
 F-PLACE1009368
 F-PLACE1009375
 F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:317:81//Hs.43681:AL022394
 F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs.9450:M27878
 F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61//Hs.101174:AF047863
 F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4e-27:210:86//Hs.3404:AF035262
 F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-45:599:68//Hs.155291:D13630
 F-PLACE1009443//H.sapiens 5T4 gene for 5T4 Oncofetal antigen//0.11:350:58//Hs.82128:AJ012159
 F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:93//Hs.76987:AF012872
 F-PLACE1009459//H.sapiens gap gene mRNA, complete CDS//1.0:241:60//Hs.151641:Z24680
 F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.00039:347:60//Hs.994:M95678
 F-PLACE1009476//Homo sapiens Chromosome 16 BAC clo

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ne CIT987SK-A-67A1//4.1e-91:464:96//Hs.155049:AC004531
 F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:AI308839
 F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-30:608:63//Hs.16165:AB002405
 F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-68:526:78//Hs.8517:U70728
 F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
 F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:AI416956
 F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
 F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs.147918:U38291
 F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
 F-PLACE1009596//ESTs, Weakly similar to LIS-1 protein [H.sapiens]//4.1e-16:281:66//Hs.13889:AI341394
 F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9e-52:313:79//Hs.113283:AF018080
 F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:AI074011
 F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:AI094085
 F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
 F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
 F-PLACE1009639
 F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//4.4e-173:816:98//Hs.21862:AB011159
 F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
 F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1e-149:701:98//Hs.109590:AF062534
 F-PLACE1009708//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN EXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926
 F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650
 F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989
 F-PLACE1009798//Human DNA sequence from clone 1189

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B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-proteinKinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins *S. pombe* C22F3.14C and *C. elegans* C16A3.8. Contains ESTs and GSSs //5.5e-130:600:95//Hs.16411:AL030996

F-PLACE1009845

F-PLACE1009861

F-PLACE1009879//ESTs//6.3e-12:293:66//Hs.147071:AI200021

F-PLACE1009886

F-PLACE1009888//EST//0.044:255:58//Hs.160695:AI282889

F-PLACE1009908

F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717

F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379

F-PLACE1009925

F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153

F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:AI306446

F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345

F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:AI139114

F-PLACE1009995//ESTs, Weakly similar to C01A2.4 [C.elegans]//3.3e-24:174:88//Hs.11449:AI201540

F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529

F-PLACE1010023

F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:W02878

F-PLACE1010053//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//5.2e-63:312:98//Hs.142151:AA984061

F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482

F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925

F-PLACE1010089//ESTs, Highly similar to PROBABLE

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UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822

F-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//1.8e-08:100:89//Hs.11469:U69567

F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761

F-PLACE1010105//Homo sapiens actin binding protein

10 MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569

F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682

F-PLACE1010134//H.sapiens hbrm mRNA//1.2e-14:380:64//Hs.77590:X72889

F-PLACE1010148//Human trans-Colgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740

F-PLACE1010152

F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792

20 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582

F-PLACE1010202//ESTs, Weakly similar to No definition line found [C.elegans]//2.3e-72:391:94//Hs.35225:H69637

F-PLACE1010231

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917

30 F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590

F-PLACE1010274//ESTs, Weakly similar to C01A2.4 [C.elegans]//6.8e-25:149:93//Hs.11449:AI201540

F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813

F-PLACE1010310//HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433

F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248

40 F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:AI367875

F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659

F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117

F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855

F-PLACE1010364//EST//0.11:292:58//Hs.135771:AI005648

50 F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA5

- 64986
F-PLACE1010401
F-PLACE1010481//Human BLu protein (BLu) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081
F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:AI038500
F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:AI 10 302100
F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177
F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
F-PLACE1010562//EST//1.0:164:66//Hs.147868:AI222979
F-PLACE1010579//EST//0.39:279:58//Hs.158960:AI380148
F-PLACE1010580//ESTs, Moderately similar to PUTATIVE ATP-DEPENDENT RNAHELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.79110:M60858
F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
F-PLACE1010628//EST, Weakly similar to line-1 protein ORF2 [H. sapiens]//0.012:258:62//Hs.144375:AA484200
F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
F-PLACE1010630//EST//0.29:319:58//Hs.137277:N62225
F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:W27076
F-PLACE1010662
F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376
F-PLACE1010714//EST//0.018:253:59//Hs.148028:AI270027
F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244
F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
F-PLACE1010761//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
F-PLACE1010771//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
F-PLACE1010786
F-PLACE1010800
F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:N48085
20 F-PLACE1010833//ESTs, Weakly similar to allograft inflammatory factor-1[H. sapiens]//2.9e-28:245:79//Hs.132736:AA583494
F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:W81048
F-PLACE1010857//ESTs, Weakly similar to KIAA0157 gene product is novel. [H. sapiens]//5.8e-67:336:97//Hs.130135:AA905493
F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
30 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182
F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169
F-PLACE1010900
F-PLACE1010916//EST//0.55:151:66//Hs.145800:AI269981
40 F-PLACE1010917
F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:H26537
F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:AB011126
F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:AF064244
F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:W30985

- F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA55515
4
F-PLACE1010954//Apolipoprotein B (including Ag(x)
antigen)//0.28:444:59//Hs.585:X04506
F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506
632
F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:AI
379721
F-PLACE1011026//EST//0.022:222:60//Hs.47154:N50931
F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N340 10
32
F-PLACE1011041//Human density enhanced phosphatase
-1 mRNA, complete cds//0.28:179:67//Hs.1177:U10886
F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOS
PHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//H
s.994:M95678
F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer b
inding factor 1//6.1e-35:310:78//Hs.2407:Z49194
F-PLACE1011056//Human putative serine/threonine pr
oteins kinase PRK (prk)mRNA, complete cds//0.74:22 20
8:61//Hs.153640:U56998
F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA9
13320
F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R7
6663
F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA4180
37
F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:AI
214317
F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:AI370 30
857
F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA62
9949
F-PLACE1011160
F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//H
s.129228:M84443
F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA7
08114
F-PLACE1011203//Homo sapiens chromosome 18q11 beta
-1.4-galactosyltransferase mRNA, complete cds//6.9 40
e-124:576:99//Hs.159140:AF038664
F-PLACE1011214//ESTs, Weakly similar to B0035.14
[C.elegans]//9.7e-101:469:99//Hs.8241:AA283057
F-PLACE1011219//ESTs, Weakly similar to coded for
by C. elegans cDNA CEESL70F [C.elegans]//2.6e-62:2
21:88//Hs.101821:W27452
F-PLACE1011221//ESTs//0.46:238:62//Hs.32853:AA0157
51
F-PLACE1011229//Homo sapiens mRNA for KIAA0529 pro
tein, partial cds//1.4e-147:675:99//Hs.23168:AB011 50
101
F-PLACE1011263//Homo sapiens BAC clone GS166A23 fr
om 7p21//5.9e-71:350:98//Hs.15144:AC005014
F-PLACE1011273//ESTs//1.0:222:59//Hs.35274:AA49580
3
F-PLACE1011291//Homo sapiens clone 24712 unknown m
RNA, partial cds//3.4e-09:191:65//Hs.140950:AF0706
37
F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA86
5915
F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584
160
F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08
310
F-PLACE1011332//Homo sapiens N-acetylglucosamine-p
hosphate mutase mRNA, complete cds//4.8e-151:696:99
//Hs.5819:AF102265
F-PLACE1011340//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0501//1.5e-20:120:81//Hs.159
897:AB007970
F-PLACE1011371//Human mRNA for PK-120//9.5e-35:68
4:63//Hs.76415:D38535
F-PLACE1011375//ESTs, Moderately similar to potass
ium channel protein Raw3 [R.norvegicus]//6.7e-68:3
25:99//Hs.107245:AA627053
F-PLACE1011399//ESTs//8.6e-05:285:61//Hs.130105:AA
904868
F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:N9555
2
F-PLACE1011433//Homo sapiens mRNA for KIAA0530 pro
tein, partial cds//1.5e-158:743:98//Hs.10801:AB011
102
F-PLACE1011452//Human Line-1 repeat mRNA with 2 op
en reading frames//1.9e-53:557:72//Hs.23094:M19503
F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:AI0
25204
F-PLACE1011472//Homo sapiens mRNA for KIAA0712 pro
tein, complete cds//1.5e-152:703:99//Hs.111138:AB0
18255
F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX
2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:A
F065482
F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA
884264
F-PLACE1011503//EST//0.67:149:65//Hs.149774:AI2859
97
F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA
705319
F-PLACE1011563//ESTs//2.2e-61:394:86//Hs.117718:AA
883476

3959

F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:325:84//Hs.153563:AF011333
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180
 F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462
 F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029:585:57//Hs.106387:AF029778
 F-PLACE1011641
 F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds//0.00058:499:58//Hs.12784:AB006631
 F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661
 F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086
 F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745
 F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs.56045:D86640
 F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78234
 F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:N23366
 F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:365:60//Hs.17262:AB002350
 F-PLACE1011725
 F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853
 F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891
 F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:AI208240
 F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:AI393693
 F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660
 F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protein//8.9e-05:477:59//Hs.37035:U07664
 F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775
 F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cds//5.3e-110:526:98//Hs.22572:AB011152
 F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
 F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4e-09:478:56//Hs.107747:AI357868
 F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817

3960

F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617
 F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
 F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
 F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:AI261591
 10 F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
 F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//4.0e-148:690:98//Hs.88756:AB018256
 F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.5e-54:290:81//Hs.92381:AB007956
 F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:AI205503
 20 F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
 F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627
 F-PLACE2000014//EST//0.10:214:61//Hs.160247:AI138831
 F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627
 F-PLACE2000017
 F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082557
 F-PLACE2000030
 F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cds//0.85:234:66//Hs.11342:U91512
 F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cds//0.058:348:62//Hs.94653:AB011179
 F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:473:59//Hs.79706:U53204
 F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:HO7128
 F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
 F-PLACE2000061
 F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9e-114:662:86//Hs.23759:M98457
 F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219
 F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:AI034333

F-PLACE2000100
 F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:AI219219
 F-PLACE2000111//H. sapiens mRNA for 1-acylglycerol-3-phosphate O-acyl transferase//0.76:215:65//Hs.6587:U56417
 F-PLACE2000115
 F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:400:79//Hs.153014:AB002353
 F-PLACE2000132
 F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H. sapiens]//1.2e-08:245:64//Hs.140343:AA718911
 F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.83833:U54645
 F-PLACE2000164
 F-PLACE2000170
 F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:AI219179
 F-PLACE2000176
 F-PLACE2000187
 F-PLACE2000216
 F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
 F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-38:792:63//Hs.21560:AB002296
 F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.5e-74:367:98//Hs.22926:AB018338
 F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete cds//2.0e-29:366:73//Hs.119387:AB007958
 F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23:650:62//Hs.144672:AJ000522
 F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
 F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
 F-PLACE2000317
 F-PLACE2000335//Fc fragment of IgE, high affinity I, receptor for; betapolyptide//6.1e-24:295:76//Hs.30:W89796
 F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds//6.8e-21:593:61//Hs.103983:U66088
 F-PLACE2000342//Centromere protein B (80kD)//1.4e-06:326:61//Hs.85004:X05299
 F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H. sapiens]//3.7e-16:139:82//Hs.28209:AI073817
 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645

F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:AI358861
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:AI131032
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638
 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953
 F-PLACE2000398
 F-PLACE2000399
 F-PLACE2000404
 F-PLACE2000411
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
 F-PLACE2000427
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
 F-PLACE2000438//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetyl galactosaminyl transferase (T2)//1.9e-20:418:64//Hs.130181:X85019
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080
 F-PLACE2000455//ESTs, Moderately similar to !!!!! A LU SUBFAMILY SC WARNING ENTRY !!!!! [H. sapiens]//4.0e-05:100:73//Hs.104239:AA488082
 F-PLACE2000458//H. sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080
 F-PLACE3000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262
 F-PLACE3000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
 F-PLACE3000020//Prostaglandin I2 (prostacyclin) receptor (IP)//0.00081:500:61//Hs.393:D38128
 F-PLACE3000029
 F-PLACE3000059//ESTs//0.0026:49:100//Hs.42913:AI082248
 F-PLACE3000070//ESTs//5.6e-15:202:74//Hs.154993:AA142842
 F-PLACE3000103//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete cds//1.0:186:62/

- /Hs.122752:AF026445
F-PLACE3000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
F-PLACE3000121
F-PLACE3000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
F-PLACE3000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
F-PLACE3000142//EST//0.41:179:59//Hs.137438:AA282243
F-PLACE3000145//ESTs//3.5e-25:145:96//Hs.163950:AA683016
F-PLACE3000147//EST//5.0e-43:285:86//Hs.160895:AI365871
F-PLACE3000148
F-PLACE3000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572
F-PLACE3000156//ESTs//0.00015:277:62//Hs.156834:AI336023
F-PLACE3000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666
F-PLACE3000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147
F-PLACE3000160
F-PLACE3000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
F-PLACE3000194
F-PLACE3000197
F-PLACE3000199//EST//1.0:108:68//Hs.98488:AA426546
F-PLACE3000207//EST//1.0e-32:184:75//Hs.160146:AI049975
F-PLACE3000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744
F-PLACE3000218//EST//1.3e-46:317:84//Hs.162197:AA535216
F-PLACE3000220//EST//9.3e-95:443:99//Hs.112702:AA609377
F-PLACE3000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019
F-PLACE3000226
F-PLACE3000230//EST//6.1e-16:173:72//Hs.148578:AI201568
F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha
-Trypsin Inhibitor Heavy Chain LIKE gene, alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046
F-PLACE3000244
F-PLACE3000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
F-PLACE3000271//ESTs//1.6e-25:195:72//Hs.108452:H78650
F-PLACE3000276//ESTs//1.0e-13:274:66//Hs.28589:AI004944
F-PLACE3000304//EST//0.043:210:61//Hs.132378:AI026770
F-PLACE3000310
F-PLACE3000320//EST//1.2e-12:188:70//Hs.145771:AI269586
F-PLACE3000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
F-PLACE3000331
F-PLACE3000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545
F-PLACE3000341//EST//1.8e-05:394:58//Hs.112894:AA620741
F-PLACE3000350//ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASESULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355
F-PLACE3000352//H. sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
F-PLACE3000353//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514
F-PLACE3000362//EST//6.5e-25:302:73//Hs.140504:AA810441
F-PLACE3000363
F-PLACE3000365//ESTs//0.81:200:60//Hs.141556:N49928
F-PLACE3000373//ESTs//0.0071:82:73//Hs.136310:AA442641
F-PLACE3000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
F-PLACE3000399//Clathrin, light polypeptide (Lcb)/5.2e-70:391:81//Hs.73919:X81637
F-PLACE3000400//ESTs//0.53:162:66//Hs.49303:AA810785
F-PLACE3000401//EST//2.3e-35:178:100//Hs.162851:AA632270
F-PLACE3000402//ESTs//2.4e-84:425:96//Hs.148962:AI

- 219715
F-PLACE3000405//EST//2.1e-39:452:73//Hs.140414:AA778541
F-PLACE3000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263
F-PLACE3000413//ESTs, Weakly similar to methyl sterol oxidase [H.sapiens]//1.6e-51:260:98//Hs.122512:H61502
F-PLACE3000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344
F-PLACE3000425//EST//3.8e-34:286:79//Hs.135301:AI039161
F-PLACE3000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202
F-PLACE3000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
F-PLACE3000477//H.sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
F-PLACE4000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:AB018352
F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12//1.1e-06:244:63//Hs.154050:AC004131
F-PLACE4000049//Homo sapiens clone 24619 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
F-PLACE4000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148
F-PLACE4000063
F-PLACE4000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
F-PLACE4000093//ESTs//0.0053:273:60//Hs.136952:AA825819
F-PLACE4000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931
F-PLACE4000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
F-PLACE4000129
F-PLACE4000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
F-PLACE4000147//ESTs//0.0060:324:60//Hs.85640:AA535856
F-PLACE4000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
F-PLACE4000192
F-PLACE4000211
F-PLACE4000222//EST//1.9e-15:317:66//Hs.149206:AI246594
F-PLACE4000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
F-PLACE4000233//ESTs//4.4e-38:240:80//Hs.114605:AI304317
F-PLACE4000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
F-PLACE4000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
F-PLACE4000252//ESTs//1.0:196:64//Hs.144869:AA493886
F-PLACE4000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200
F-PLACE4000261
F-PLACE4000269//ESTs, Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
F-PLACE4000270
F-PLACE4000300
F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//Hs.155952:U88966
F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798
F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:AI147292
F-PLACE4000367
F-PLACE4000369
F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:AI379823
F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046
F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.1e-47:605:71//Hs.153026:AB014540
F-PLACE4000411//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//4.7e-33:159:81//Hs.154257:AI275982
F-PLACE4000431//Homo sapiens mRNA for KIAA0788 pro

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- tein, partial cds//1.3e-45:263:92//Hs.2397:Z70200
 F-PLACE4000445
 F-PLACE4000450
 F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA
 081874
 F-PLACE4000487//Sialophorin (gpL115, leukosialin,
 CD43)//3.0e-14:189:71//Hs.80738:X52075
 F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R3895
 1
 F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:AI1262
 89
 F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA6
 51731
 F-PLACE4000522//ESTs, Highly similar to NEUROGENI
 C LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR [Homo sap
 iens]//0.047:119:65//Hs.129053:AA767022
 F-PLACE4000548
 F-PLACE4000558//Homo sapiens mRNA for DFFRY protei
 n, abundant transcript//0.0035:510:59//Hs.39163:AF
 000986
 F-PLACE4000581
 F-PLACE4000590//ESTs, Highly similar to POL POLYP
 ROTEIN [Friend murine leukemia virus (isolate 57)]/
 /3.4e-13:275:68//Hs.113980:AI034080
 F-PLACE4000593//ESTs, Weakly similar to F25D7.1
 [C.elegans]//5.2e-28:239:79//Hs.109084:AI004675
 F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z2
 9074
 F-PLACE4000638//Homo sapiens mRNA from chromosome
 5q21-22, clone:sF2//3.5e-47:562:69//Hs.129685:AB00
 2446
 F-PLACE4000650
 F-PLACE4000654
 F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:A
 1028132
 F-SKNMC1000011//Centromere protein B (80kD)//0.001
 3:243:62//Hs.85004:X05299
 F-SKNMC1000013//ESTs, Highly similar to MULTIDRUG
 RESISTANCE PROTEIN HOMOLOG 50 [Drosophila melanog
 aster]//2.5e-36:197:96//Hs.118634:U66688
 F-SKNMC1000046//Homo sapiens mRNA for KIAA0654 pro
 tein, partial cds//2.5e-148:706:98//Hs.109299:AB01
 4554
 F-SKNMC1000050//Calpain, large polypeptide L2//4.1
 e-53:330:90//Hs.76288:M23254
 F-SKNMC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA9
 46877
 F-THYR01000017//Human mRNA for KIAA0315 gene, part
 ial cds//1.0:310:60//Hs.3989:AB002313
 F-THYR01000026//H.sapiens OBF-1 mRNA for octamer b
 50
 inding factor 1//2.9e-35:299:81//Hs.2407:Z49194
 F-THYR01000034
 F-THYR01000035//ESTs//4.1e-37:317:79//Hs.141254:AI
 334099
 F-THYR01000040//ESTs//0.30:331:59//Hs.87176:AI1483
 26
 F-THYR01000070//Human mRNA for KIAA0347 gene, comp
 lete cds//0.069:278:63//Hs.101996:AB002345
 F-THYR01000072//Homo sapiens clone 23584 mRNA sequ
 ence//8.7e-86:722:77//Hs.6654:AB014557
 F-THYR01000085
 F-THYR01000092//ESTs//3.1e-100:469:99//Hs.132207:A
 I148065
 F-THYR01000107
 F-THYR01000111//Human Line-1 repeat mRNA with 2 op
 en reading frames//6.8e-106:690:86//Hs.23094:M1950
 3
 F-THYR01000121
 F-THYR01000124//Human mRNA for alanine aminotransf
 erase//0.0026:420:58//Hs.103502:U70732
 F-THYR01000129//Homo sapiens TED protein (TED) mRN
 A, complete cds//2.8e-155:732:98//Hs.87619:AF08714
 2
 F-THYR01000132//ESTs//1.9e-35:164:79//Hs.139179:AA
 650203
 F-THYR01000156//EST//0.32:102:68//Hs.139634:AA4784
 16F-THYR01000163//Small inducible cytokine A5 (RAN
 TES)//5.2e-50:331:85//Hs
 .155464:AF088219
 F-THYR01000173//Human clathrin assembly protein 50
 (AP50) mRNA, complete cds//1.1e-05:261:61//Hs.1529
 36:D63475
 F-THYR01000186//H.sapiens mRNA for phosphoinositid
 e 3-kinase//3.7e-41:270:87//Hs.101238:Y11312
 F-THYR01000187//EST//0.11:227:62//Hs.101773:H23270
 F-THYR01000190//ESTs//0.82:194:63//Hs.128818:AA976
 883
 F-THYR01000197//Homo sapiens mRNA for poly(A)-spec
 ific ribonuclease//2.4e-175:805:99//Hs.43445:AJ005
 698
 F-THYR01000199//Homo sapiens mRNA for KIAA0652 pro
 tein, complete cds//4.0e-88:616:84//Hs.79672:AB014
 552
 F-THYR01000206//EST//0.96:291:61//Hs.104962:AA4438
 48
 F-THYR01000221//Human clone 23589 mRNA sequence//
 0.035:242:62//Hs.11506:U79297
 F-THYR01000241//EST//0.48:102:69//Hs.160764:AI3133
 22
 F-THYR01000242//Zinc finger protein 84 (HPF2)//1.2

- e-42: 534: 64//Hs. 9450: M27878
 F-THYR01000253//Homo sapiens mRNA for KIAA0690 protein, partial cds//0.61:211:64//Hs.60103:AB014590
 F-THYR01000270
 F-THYR01000279//ESTs//0.0020:104:72//Hs.121476:AI215500
 F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3e-180:848:98//Hs.25846:AB016068
 F-THYR01000320//ESTs, Weakly similar to Similar to glutamate decarboxylase [C.elegans]//7.6e-92:431: 10 99//Hs.122719:AA777803
 F-THYR01000327//Autocrine motility factor receptor//2.8e-52:290:93//Hs.80731:M63175
 F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//7.2e-164:763:98//Hs.12002:AB018333
 F-THYR01000358//Human selenium-binding protein (hS BP) mRNA, complete cds//6.9e-34:177:84//Hs.7833:U29091
 F-THYR01000368//ESTs//0.0011:55:96//Hs.34994:AA252 20 919
 F-THYR01000381//Homo sapiens mRNA for KIAA0562 protein, complete cds//0.081:240:62//Hs.118401:AB01134
 F-THYR01000387//EST//3.6e-14:197:71//Hs.139399:AA416855
 F-THYR01000394//ESTs, Weakly similar to No definition line found [C.elegans]//5.8e-39:245:91//Hs.119095:T79413
 F-THYR01000395//EST//5.8e-69:333:99//Hs.156524:AA7 30 24572
 F-THYR01000401//ESTs//1.8e-24:132:98//Hs.54852:W26238
 F-THYR01000438//EST//1.9e-05:217:63//Hs.115930:AA579773
 F-THYR01000452//B cell lymphoma protein 6 (zinc finger protein 51)//0.096:306:60//Hs.155024:U00115
 F-THYR01000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.2999:X52520
 F-THYR01000484//EST, Weakly similar to putative pl 40 50 [H.sapiens]//8.9e-22:248:76//Hs.162011:AA513663
 F-THYR01000488
 F-THYR01000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X82200
 F-THYR01000502//ESTs//1.0:350:57//Hs.119749:AA689298
 F-THYR01000505//Interleukin 13//0.95:245:60//Hs.845:U31120
 F-THYR01000558//EST//1.3e-24:351:64//Hs.142326:AA351877
 F-THYR01000569//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.28:229:61//Hs.100058:AB006713
 F-THYR01000570//EST//0.80:171:61//Hs.112790:AA609949
 F-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds//2.4e-168:808:97//Hs.151411:AF075587
 F-THYR01000596//EST//9.5e-94:461:96//Hs.135397:AI056322
 F-THYR01000602//EST//4.9e-06:80:80//Hs.162135:AA526331
 F-THYR01000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62//Hs.2685:Z50053
 F-THYR01000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:D38081
 F-THYR01000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941
 F-THYR01000641//ESTs//0.00017:375:58//Hs.32703:AA054125
 F-THYR01000658//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267
 F-THYR01000662
 F-THYR01000666//ESTs//1.9e-28:149:99//Hs.105187:AI394157
 F-THYR01000676//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267
 F-THYR01000684//ESTs, Weakly similar to band-6-protein [H.sapiens]//0.46:368:57//Hs.26557:AA480380
 F-THYR01000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
 F-THYR01000712//ESTs//3.3e-42:211:99//Hs.69330:AI056324
 F-THYR01000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:631:59//Hs.79706:U53204
 F-THYR01000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
 F-THYR01000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:339:74//Hs.7977:AB007871
 F-THYR01000756//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//1.0:209:62//Hs.19492:AF061573
 F-THYR01000777//Human mRNA for KIAA0147 gene, partial cds//0.00069:636:57//Hs.158132:D63481
 F-THYR01000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084
 F-THYR01000787
 50 F-THYR01000793

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F-THYR01000796
 F-THYR01000805//Homo sapiens mRNA from chromosome 5q21-22, clone: sF2//9.4e-36:561:68//Hs.129685:AB002446
 F-THYR01000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:465:75//Hs.154326:D42087
 F-THYR01000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
 F-THYR01000843
 F-THYR01000852//ESTs//6.2e-23:204:81//Hs.144452:AA 10 838788
 F-THYR01000855//ESTs//0.049:159:64//Hs.163532:AI424170
 F-THYR01000865//ESTs, Weakly similar to !!!! ALU S UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103
 F-THYR01000895//ESTs//3.8e-24:191:84//Hs.132722:AA 618531
 F-THYR01000916//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-43:318:79//Hs.923 20 81:AB007956
 F-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529
 F-THYR01000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63//Hs.79217:M77836
 F-THYR01000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:56//Hs.112432:AC005263
 F-THYR01000952//Human mRNA for KIAA0208 gene, complete cds//0.98:177:65//Hs.83558:D86963
 F-THYR01000974//Homo sapiens putative ATP-dependent mitochondrial RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.7e-15:123:90//Hs.106469:AF042169
 F-THYR01000975//EST//0.45:172:62//Hs.105449:AA513907
 F-THYR01000983
 F-THYR01000984//EST//0.0075:119:65//Hs.150347:AA984646
 F-THYR01000988//ESTs//0.056:99:71//Hs.153409:AI224 40 307
 F-THYR01001003
 F-THYR01001031//Thiopurine S-methyltransferase//3.8e-44:568:71//Hs.51124:AF019369
 F-THYR01001033//H.sapiens mRNA for cyclicin II//0.0061:287:60//Hs.3232:Z46788
 F-THYR01001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:79//Hs.51048:X68830
 F-THYR01001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-33:421:72//Hs.153014:AB002353 50

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F-THYR01001100//Human DNA-binding protein mRNA, 3' end//2.1e-74:741:74//Hs.159249:Z99130
 F-THYR01001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-18:447:62//Hs.124024:AF053700
 F-THYR01001121//ESTs//0.92:257:61//Hs.118246:N95416
 F-THYR01001133//EST//1.1e-38:367:75//Hs.144175:H70425
 F-THYR01001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
 F-THYR01001142//ESTs//1.8e-44:332:82//Hs.146811:AA 410788
 F-THYR01001173
 F-THYR01001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
 F-THYR01001189//ESTs//2.1e-36:323:76//Hs.120206:AI 089163
 F-THYR01001204
 F-THYR01001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:81//Hs.155464:AF088219
 F-THYR01001262//ESTs//7.9e-44:279:87//Hs.138856:H47461
 F-THYR01001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:60//Hs.6467:AJ002309
 F-THYR01001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF 027156
 F-THYR01001290//ESTs//3.9e-43:145:99//Hs.147797:AA 069836
 F-THYR01001313//ESTs//1.0:244:61//Hs.127488:AA528182
 F-THYR01001320//ESTs//0.062:126:67//Hs.133296:AI311872
 F-THYR01001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:560:68//Hs.153563:AF011333
 F-THYR01001322//ESTs//0.12:238:61//Hs.29169:N66545
 F-THYR01001347//ESTs//7.5e-61:293:99//Hs.129962:AA 927207
 F-THYR01001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
 F-THYR01001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:187:79//Hs.12385:AB007877
 F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds//7.4e-157:740:97//Hs.138488:AB014607
 F-THYR01001401//EST//4.6e-14:171:76//Hs.157587:AI356993
 F-THYR01001403//ESTs//2.2e-50:464:79//Hs.118046:N49946
 F-THYR01001405//ESTs//1.7e-44:226:98//Hs.156667:AI

- 347694
F-THYR01001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:459:62//Hs.477:U05659
F-THYR01001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
F-THYR01001426//Human ring zinc-finger protein (ZN F127-Xp) gene and 5' flanking sequence//4.6e-33:153:81//Hs.102877:U41315
F-THYR01001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
F-THYR01001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:653:71//Hs.44782:Z82215
F-THYR01001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:78//Hs.51048:X68830
F-THYR01001487//EST//1.0:88:71//Hs.160760:AI311943
F-THYR01001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
F-THYR01001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
F-THYR01001541//EST//1.4e-10:158:65//Hs.145159:AI150211
F-THYR01001559//ESTs//1.4e-07:91:81//Hs.43507:N24046
F-THYR01001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
F-THYR01001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:546:95//Hs.25306:AF070572
F-THYR01001584//Human RCP3 mRNA, complete cds//0.14:335:58//Hs.82294:U27655
F-THYR01001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:84//Hs.75551:L12535
F-THYR01001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
F-THYR01001605//EST//0.11:426:57//Hs.151206:AI126071
F-THYR01001617//ESTs//5.2e-43:345:81//Hs.8710:W07046
F-THYR01001637//ESTs, Weakly similar to anion exchanger [H.sapiens]//5.2e-13:108:86//Hs.141045:AA191659
F-THYR01001656//Solute carrier family 2 (facilitated glucose transporter), member 4//0.099:540:55//Hs.95958:M91463
F-THYR01001661//ESTs//0.12:53:92//Hs.151586:W45568
F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
F-THYR01001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.78160:AF010238
F-THYR01001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:57//Hs.122908:AF070552
F-THYR01001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
F-THYR01001721//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//2.5e-51:296:92//Hs.3826:U69560
F-THYR01001738//EST//6.9e-30:180:94//Hs.58641:W81229
F-THYR01001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
F-THYR01001746//EST//0.96:119:63//Hs.144107:AI053590
F-THYR01001772//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
F-THYR01001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
F-THYR01001809//Human mRNA for KIAA0297 gene, partial cds//0.47:168:67//Hs.11711:AB002295
F-THYR01001828
F-THYR01001854//EST//0.038:128:67//Hs.160649:AI241823
F-THYR01001895//Intercellular adhesion molecule 1 (CD54), human rhinovirus receptor//9.6e-13:288:65//Hs.51061:W24283
F-THYR01001907//EST//1.9e-12:126:80//Hs.139296:AA350198
F-VESEN1000122
F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
F-Y79AA1000033
F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.8e-21:230:66//Hs.431:L13689
F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds//7.3e-40:629:64//Hs.75305:U78521
F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:W33680
F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:58//Hs.2685:Z50053
F-Y79AA1000181//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U29344
F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860
F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds//3.9e-73:345:100//Hs.9242:AF081192
F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//Hs.842:X73079

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F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623
 F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.30:444:61//Hs.99941:L23134
 F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-11:300:64//Hs.23311:AB002365
 F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:744:56//Hs.44361:D50919
 F-Y79AA1000328
 F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete cds//8.4e-15:223:75//Hs.85313:AF071309
 F-Y79AA1000346
 F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//Hs.123022:J03853
 F-Y79AA1000355
 F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908
 F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897
 F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219
 F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018
 F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516
 F-Y79AA1000480
 F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871
 F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521
 F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356
 F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706
 F-Y79AA1000574//Human mRNA for GC box binding protein, complete cds//0.95:258:62//Hs.150557:D31716
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503
 F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513
 F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670

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F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969
 F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:AI198377
 F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067
 F-Y79AA1000782//EST//0.97:78:69//Hs.147351:AI208468
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799
 F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231
 F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085
 F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:AF059569
 F-Y79AA1000805
 F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568
 F-Y79AA1000827//Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344
 F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956
 F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.86660:AA398644
 F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor BD73 mRNA, 3' end//0.14:499:58//Hs.37288:D16815
 F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:AI341699
 F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:AI359536
 F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
 F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
 F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
 F-Y79AA1001023
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
 F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
 F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
 F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:AI357511
 F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047

- F-Y79AA1001078
F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
F-Y79AA1001177//Human hSIAH2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110I13307 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:AI393240
F-Y79AA1001299//Human Ini1 mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:AI017555
F-Y79AA1001384
F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
F-Y79AA1001394//ESTs, Weakly similar to F54B3.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167
F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:AI088489
F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POLYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:AI360447
F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
- F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA93109
F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:AI363426
F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583
F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244
F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526
F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:AI018620
F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213
F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124
F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332
F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778
F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173
F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720
F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI

- 424382
F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620
611
F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W8
8943
F-Y79AA1002089//ESTs, Weakly similar to putative p
150 [H. sapiens]//8.3e-53:348:88//Hs.18122:AI338045
F-Y79AA1002093
F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA4
11865
F-Y79AA1002115
F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N4
0395
F-Y79AA1002139//ESTs, Weakly similar to B0035.14
[C. elegans]//1.2e-24:165:90//Hs.6473:AA853955
F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 pro
tein, partial cds//9.5e-05:393:62//Hs.77864:AB0145
38
F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA
598515
F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TR
NA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568:
96//Hs.111637:AA305890
F-Y79AA1002210//ESTs, Weakly similar to D2045.8
[C. elegans]//8.6e-33:338:73//Hs.26662:U55984
F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA
524477
F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482
508
F-Y79AA1002229//Human mRNA for KIAA0086 gene, comp
lete cds//0.0041:203:63//Hs.1560:D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 pro
tein, partial cds//4.1e-176:821:98//Hs.100729:AB01
4592
F-Y79AA1002246//Human involucrin mRNA//5.6e-05:52
5:59//Hs.157091:M13903
F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 pro
tein, partial cds//2.2e-160:748:98//Hs.96731:AB014
555
F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84
489
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 pro
tein, partial cds//2.1e-130:622:97//Hs.30898:AB014
534
F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA8
30999
F-Y79AA1002351//Human high conductance inward rect
ifier potassium channel alpha subunit mRNA, comple
te cds//0.028:587:58//Hs.2363:L36069
F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:A
- A824377
F-Y79AA1002399
F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T5
2569
F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//H
s.84112:X52142
F-Y79AA1002431
F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772
318
10 F-Y79AA1002472//Homo sapiens DNA from chromosome 1
9, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973
F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI
160765
F-Y79AA1002487//Insulin-like growth factor binding
protein 2//0.43:249:61//Hs.162:X16302
【1126】 相同性検索結果データ 5.
3' 末端クローン配列に対する Human Unigene 相同性検索
結果データ
各データは、クローン配列名、トップヒットデータの Ti
tle、P 値: 比較配列の長さ (base): 相同性 (%), トップヒ
ットデータの Accession No. の順に // で区切って記載し
た。なお、同一クローンで 5' 末端配列に対応する 3' 末端
配列が決定されていないものは空欄とした。相同性のス
コアの P 値が 1 より大であった場合はデータは示さな
い。
R-HEMBA1000005//ESTs, Highly similar to HYPOTHETI
CAL 31.6 KD PROTEIN F54F2.9 IN CHROMOSOME III [Cae
norhabditis elegans]//5.6e-93:501:93//Hs.13015:AA6
28434
30 R-HEMBA1000030//Human POU domain protein (Brn-3b)
mRNA, complete cds//0.83:314:61//Hs.266:U06233
R-HEMBA1000042//Archain//1.4e-45:282:89//Hs.33642:
X81198
R-HEMBA1000046//Human mRNA for KIAA0118 gene, part
ial cds//8.3e-52:528:72//Hs.154326:D42087
R-HEMBA1000050//EST//0.043:155:63//Hs.149031:AI243
340
R-HEMBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R3
9329
40 R-HEMBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA
410788
R-HEMBA1000129//ESTs, Weakly similar to contains s
imilarity to helicases [C. elegans]//4.4e-90:502:90/
/Hs.55918:AA151667
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 pro
tein, partial cds//2.1e-100:514:94//Hs.27197:AB018
340
R-HEMBA1000150//Homo sapiens mRNA for KIAA0640 pro
tein, partial cds//3.1e-45:435:77//Hs.153026:AB014
540

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R-nnnnnnnnnnnn/ESTs, Moderately similar to The KIAA0138 gene product isnovel. [H.sapiens]//7.7e-92: 428:100//Hs.126925:AA931237
 R-HEMBA1000158
 R-nnnnnnnnnnnn/ESTs, Weakly similar to F13B12.1 [C.elegans]//1.3e-05:58:91//Hs.5570:AI377863
 R-HEMBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545
 R-HEMBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366
 R-HEMBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769927
 R-HEMBA1000201//Human Ini1 mRNA, complete cds//3.0e-25:137:99//Hs.155626:U04847
 R-HEMBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311
 R-HEMBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532
 R-nnnnnnnnnnnn/EST//2.2e-100:498:96//Hs.161570:W80404
 R-HEMBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:287:70//Hs.127649:AB007874
 R-HEMBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete cds//1.3e-23:276:75//Hs.5737:AB007944
 R-HEMBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019
 R-HEMBA1000251//ESTs//0.96:411:56//Hs.120277:AI243808
 R-HEMBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424
 R-nnnnnnnnnnnn/ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.9e-14:208:73//Hs.93332:AA811920
 R-HEMBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485
 R-HEMBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962
 R-HEMBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409
 R-HEMBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cds//1.0:122:67//Hs.129748:AB011099
 R-nnnnnnnnnnnn/ESTs//7.4e-76:386:97//Hs.22276:AA191323
 R-nnnnnnnnnnnn//Human Ca2+-dependent activator protein for secretion mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448
 R-HEMBA1000307//ESTs, Highly similar to 8A-2V protein [M.musculus]//1.1e-103:489:99//Hs.108881:AI018024

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R-nnnnnnnnnnnn/ESTs//9.3e-99:472:98//Hs.163512:AA903238
 R-HEMBA1000338//EST//5.1e-49:278:92//Hs.150815:AI302560
 R-HEMBA1000351//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460
 R-HEMBA1000355//ESTs//1.0e-105:531:96//Hs.61762:AI422243
 10 R-HEMBA1000357//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//9.4e-89:432:87//Hs.139107:K00629
 R-HEMBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857
 R-HEMBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938
 R-HEMBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-44:388:77//Hs.3610:D86960
 R-HEMBA1000387//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460
 20 R-HEMBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878
 R-HEMBA1000392//ESTs//3.9e-105:531:96//Hs.130661:AI340248
 R-HEMBA1000396//ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]//1.1e-44:447:75//Hs.42849:N31920
 R-HEMBA1000411//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//6.1e-92:373:99//Hs.48675:AI005282
 R-HEMBA1000418//ESTs//3.1e-66:315:100//Hs.94133:AI270700
 R-HEMBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
 R-HEMBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:87//Hs.158122:AJ001189
 R-HEMBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
 40 R-HEMBA1000442//ESTs//0.93:322:57//Hs.144763:AI218014
 R-HEMBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
 R-HEMBA1000459//ESTs//0.010:184:63//Hs.128797:AI246316
 R-HEMBA1000460
 R-HEMBA1000464//EST//0.082:87:70//Hs.147977:AI262370
 R-HEMBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:81//Hs.155464:AF088219
 50

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R-HEMBA1000488//ESTs, Weakly similar to The KIAA0132 gene product is related to Drosophila melanogaster ring canel protein. [H.sapiens]//1.1e-31:181:94//Hs.61454:AA312449

R-HEMBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528

R-HEMBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087

R-HEMBA1000504//ESTs//0.016:282:58//Hs.130778:AI077571

R-HEMBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318

R-HEMBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531

R-HEMBA1000518//EST//0.60:141:60//Hs.97831:AA400885

R-HEMBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414

R-HEMBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280

R-HEMBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD//4.0e-55:203:92//Hs.155510:U15782

R-HEMBA1000531//ESTs, Weakly similar to HEAT SHOCK 70 KD PROTEIN 1 [H.sapiens]//1.3e-117:550:99//Hs.99722:AI422277

R-HEMBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809

R-HEMBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:549:80//Hs.91916:AF035317

R-nnnnnnnnnnnnn//ESTs//2.3e-66:342:97//Hs.71916:AA219699

R-HEMBA1000557//EST//1.5e-49:297:90//Hs.149580:AI281881

R-HEMBA1000561//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//1.8e-108:550:96//Hs.26799:W74481

R-HEMBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196

R-HEMBA1000568//ESTs//5.1e-42:321:82//Hs.141024:HO7128

R-nnnnnnnnnnnnn

R-HEMBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788

R-HEMBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//3.9e-113:591:94//Hs.155218:AJ007509

R-HEMBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK// 50

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0.024:309:61//Hs.89519:L10717

R-HEMBA1000594//ESTs//8.6e-07:172:68//Hs.160289:AI168041

R-HEMBA1000604//Human telomerase-associated protein TP-1 mRNA, completecds//1.5e-19:129:93//Hs.158334:U86136

R-HEMBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424

10 R-HEMBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438

R-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//1.4e-86:422:97//Hs.26252:AA643235

R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.7e-99:443:97//Hs.60103:AB014590

R-HEMBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-50:426:79//Hs.40100:AB002390

20 R-HEMBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929

R-HEMBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136

R-HEMBA1000673//ESTs//1.2e-101:473:99//Hs.138215:AI123922

R-HEMBA1000682//ESTs, Weakly similar to putative p150 [H.sapiens]//3.5e-114:553:97//Hs.111730:AA604403

R-HEMBA1000686//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//6.8e-18:137:86//Hs.7049:AI141736

30 R-HEMBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//7.4e-52:345:84//Hs.144563:AF057280

R-HEMBA1000705//EST//0.21:139:63//Hs.132687:AI033672

R-HEMBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213

R-HEMBA1000722//ESTs, Weakly similar to similar to enoyl-CoA hydratases/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:AI018612

R-HEMBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8e-40:449:75//Hs.74478:U33931

R-HEMBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777

R-HEMBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110

R-HEMBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:82//Hs.155464:AF088219

R-HEMBA1000752//EST//0.041:39:94//Hs.127772:AA961131

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- R-HEMBA1000769//Homo sapiens mRNA for chemokine LE C precursor, complete cds//1.6e-32:309:75//Hs.10458:AF088219
- R-HEMBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612
- R-HEMBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody I A4))//1.3e-48:284:90//Hs.103458:X53795
- R-HEMBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-45:291:87//Hs.154326:D42087
- R-HEMBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939
- R-HEMBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027
- R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977
- R-HEMBA1000843//Homo sapiens LIM protein mRNA, complete cds//6.6e-46:410:77//Hs.154103:AF061258
- R-HEMBA1000851
- R-HEMBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrogenase)//3.7e-33:284:80//Hs.159608:U46689
- R-HEMBA1000867//EST//2.0e-17:211:74//Hs.145670:AI265794
- R-HEMBA1000869//ESTs//3.1e-16:237:71//Hs.116518:AA653202
- R-HEMBA1000870//ESTs//1.6e-43:222:98//Hs.69564:AA203608
- R-HEMBA1000872//ESTs//1.9e-93:453:98//Hs.152622:AA594951
- R-HEMBA1000876//Small inducible cytokine A5 (RANTE S)//3.0e-41:329:79//Hs.155464:AF088219
- R-HEMBA1000908//ESTs//1.6e-51:291:92//Hs.12247:AI203154
- R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672
- R-HEMBA1000918//EST//9.6e-30:152:84//Hs.162136:AA526508
- R-HEMBA1000919
- R-HEMBA1000934//ESTs//4.1e-38:254:89//Hs.87784:AA460597
- R-HEMBA1000942//ESTs//3.5e-20:172:69//Hs.160065:AI018619
- R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291
- R-HEMBA1000946//ESTs//1.6e-68:352:96//Hs.21331:H93074
- R-HEMBA1000960//Homo sapiens tapasin (NGS-17) mRNA, complete cds//4.0e-61:347:81//Hs.5247:AF029750
- R-HEMBA1000968//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362:84//Hs.159187:AB007977
- R-HEMBA1000971//ESTs//2.8e-41:246:91//Hs.104287:AI363498
- R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341:81//Hs.44766:AJ007590
- R-HEMBA1000974//ESTs//1.4e-32:166:100//Hs.149274:AI018170
- R-HEMBA1000975//Oxytocin receptor//2.7e-46:563:73//Hs.2820:X64878
- R-HEMBA1000985//ESTs//4.4e-05:125:69//Hs.147434:AI214464
- R-HEMBA1000986//ESTs//7.8e-44:266:84//Hs.163784:N54902
- R-HEMBA1000991//EST//1.4e-42:162:86//Hs.149580:AI281881
- R-HEMBA1001007
- R-HEMBA1001008//ESTs//2.3e-82:463:92//Hs.10339:AA058764
- R-HEMBA1001009//ESTs, Weakly similar to non-lens beta eta gamma-crystallin like protein [H.sapiens]//2.6e-58:280:100//Hs.128738:AA970836
- R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587:95//Hs.158287:AB007937
- R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140:95//Hs.58393:X05360
- R-HEMBA1001020//ESTs//0.52:86:72//Hs.69683:AA115292
- R-HEMBA1001022//ESTs//3.4e-18:102:100//Hs.63243:AI123912
- R-HEMBA1001024//ESTs//1.9e-07:262:61//Hs.124399:AA832336
- R-HEMBA1001026//ESTs//0.0017:142:67//Hs.144109:AI345543
- R-nnnnnnnnnnnnn//Ankyrin G//0.23:244:60//Hs.75893:U13616
- R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186:79//Hs.132942:AB014521
- R-HEMBA1001052//ESTs//5.4e-107:497:99//Hs.121773:AI357886
- R-HEMBA1001060//ESTs//1.1e-31:298:80//Hs.24821:AA044813
- R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179:98//Hs.119571:X14420
- R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 sp

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- ecific transcript KIAA0492//2.7e-21:417:64//Hs.127338:AB007961
 R-HEMBA1001080
 R-HEMBA1001085//ESTs//1.9e-47:385:79//Hs.146811:AA410788
 R-HEMBA1001088//ESTs//2.8e-102:548:93//Hs.127273:AA522674
 R-HEMBA1001094
 R-HEMBA1001099//ESTs//0.24:41:97//Hs.18612:T99245
 R-HEMBA1001109//Small inducible cytokine A5 (RANTE S)//2.4e-46:396:80//Hs.155464:AF088219
 R-HEMBA1001121//ESTs//1.7e-15:216:71//Hs.141605:H92974
 R-HEMBA1001122//ESTs//2.0e-90:474:94//Hs.107884:AA131320
 R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319:84//Hs.99879:M15530
 R-HEMBA1001133//ESTs//1.2e-92:443:99//Hs.99626:AA632341
 R-HEMBA1001137//ESTs//2.0e-86:426:97//Hs.157103:W60265
 R-HEMBA1001140//Small inducible cytokine A5 (RANTE S)//2.9e-45:323:83//Hs.155464:AF088219
 R-HEMBA1001172//ESTs, Moderately similar to !!!! A LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//1.1e-39:309:82//Hs.96337:AA225358
 R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238:60//Hs.127338:AB007961
 R-HEMBA1001197//ESTs//0.010:388:61//Hs.14881:R91896
 R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305:62//Hs.100238:U69194
 R-HEMBA1001226//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.0e-54:333:81//Hs.113283:AF018080
 R-HEMBA1001235//EST//2.3e-07:42:92//Hs.141620:N63316
 R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160:87//Hs.103102:W55932
 R-HEMBA1001257//ESTs//3.3e-112:544:97//Hs.128749:AA779728
 R-HEMBA1001265//ESTs//8.7e-116:564:98//Hs.155150:AA1061435
 R-nnnnnnnnnnnn//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239:87//Hs.103919:AA159181
 R-HEMBA1001286//ESTs//1.4e-97:507:95//Hs.26244:AI352674
 R-HEMBA1001289//ESTs//8.2e-44:122:96//Hs.76267:AA877534
- R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
 R-HEMBA1001299//Small inducible cytokine A5 (RANTE S)//1.1e-45:307:84//Hs.155464:AF088219
 R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
 R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
 R-HEMBA1001310//ESTs//1.4e-91:486:93//Hs.86228:AA206019
 R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
 R-HEMBA1001323//ESTs//6.2e-83:401:98//Hs.47343:AI282950
 R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN INFAB1-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458:92//Hs.9398:N41838
 R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
 R-HEMBA1001330//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
 R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
 R-HEMBA1001361//ESTs//3.5e-107:570:94//Hs.7727:AA142837
 R-HEMBA1001375//ESTs//1.1e-96:454:99//Hs.59584:AA587334
 R-HEMBA1001377//ESTs//8.5e-91:459:95//Hs.61859:AA628550
 R-HEMBA1001383//ESTs//0.077:381:58//Hs.163093:AA745458
 R-HEMBA1001387//ESTs//2.0e-85:405:99//Hs.152127:AI246482
 R-HEMBA1001388//ESTs//1.5e-83:395:99//Hs.105191:AA133439
 R-HEMBA1001391//ESTs//7.7e-90:455:96//Hs.120905:R22204
 R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279:89//Hs.89887:D38081
 R-HEMBA1001405//ESTs//1.2e-98:485:97//Hs.73287:W16714
 R-HEMBA1001407//ESTs//2.2e-76:365:99//Hs.110128:AA584364
 R-HEMBA1001411//ESTs//1.2e-102:476:100//Hs.143162:AI380343
 R-HEMBA1001413//ESTs//3.7e-66:321:98//Hs.152472:AA041199
 R-HEMBA1001415
 R-HEMBA1001432//Putative mismatch repair/binding protein hMSH3//7.9e-42:183:82//Hs.42674:U61981

- R-HEMBA1001433//ESTs//1.4e-34:240:77//Hs.95611:U51704
- R-HEMBA1001435//ESTs//5.6e-23:292:70//Hs.116315:AA629263
- R-HEMBA1001442//ESTs//0.76:414:58//Hs.156189:AI419982
- R-HEMBA1001446//ESTs//2.2e-95:447:99//Hs.154091:AA767546
- R-HEMBA1001450//ESTs//1.0e-93:491:94//Hs.16130:AA195077
- R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-47:304:88//Hs.23094:M19503
- R-HEMBA1001455//ESTs//7.1e-103:482:99//Hs.97407:AI417220
- R-HEMBA1001463
- R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409:66//Hs.36232:D80008
- R-HEMBA1001478
- R-HEMBA1001497
- R-HEMBA1001510//ESTs//3.3e-44:381:78//Hs.139882:AA864426
- R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-79:528:84//Hs.23094:M19503
- R-HEMBA1001517//ESTs//5.8e-32:272:81//Hs.119512:AA487269
- R-HEMBA1001522//ESTs//1.7e-84:364:95//Hs.117858:AA702493
- R-HEMBA1001526//ESTs//1.8e-93:527:93//Hs.10624:N64723
- R-HEMBA1001533//ESTs//1.9e-42:211:100//Hs.55830:AA580270
- R-HEMBA1001557//ESTs//4.2e-83:413:97//Hs.47546:AA181348
- R-HEMBA1001566//Small inducible cytokine A5 (RANTE S)//3.4e-50:304:88//Hs.155464:AF088219
- R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259:62//Hs.2229:X82324
- R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456:77//Hs.159275:AF030880
- R-HEMBA1001579//ESTs//0.11:299:60//Hs.106090:AA457030
- R-HEMBA1001581//ESTs//0.016:350:61//Hs.124664:AI015652
- R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329
- R-HEMBA1001589
- R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431:88//Hs.26625:W25874
- R-HEMBA1001608//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.3e-73:533:82//Hs.103948:X00627
- R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537:90//Hs.20218:AA628530
- R-nnnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRNA A, complete cds//0.054:362:60//Hs.132206:AF039694
- R-HEMBA1001636//ESTs//4.9e-53:267:97//Hs.47459:AA700158
- R-HEMBA1001640//ESTs//2.9e-27:299:72//Hs.65236:AA927623
- R-nnnnnnnnnnnnn//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442:95//Hs.63888:AA203398
- R-HEMBA1001655//ESTs//1.5e-101:516:95//Hs.86541:AA214554
- R-HEMBA1001658
- R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH 68) mRNA, complete cds//1.3e-16:427:61//Hs.106511:AF029343
- R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943
- R-HEMBA1001675
- R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962
- R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424
- R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916
- R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds//6.3e-98:483:96//Hs.31720:AB014598
- R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960
- R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095
- R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA194452
- R-HEMBA1001718//Small inducible cytokine A5 (RANTE S)//8.6e-43:166:88//Hs.155464:AF088219
- R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRP L2 INTERGENIC REGION [Saccharomyces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105
- R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712
- R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353 R-HEMBA1001744

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R-HEMBA1001745//ESTs//6. 6
e-05:244:62//Hs. 157663:AI
358623
R-HEMBA1001746//EST//4. 9e
-65:409:88//Hs. 124673:AA8
58162
R-HEMBA1001761//ESTs//1. 9
e-44:315:84//Hs. 159510:AA
297145
R-HEMBA1001781//ESTs//3. 0
e-98:462:99//Hs. 60059:AI0
57306
R-HEMBA1001784//EST//1. 0e
-12:250:68//Hs. 152366:AA4
86721
R-HEMBA1001791//EST//1. 4e
-47:292:89//Hs. 163333:AA8
79053
R-HEMBA1001800//ESTs//8. 4
e-37:314:79//Hs. 105151:AA
970243
R-HEMBA1001803//ESTs//4. 5
e-99:465:99//Hs. 135159:AI
095823
R-nnnnnnnnnnnnn//Zinc fing
er protein 148 (pHZ-52)//
0. 78:232:57//Hs. 112180:AF
039019
R-HEMBA1001808//Homo sapi
ens mRNA, chromosome 1 sp
ecific transcript KIAA050
0//9. 0e-114:548:98//Hs. 11
8164:AB007969
R-HEMBA1001809//EST//3. 8e
-63:292:89//Hs. 158591:AI3
69334
R-HEMBA1001815//Calcium m
odulating ligand//1. 1e-4
7:299:87//Hs. 13572:AF0681
79
R-HEMBA1001819//ZINC FING
ER PROTEIN HF. 12//1. 2e-1
6:259:69//Hs. 155470:X0729
0
R-HEMBA1001820//ESTs//2. 6
e-86:404:100//Hs. 112881:A
A620707
R-nnnnnnnnnnnnn//ESTs//2. 2
e-101:480:99//Hs. 159940:A
A971578

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R-HEMBA1001824//ESTs, Wea
kly similar to MATRIN 3
[H. sapiens]//6. 2e-27:147:
97//Hs. 23476:AA401210
R-HEMBA1001835//EST//0. 7
9:216:64//Hs. 47437:N52250
R-HEMBA1001844//ESTs//4. 7
e-62:319:95//Hs. 55200:N98
513
R-HEMBA1001847//ESTs//2. 3
e-102:522:95//Hs. 20879:AA
845446
R-HEMBA1001861//Homo sapi
ens mRNA for KIAA0617 pro
tein, complete cds//1. 1e-
109:553:96//Hs. 78946:AB01
4517
R-HEMBA1001864//ESTs//7. 4
e-94:449:99//Hs. 132776:AI
142853
R-HEMBA1001866//Myelin ol
igodendrocyte glycoprotei
n {alternative products}/
/1. 9e-37:357:76//Hs. 5321
7:Z48051
R-nnnnnnnnnnnnn//ESTs, Wea
kly similar to trithorax
homolog HTX, version 2 [H.
sapiens]//2. 3e-32:193:94/
/Hs. 9489:R84329
R-HEMBA1001888//H. sapiens
mRNA for urea transporte
r//2. 0e-47:425:78//Hs. 667
10:X96969
R-HEMBA1001896//ESTs//3. 5
e-56:274:99//Hs. 129018:HO
3128
R-HEMBA1001910
R-HEMBA1001912//ESTs, Wea
kly similar to !!!! ALU S
UBFAMILY J WARNING ENTRY
!!!! [H. sapiens]//1. 5e-7
3:347:100//Hs. 30991:AA994
438
R-HEMBA1001913//ESTs, Hig
hly similar to GCN20 PRO
TEIN [Saccharomyces cerev
isiae]//5. 1e-57:320:91//H
s. 91251:U66685
R-HEMBA1001915//ESTs//4. 9

3993

3994

e-88:459:95//Hs. 122810:AI
273706
R-HEMBA1001918//ESTs//1.2
e-106:505:99//Hs. 98518:AI
027125
R-HEMBA1001921//Homo sapi
ens germinal center kinas
e related protein kinase
mRNA, complete cds//5.5e-
107:534:96//Hs. 154934:AF0
00145
R-HEMBA1001939//ESTs, Mod
erately similar to !!!!! A
LU SUBFAMILY J WARNINGENT
RY !!!!! [H. sapiens]//2.9e-
99:482:98//Hs. 96849:AA87
9470
R-HEMBA1001940//Human mRN
A for KIAA0392 gene, part
ial cds//5.6e-45:336:82//
Hs. 40100:AB002390
R-HEMBA1001942//EST//2.6e-
84:397:99//Hs. 145444:AI2
03668
R-HEMBA1001945//ESTs//1.4
e-92:437:99//Hs. 144565:AI
192452
R-HEMBA1001950//ESTs//3.9
e-43:280:88//Hs. 84429:N28
866
R-HEMBA1001960//ESTs//0.0
40:243:62//Hs. 29567:AA640
421
R-HEMBA1001962//ESTs//0.0
071:113:69//Hs. 49792:N700
48
R-HEMBA1001964//ESTs//3.0
e-38:239:87//Hs. 158126:W2
6825
R-HEMBA1001967//Human DNA
sequence from clone 341E
18 on chromosome 6p11.2-1
2.3. Contains a Serine/Th
reonine Protein Kinase ge
ne (presumptive isolog of
a Rat gene) and a novel
alternatively spliced gen
e. Contains a putative Cp
G island, ESTs and GSSs//
1.8e-106:517:97//Hs. 1105

O:AL031178

R-HEMBA1001979//EST//0.039:167:63//Hs. 129451:AA993
932
R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs. 136839:H9
3717
R-HEMBA1001991//Human mRNA for KIAA0355 gene, comp
lete cds//9.5e-47:303:88//Hs. 153014:AB002353
R-HEMBA1002003//Homo sapiens mRNA for protein phos
phatase 2C (beta)//1.6e-91:448:97//Hs. 5687:AJ00580
1
R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs. 142314:AA
347930
R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs. 7871:AI04
1837
R-HEMBA1002022//Human mRNA for KIAA0075 gene, part
ial cds//0.25:196:63//Hs. 1189:D38550
R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs. 8858:AI1
31538
R-HEMBA1002039//H. sapiens mRNA for phosphoinositid
e 3-kinase//0.68:256:64//Hs. 101238:Y11312
R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 pro
tein, complete cds//2.4e-51:254:85//Hs. 15731:AB011
135
R-HEMBA1002084//EST//0.31:219:60//Hs. 162396:AA5727
64
R-HEMBA1002092//EST//6.4e-72:342:99//Hs. 148533:AI2
00996
R-HEMBA1002100//EST//5.6e-38:258:85//Hs. 103094:W52
354
30 R-HEMBA1002102//Thiopurine S-methyltransferase//1.
4e-46:403:79//Hs. 51124:AF019369
R-HEMBA1002113//Prostaglandin I2 (prostacyclin) sy
nthase //1.4e-76:280:90//Hs. 61333:D83402
R-HEMBA1002119//Homo sapiens OR7E12P pseudogene, c
omplete sequence//1.4e-87:362:94//Hs. 103443:AF0658
54
R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3
[C. elegans]//1.7e-16:94:100//Hs. 107747:AI357868
R-HEMBA1002139//H. sapiens mRNA for nebulin//0.001
9:68:88//Hs. 83870:X83957
R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs. 141575:AA
211734
R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs. 32275:AA
595199
R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs. 77703:W1
9642
R-HEMBA1002153//EST//4.5e-49:458:77//Hs. 141708:W44
337
R-HEMBA1002160//Homo sapiens nephrocystin (NPHP1)
mRNA, partial cds//1.4e-36:400:75//Hs. 75474:AF0236

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R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:N64043
R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622
R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.4e-29:244:72//Hs.119387:AB007958
R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frames//4.3e-84:557:84//Hs.23094:M19503
R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete cds//5.1e-21:230:75//Hs.139648:AB014606
R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//1.5e-47:238:98//Hs.25664:AF089814
R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
R-HEMBA1002257
R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN INVMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818
R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-130:642:96//Hs.6162:AB018314
R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04 50
- 822
R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
R-nnnnnnnnnnnn//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563
R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849
R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267
R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-22:181:80//Hs.74554:D38522
R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069
R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085
R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395
R-nnnnnnnnnnnn//ESTs, Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193
R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394
R-HEMBA1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219
30 R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:AI188995
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449
R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990
R-nnnnnnnnnnnn//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972
40 R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923
R-HEMBA1002542//ESTs//1.0e-101:539:93//Hs.93872:AA524700
R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:AI041804
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:AI281881

3997

3998

- R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012
- R-HEMBA1002558//Homo sapiens 4F5S mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519
- R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219
- R-nnnnnnnnnnnn//Homo sapiens protein associated with Myc mRNA, completecds//1.4e-120:587:97//Hs.151411:AF075587
- R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904
- R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838
- R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055
- R-HEMBA1002621
- R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351
- R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881
- R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715
- R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041
- R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970
- R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696
- R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307
- R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945
- R-HEMBA1002678//EST, Moderately similar to !!!!! ALU SUBFAMILY J WARNINGENTRY !!!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896
- R-nnnnnnnnnnnn//EST//0.15:136:69//Hs.129570:AA995396
- R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282
- R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477
- R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//6.0e-46:302:86//Hs.15519:AB018315
- R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884
- R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521
- R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168
- R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163
- R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526
- R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:AI375792
- R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090
- R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126
- R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127
- R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491
- R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717
- R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333
- R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:AI279709
- R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320
- R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:AF071185
- R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204
- R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:AI092013
- R-HEMBA1002833//ESTs, Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.5337:AA243757
- R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514
- R-HEMBA1002863//ESTs//1.1e-67:359:94//Hs.124699:W27830
- R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:AI220827
- R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
- R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//Hs.33787:AF037261
- R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
- R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34

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R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:AI254165
R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA 10229723
R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:AI190892
R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:AI00405
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
R-nnnnnnnnnnnn//ESTs//3.2e-18:102:100//Hs.146255:AA197064
R-HEMBA1002999//ESTs, Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//7.9e-113:560:96//Hs.125749:AI377682
R-HEMBA1003021//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080
R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:AI038577
R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:AI240366
R-HEMBA1003041//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182
R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238
R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA7 50
01903
R-HEMBA1003077//ESTs, Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235
R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:AI075249
R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219
R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
R-HEMBA1003096//ESTs, Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155
R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:AI150058
R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751
R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:AI370845
R-HEMBA1003136//ESTs, Weakly similar to MANNULOSE-1-PHOSPHATE GUANYLTRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:AI088615
R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219
R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670
R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804
R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540
R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265
R-HEMBA1003220//ESTs, Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817
R-HEMBA1003222//ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.232

94:W27666
 R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
 R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
 R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864
 R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
 R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219
 R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392
 R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785
 R-HEMBA1003281
 R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109
 R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266
 R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353
 R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504
 R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872
 R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869
 R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119
 R-HEMBA1003328//H.sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173
 R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029
 R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357
 R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540
 R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651
 R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588
 R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247
 R-HEMBA1003380//ESTs, Moderately similar to ILLI A LU SUBFAMILY J WARNINGENTRY ILLI [H.sapiens]//1.8e

-11:261:65//Hs.87578:AI125363
 R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847
 R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127
 R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA74204
 R-nnnnnnnnnnnn//ESTs//1.7e-24:188:85//Hs.70266:Z78309
 10 R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:D11563
 R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013
 R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696
 R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121
 R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA885516
 20 R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080
 R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688
 R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760
 R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:M14058
 R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817
 30 R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673
 R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN [H.sapiens]//2.8e-93:495:93//Hs.91619:AA552351
 R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734
 R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522
 R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058
 40 R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H.sapiens]//4.0e-63:343:93//Hs.58598:AA625440
 R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099
 R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892
 R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065
 50 R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI

- 244212
R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087
R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042
R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374
R-HEMBA1003615
R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167
R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387
R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888
R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021
R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//9.3e-24:189:84//Hs.142208:AA209438
R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830
R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010
R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783
R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957
R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049
R-HEMBA1003667//Farnesyl transferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635
R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2[H.sapiens]//4.1e-87:434:97//Hs.9489:R84329
R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379
R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
R-HEMBA1003692//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873
R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279064
R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777
R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K⁺ channel (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823
R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847
R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040
R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
R-HEMBA1003783//ESTs, Weakly similar to C01H6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868
R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219
R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333
R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTINGXP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911
R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621
R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930

- R-HEMBA1003893//Calcium modulating ligand//2.1e-4
3: 294: 86//Hs. 13572: AF068179
- R-HEMBA1003902//ESTs//1.8e-43: 300: 85//Hs. 146811: AA
410788
- R-HEMBA1003908//ESTs//3.5e-91: 477: 94//Hs. 6638: AA53
6187
- R-HEMBA1003926//ESTs//7.9e-44: 294: 87//Hs. 164036: AA
845659
- R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 pro
tein, partial cds//3.5e-48: 276: 81//Hs. 72660: AB0111 10
57
- R-HEMBA1003939
- R-HEMBA1003942//ESTs//1.6e-81: 428: 94//Hs. 50418: AA5
24669
- R-HEMBA1003950//ESTs//8.1e-54: 283: 95//Hs. 145528: AI
261545
- R-HEMBA1003953//ESTs//3.8e-30: 194: 89//Hs. 99681: AA5
04591
- R-HEMBA1003958//ESTs//4.0e-45: 394: 77//Hs. 141602: N6
3562
- R-HEMBA1003959//ESTs//5.2e-28: 197: 86//Hs. 9951: W562
53
- R-HEMBA1003976//ESTs//2.0e-29: 232: 84//Hs. 133947: AI
074525
- R-HEMBA1003978//ESTs//3.2e-115: 549: 98//Hs. 76798: AI
050882
- R-HEMBA1003985//ESTs, Weakly similar to !!!!! ALU S
UBFAMILY J WARNING ENTRY !!!!! [H. sapiens]//2.2e-9
1: 448: 97//Hs. 117834: AA766771
- R-HEMBA1003987//ESTs//8.1e-36: 193: 88//Hs. 151844: N9 30
2756
- R-HEMBA1003989//Human mRNA for KIAA0241 gene, part
ial cds//3.6e-43: 360: 81//Hs. 150275: D87682
- R-HEMBA1004000//EST//5.5e-62: 308: 97//Hs. 50438: N741
05
- R-HEMBA1004011//ESTs//8.6e-85: 431: 96//Hs. 36185: R99
899
- R-HEMBA1004012//ESTs//1.3e-40: 309: 83//Hs. 140329: AA
714011
- R-HEMBA1004015//ESTs//5.1e-97: 453: 99//Hs. 111446: AI 40
333774
- R-HEMBA1004024//ESTs//5.2e-19: 159: 79//Hs. 138856: H4
7461
- R-HEMBA1004038//ESTs//1.3e-41: 346: 79//Hs. 146173: AA
906191
- R-HEMBA1004042//ESTs//0.0012: 201: 69//Hs. 24248: AA52
8253
- R-HEMBA1004045//ESTs, Weakly similar to putative p
150 [H. sapiens]//1.5e-22: 365: 70//Hs. 99692: AA811804
- R-HEMBA1004048//ESTs//9.5e-104: 497: 98//Hs. 77735: AI 50
- 125469
- R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-3
1: 176: 96//Hs. 8997: M11717
- R-HEMBA1004055//ESTs//1.7e-115: 577: 96//Hs. 59503: W6
3754
- R-HEMBA1004056//Homo sapiens PYRIN (MEFV) mRNA, co
mplete cds//5.2e-78: 577: 82//Hs. 113283: AF018080
- R-HEMBA1004074//EST//1.0: 152: 61//Hs. 149093: AI 24398
8
- R-HEMBA1004086//ESTs//4.0e-53: 266: 98//Hs. 34658: N98
652
- R-HEMBA1004097//ESTs//4.4e-46: 279: 91//Hs. 110533: H1
6251
- R-HEMBA1004131//Human mRNA for KIAA0128 gene, part
ial cds//3.0e-43: 534: 69//Hs. 90998: D50918
- R-HEMBA1004132//ESTs//4.6e-47: 316: 86//Hs. 141602: N6
3562
- R-HEMBA1004133
- R-HEMBA1004138//EST//1.7e-08: 211: 64//Hs. 129189: AA9
20 88736
- R-HEMBA1004143//ESTs//4.0e-25: 137: 97//Hs. 21307: AA2
03320
- R-HEMBA1004146//Small inducible cytokine A5 (RANTE
S)//4.1e-27: 191: 86//Hs. 155464: AF088219
- R-HEMBA1004150//GRANALCIN//0.99: 357: 59//Hs. 79381:
M81637
- R-HEMBA1004164//Human mRNA for KIAA0118 gene, part
ial cds//9.5e-47: 313: 84//Hs. 154326: D42087
- R-HEMBA1004168//Homo sapiens geminin mRNA, complet
e cds//7.7e-112: 563: 96//Hs. 59988: AF067855
- R-HEMBA1004199
- R-HEMBA1004200//EST//3.1e-89: 441: 97//Hs. 141173: R97
701
- R-HEMBA1004202//ESTs, Weakly similar to GTP-BINDIN
G PROTEIN YPTM1 [Zea mays]//1.7e-107: 552: 94//Hs. 10
092: AI 189282
- R-HEMBA1004203//Homo sapiens mRNA for KIAA0618 pro
tein, complete cds//1.5e-96: 275: 98//Hs. 15832: AB014
518
- R-HEMBA1004207//Leptin receptor//1.1e-117: 573: 97//
Hs. 54515: U50748
- R-HEMBA1004225//EST//9.7e-34: 186: 95//Hs. 137567: R20
617
- R-HEMBA1004227//ESTs, Moderately similar to !!!!! A
LU SUBFAMILY SQ WARNING ENTRY !!!!! [H. sapiens]//4.
0e-16: 117: 91//Hs. 92033: AA255832
- R-HEMBA1004238//Human mRNA for KIAA0355 gene, comp
lete cds//3.0e-46: 338: 83//Hs. 153014: AB002353
- R-HEMBA1004241//ESTs//1.3e-10: 93: 87//Hs. 137511: AA4
56389

4007

R-HEMBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258
 R-HEMBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284
 R-HEMBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962
 R-HEMBA1004267//ESTs, Moderately similar to !!!! A LU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018
 R-HEMBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931
 R-nnnnnnnnnnnnn//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081
 R-HEMBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795
 R-HEMBA1004289//Sulfotransferase, dehydroepiandrosterone (DHEA) -preferring//1.7e-34:223:75//Hs.81884:U13061
 R-HEMBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961
 R-HEMBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426
 R-HEMBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679
 R-HEMBA1004321//Zinc finger protein 44 (KOX 7)//2.6e-37:415:64//Hs.51199:X16281
 R-HEMBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904
 R-HEMBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714
 R-HEMBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA56561
 R-HEMBA1004334//ESTs//1.6e-46:234:98//Hs.47159:AI310231
 R-HEMBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336
 R-HEMBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667
 R-HEMBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353

4008

R-HEMBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494
 R-HEMBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869
 R-HEMBA1004372//EST//0.27:198:60//Hs.162665:AA605057
 R-HEMBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264
 R-HEMBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084
 R-HEMBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219
 R-HEMBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717
 R-HEMBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933
 R-HEMBA1004429//ESTs, Weakly similar to homeotic protein protein zhx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:AI123518
 R-HEMBA1004433//Human Line-1 repeat mRNA with 2 open reading frames//2.9e-32:463:68//Hs.23094:M19503
 R-HEMBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
 R-HEMBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
 R-HEMBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
 R-HEMBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA59306
 R-HEMBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
 R-HEMBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
 R-HEMBA1004507
 R-HEMBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPR1-GCN20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
 R-HEMBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
 R-HEMBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
 R-HEMBA1004554
 R-HEMBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924
 R-HEMBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913

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R-HEMBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA5
82243
R-HEMBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R397
69
R-nnnnnnnnnnnnn//ESTs//6.0e-22:190:82//Hs.42530:N41
661
R-HEMBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA7
80767
R-HEMBA1004617//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0501//4.6e-52:327:85//Hs.159 10
897:AB007970
R-HEMBA1004629//ESTs//2.3e-19:215:76//Hs.111995:AI
375915
R-HEMBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA8
10785
R-HEMBA1004632//ESTs//1.0:128:66//Hs.159182:AA8311
52
R-HEMBA1004637//ESTs, Highly similar to HYPOTHETI
CAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [Cae
norhabditis elegans]//4.8e-111:532:98//Hs.12263:AA 20
282393
R-HEMBA1004638//ESTs//1.2e-66:341:95//Hs.122687:AI
278454
R-HEMBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA6
25442
R-HEMBA1004669//ESTs//0.00039:116:74//Hs.138725:N7
6348
R-HEMBA1004670//ESTs//1.7e-16:116:89//Hs.56825:AI0
57560
R-HEMBA1004672//EST//6.7e-76:315:97//Hs.20821:R193 30
68
R-HEMBA1004693//ESTs//6.4e-68:327:99//Hs.159066:AI
093252
R-HEMBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA0
43562
R-HEMBA1004705//EST//0.0034:271:58//Hs.112503:AA59
9042
R-HEMBA1004709//EST//1.3e-55:392:85//Hs.149580:AI2
81881
R-HEMBA1004711//Small inducible cytokine A5 (RANTE 40
S)//1.9e-47:449:76//Hs.155464:AF088219
R-HEMBA1004725//EST//1.8e-71:424:88//Hs.155712:AI3
09235
R-HEMBA1004730//Homo sapiens clone 23892 mRNA sequ
ence//2.1e-44:467:73//Hs.91916:AF035317
R-HEMBA1004733//EST//0.99:84:65//Hs.161372:AI42315
1
R-HEMBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73
275
R-HEMBA1004736//Ataxia telangiectasia mutated (inc 50

4010

ludes complementation groups A, C and D)//9.5e-39:2
96:82//Hs.51187:U82828
R-HEMBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59
651
R-HEMBA1004751//ESTs//8.0e-23:155:88//Hs.149464:AI
279428
R-HEMBA1004752//Thromboxane A2 receptor//2.7e-45:2
81:89//Hs.89887:D38081
R-HEMBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-6
7:475:84//Hs.8102:L06498
R-HEMBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N6
8679
R-HEMBA1004758//EST//2.0e-43:367:80//Hs.133006:AI0
49504
R-HEMBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87
380
R-HEMBA1004768//ESTs, Weakly similar to RETROVIRUS
-RELATED POLYPROTEIN [Mus musculus]//1.4e-47:3
79:81//Hs.141273:H66705
R-HEMBA1004770//ESTs//0.0014:246:61//Hs.124857:AA6
87092
R-HEMBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA
699633
R-HEMBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W7
4476
R-HEMBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA
848167
R-nnnnnnnnnnnnn
R-HEMBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W8
7732
R-HEMBA1004806
R-HEMBA1004807//ESTs//6.2e-77:362:100//Hs.140945:N
47676
R-HEMBA1004816//EST//4.3e-18:246:72//Hs.150552:AI0
53784
R-HEMBA1004820//Human arginine-rich nuclear protei
n mRNA, complete cds//5.0e-14:141:85//Hs.80510:W74
002
R-HEMBA1004847
R-HEMBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA5
77120
R-HEMBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95
267
R-HEMBA1004864
R-HEMBA1004865//EST//6.7e-18:191:75//Hs.129944:AA4
29362
R-HEMBA1004880//EST//4.4e-70:346:98//Hs.145094:AA4
52409
R-HEMBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W6
3676

- R-HEMBA1004900//ESTs//1.2e-15:283:68//Hs.157606:AI357470
- R-HEMBA1004909//ESTs//7.3e-44:366:79//Hs.140329:AA714011
- R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-50:313:89//Hs.40100:AB002390
- R-HEMBA1004923//ESTs//0.013:162:64//Hs.143655:AI128388
- R-HEMBA1004929//EST//2.3e-48:250:97//Hs.131589:AI025053
- R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.2e-70:547:80//Hs.1361:M55053
- R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-110:530:98//Hs.18029:AI422883
- R-HEMBA1004934//ESTs//1.3e-103:522:96//Hs.40415:AA037215
- R-HEMBA1004944//ESTs//6.0e-21:97:84//Hs.141973:N21434
- R-HEMBA1004954//ESTs//7.9e-112:596:93//Hs.6226:W61007
- R-HEMBA1004956//ESTs//3.1e-58:280:100//Hs.120750:AA741074
- R-HEMBA1004960//ESTs//6.9e-89:476:93//Hs.163738:AA601040
- R-HEMBA1004972//ESTs//3.0e-72:381:95//Hs.55014:AA934035
- R-HEMBA1004973//ESTs//2.7e-91:441:98//Hs.28144:AI292065
- R-HEMBA1004977//ESTs//2.0e-95:446:99//Hs.29690:AI168404
- R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F) mRNA, complete cds//0.43:187:67//Hs.129734:AJ001683
- R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-53:305:91//Hs.146395:AB002329
- R-HEMBA1004983//ESTs//0.16:482:57//Hs.131929:AI021894
- R-HEMBA1004995
- R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapiens]//6.9e-51:482:78//Hs.141601:N63520
- R-HEMBA1005009//ESTs, Highly similar to ACTIN I [Naegleria fowleri]//3.8e-109:551:96//Hs.103180:AI365212
- R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//2.0e-105:542:94//Hs.31921:AB014548
- R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-9
- 5:491:94//Hs.16085:AI261382
- R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-64:312:85//Hs.22271:D26067
- R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sapiens]//2.6e-48:443:78//Hs.139019:N99348
- R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5A [Canis familiaris]//1.2e-87:542:87//Hs.16258:AI376436
- 10 R-HEMBA1005050//ESTs//6.3e-46:311:86//Hs.159510:AA297145
- R-HEMBA1005062//ESTs//1.1e-14:216:68//Hs.129935:AA994451
- R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303:73//Hs.79385:U90905
- R-HEMBA1005075//EST//0.65:214:62//Hs.133991:AI075789
- R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304:83//Hs.85889:U17077
- 20 R-HEMBA1005083//ESTs//2.8e-74:356:98//Hs.132272:AI393958
- R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//1.7e-111:545:96//Hs.11170:AF080561
- R-HEMBA1005113//ESTs//1.1e-101:512:95//Hs.7972:AI052739
- R-HEMBA1005123//Ley I-L//3.6e-58:519:77//Hs.37062:AC005952
- R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:309:85//Hs.19949:X98173
- 30 R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//4.7e-36:394:75//Hs.67619:AB007957
- R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//3.6e-32:362:77//Hs.132206:AF039694
- R-HEMBA1005159//EST//7.4e-47:252:94//Hs.134930:AI093397
- R-HEMBA1005185//ESTs//5.2e-48:305:89//Hs.14920:AA910914
- R-HEMBA1005201//ESTs//4.7e-58:293:97//Hs.23752:C05766
- R-HEMBA1005202//ESTs//1.0:169:59//Hs.153423:AI198239
- R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (123F2) mRNA, complete cds//0.84:191:61//Hs.26931:AF061836
- R-HEMBA1005223//ESTs//0.75:90:70//Hs.127446:AA167284
- 50 R-HEMBA1005232//EST//0.056:162:67//Hs.65649:F13687

- R-HEMBA1005241//ESTs//3.6e-113:564:96//Hs.12770:W8
4331
- R-HEMBA1005244//ESTs//6.4e-22:118:100//Hs.21396:AA
114834
- R-HEMBA1005251//ESTs//8.5e-36:213:92//Hs.161554:AA
393896
- R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 pro
tein, partial cds//6.1e-49:277:93//Hs.72660:AB0111
57
- R-HEMBA1005274//ESTs//3.7e-65:322:98//Hs.105166:AA 10
668862
- R-HEMBA1005275//ESTs//2.1e-29:298:73//Hs.33393:R83
391
- R-HEMBA1005293//ESTs//3.5e-93:448:98//Hs.12066:AI2
08611
- R-HEMBA1005296//ESTs//4.3e-33:168:100//Hs.13916:AI
025750
- R-HEMBA1005304//Small inducible cytokine A5 (RANTE
S)//2.8e-50:315:82//Hs.155464:AF088219
- R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete c 20
ds//1.3e-44:318:83//Hs.32567:AF073519
- R-HEMBA1005314//ESTs//3.0e-103:491:98//Hs.41606:AI
095046
- R-HEMBA1005315//EST//1.9e-29:370:72//Hs.161483:N59
169
- R-HEMBA1005318//ESTs//3.9e-110:535:97//Hs.26771:AA
126472
- R-HEMBA1005331//Intercellular adhesion molecule 2/
//7.6e-39:256:87//Hs.83733:X15606
- R-HEMBA1005353//ESTs//1.7e-81:406:96//Hs.155374:AI 30
341467
- R-HEMBA1005359//Homo sapiens neuronal thread prote
in AD7c-NTP mRNA, complete cds//4.7e-46:294:81//H
s.129735:AF010144
- R-HEMBA1005367//Alcohol dehydrogenase 2 (class I),
beta polypeptide//1.0:210:62//Hs.4:X03350
- R-HEMBA1005372//ESTs//6.2e-95:451:99//Hs.135219:AI
091653
- R-HEMBA1005374//ESTs//1.5e-107:502:99//Hs.118208:A
A947305
- R-HEMBA1005389//Fc fragment of IgA, receptor for//
1.0e-39:311:80//Hs.54486:X54150
- R-HEMBA1005394//ESTs, Weakly similar to coded for
by C. elegans cDNA yk30b3.5 [C.elegans]//4.0e-88:4
89:92//Hs.43864:AA131568
- R-HEMBA1005403//EST//0.0011:78:75//Hs.127061:AA863
278
- R-HEMBA1005408//ESTs//3.2e-29:395:71//Hs.117532:AA
676725
- R-HEMBA1005410//ESTs//1.5e-18:271:70//Hs.144604:AI 50
- 052059
- R-HEMBA1005411//ESTs//1.1e-35:335:77//Hs.141181:R9
8757
- R-HEMBA1005423//Homo sapiens cyclin-dependent kina
se inhibitor (CDKN2C)mRNA, complete cds//1.8e-118:
453:99//Hs.4854:AF041248
- R-HEMBA1005426//Chromosome 1 specific transcript K
IAA0491//0.25:264:61//Hs.136309:AB007960
- R-HEMBA1005443//Homo sapiens (clone s153) mRNA fra
gment//1.7e-47:305:87//Hs.6445:L40391
- R-HEMBA1005447//ESTs//5.7e-83:529:86//Hs.114253:AA
745961
- R-HEMBA1005468//ESTs//7.3e-23:249:73//Hs.61199:AA0
24494
- R-HEMBA1005469//Human mRNA for KIAA0355 gene, comp
lete cds//4.5e-45:320:85//Hs.153014:AB002353
- R-HEMBA1005472//Human kpni repeat mrna (cdna clone
pcd-kpni-8), 3' end//8.4e-73:464:87//Hs.103948:KO
0627
- R-HEMBA1005475//ESTs//0.32:192:59//Hs.62694:AA1004
45
- R-HEMBA1005497
- R-HEMBA1005500//ESTs//2.2e-43:307:85//Hs.146811:AA
410788
- R-HEMBA1005506//75 kda infertility-related sperm p
rotein [human, testis,mRNA Partial, 2427 nt]//0.1
1:295:60//Hs.62608:S58544
- R-HEMBA1005508//ESTs//2.8e-55:319:93//Hs.50150:N90
870
- R-HEMBA1005511//ESTs, Weakly similar to similar to
mouse MNRI [C.elegans]//2.6e-82:387:99//Hs.67466:
AI219740
- R-HEMBA1005517//ESTs//4.6e-77:469:90//Hs.126787:AA
203322
- R-HEMBA1005518//ESTs//1.5e-108:561:94//Hs.123167:A
A601045
- R-HEMBA1005520//Putative mismatch repair/binding p
rotein hMSH3//7.5e-44:179:84//Hs.42674:U61981
- R-HEMBA1005526//ESTs//8.7e-46:308:86//Hs.146811:AA
410788
- R-HEMBA1005528//ESTs, Highly similar to POP2 PROT
EIN [Saccharomyces cerevisiae]//8.6e-115:578:95//H
s.17035:AI080471
- R-HEMBA1005530//ESTs//1.5e-110:551:96//Hs.107294:W
72350
- R-HEMBA1005548//ESTs//1.7e-100:510:96//Hs.9115:N90
926
- R-HEMBA1005552//Interleukin 10//2.4e-38:306:80//H
s.2180:M57627
- R-HEMBA1005558//ESTs, Weakly similar to unknown

4015

[S.cerevisiae]//5.3e-77:439:91//Hs.22897:R43193
 R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-3
 1:182:76//Hs.133526:N21103
 R-HEMBA1005570//ESTs//3.3e-67:411:88//Hs.142245:AA
 489709
 R-HEMBA1005576//EST//0.91:52:73//Hs.149518:AI28049
 7
 R-HEMBA1005577
 R-HEMBA1005581//Homo sapiens mRNA for MEGF5, parti 10
 al cds//3.1e-28:561:64//Hs.57929:AB011538
 R-HEMBA1005582//ESTs//6.0e-73:371:97//Hs.103758:CO
 6392
 R-HEMBA1005583//ESTs//8.3e-79:413:95//Hs.62348:AA
 19539
 R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403:83
 //Hs.75680:M15990
 R-HEMBA1005593//ESTs//3.3e-30:139:80//Hs.142273:W3
 7905
 R-HEMBA1005595//ESTs//1.1e-97:454:100//Hs.27497:AI 20
 274820
 R-HEMBA1005606//EST//1.0e-12:313:64//Hs.162402:AA5
 73125
 R-HEMBA1005609//ESTs//0.49:278:58//Hs.76235:W56390
 R-HEMBA1005616//EST//1.3e-98:470:99//Hs.122230:AA7
 81422
 R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MA
 D2 PROTEIN [S.cerevisiae]//2.8e-95:539:92//Hs.1940
 0:AA662845
 R-HEMBA1005627//Human mRNA for adipogenesis inhibi 30
 tory factor//5.5e-38:317:78//Hs.1721:X58377
 R-HEMBA1005631//Human mRNA for KIAA0393 gene, comp
 lete cds//2.3e-11:279:65//Hs.15245:AF041081
 R-HEMBA1005632//EST//1.5e-10:181:70//Hs.120259:AA7
 31522
 R-HEMBA1005634//Homo sapiens mRNA for chemokine LE
 C precursor, completecds//1.4e-25:234:80//Hs.1045
 8:AF088219
 R-HEMBA1005666//ESTs//2.3e-103:534:95//Hs.14512:AA
 205973
 R-HEMBA1005670//ESTs//2.6e-39:166:81//Hs.139414:AI
 279477
 R-HEMBA1005679//Esterase D/formylglutathione hydro
 lase//1.3e-50:322:88//Hs.82193:M13450
 R-HEMBA1005680//Homo sapiens LIM protein mRNA, com
 plete cds//3.3e-43:343:81//Hs.154103:AF061258
 R-HEMBA1005685//Human homeodomain protein (Prox 1)
 mRNA, complete cds//0.0050:235:64//Hs.159437:U440
 60
 R-HEMBA1005699//Human putative EPH-related PTK rec 50

4016

ceptor ligand LERK-8 (Eplg8) mRNA, complete cds//1.
 7e-47:376:84//Hs.26988:U66406
 R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA7
 72055
 R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:AI1
 59943
 R-HEMBA1005732//Homo sapiens mRNA for cartilage-as
 sociated protein (CASP)//1.2e-45:398:79//Hs.15548.
 1:AJ006470
 R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA0
 53815
 R-nnnnnnnnnnnnn//EST//0.098:125:68//Hs.136945:AA765
 672
 R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47
 096
 R-HEMBA1005765//Human peptide transporter (HPEPT1)
 mRNA, complete cds//3.9e-47:404:80//Hs.2217:U2193
 6
 R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA
 173974
 R-HEMBA1005813//Homo sapiens mRNA for chemokine LE
 C precursor, completecds//2.0e-33:195:84//Hs.1045
 8:AF088219
 R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:AI
 038601
 R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA5
 14960
 R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:AI0
 39201
 R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:AI
 080618
 R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA0
 98911
 R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA
 757917
 R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA4
 20970
 R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:AI0
 22252
 R-HEMBA1005894
 R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:AI
 215686
 R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:AI
 076363
 R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA
 970632
 R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 pro
 tein, complete cds//9.5e-45:446:75//Hs.59403:AB011
 098
 R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA3708

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R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:AI1199418
R-HEMBA1005963
R-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516
R-HEMBA1005991//Human antiseecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199
R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:AI080618
R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:AI379875
R-HEMBA1006005//EST//1.0:105:63//Hs.145273:AI249436
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268
R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951
R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490
R-nnnnnnnnnnnnn
R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612
R-HEMBA1006090//EST//5.1e-66:320:99//Hs.99551:AA461517
R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313
R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//Hs.73614:U83460
R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297
R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:AI279293
R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:AI198931
R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:AB007958
R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542
R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212
R-HEMBA1006158//Deoxyuridine triphosphatase//0.99: 50
162:62//Hs.82113:U31930
R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627
R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906
R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557
10 R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//Hs.23617:AA928683
R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:AF083384
R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881
20 R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper interactive [M.musculus]//1.2e-97:529:93//Hs.10552:AA524401
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//2.7e-88:484:92//Hs.104129:AA923278
R-nnnnnnnnnnnnn//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2 [S.cerevisiae]//1.6e-66:377:91//Hs.108674:W25821
30 R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:AI084735
R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:AI202037
R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:U33931
R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M.musculus]//5.6e-76:417:94//Hs.111754:AI204587
R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79706:U53204
R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROTEIN INSHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.4

- 2343: A1417075
 R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
 R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
 R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
 R-HEMBA1006377//EST//0.0097:145:62//Hs.133027:AI049830
 R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:AB011166
 R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:H59651
 R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frames//9.0e-87:582:84//Hs.23094:M19503
 R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:AI218923
 R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778
 R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
 R-HEMBA1006424//ESTs, Weakly similar to pot. ORF I [H. sapiens]//6.3e-13:263:66//Hs.43127:AA258004
 R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
 R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
 R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033
 R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784
 R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
 R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H. sapiens]//3.0e-17:342:63//Hs.111730:AA604403
 R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
 R-HEMBA1006474
 R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984
 R-HEMBA1006485//H. sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
 R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223
 R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350
 R-HEMBA1006492//ESTs//0.00034:52:90//Hs.163219:AA810720
 R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387
 R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117
 R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505
 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566
 R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
 R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:AI057628
 R-HEMBA1006535//CS1 PROTEIN//0.52:267:62//Hs.78991:M86934
 R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
 R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154
 R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R. norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
 R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:AI283064
 R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
 R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
 R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
 R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280
 R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
 R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219
 R-HEMBA1006612
 R-nnnnnnnnnnnnn//ESTs//1.2e-25:225:80//Hs.138852:AA284247
 R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
 R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067
 R-HEMBA1006635//ESTs, Moderately similar to !!!! A LU SUBFAMILY SP WARNING ENTRY !!!! [H. sapiens]//2.7e-91:426:100//Hs.139469:AI299889
 R-HEMBA1006639//ESTs, Highly similar to POLYADENY

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LATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185
 R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282
 R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427
 R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511
 R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102
 R-HEMBA1006674//ESTs//3.1e-32:212:83//Hs.95115:AA206594
 R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842
 R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435
 R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263
 R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695
 R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene[H.sapiens]//1.1e-92:483:94//Hs.6525:AI205313
 R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062
 R-HEMBA1006717
 R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002
 R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627
 R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099
 R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646
 R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763
 R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881
 R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562
 R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936
 R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705
 R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978

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R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333
 R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305
 R-HEMBA1006824//Homo sapiens mRNA, clone:RES4-16//6.7e-51:298:90//Hs.121493:D25272
 R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556
 R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087
 R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:AB018315
 R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453
 R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739
 R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117
 R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C.elegans]//2.9e-28:213:84//Hs.9096:AA029400
 R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308
 R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712
 R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:AJ010841
 R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321
 R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457
 R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827
 R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325
 R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679
 R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440
 R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293
 R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R.norvegicus]//2.8e-112:558:96//Hs.107905:AI248363
 R-HEMBA1007045
 R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA

- 410788
R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839
R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140
R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272
R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866
R-HEMBA1007078//EST, Moderately similar to !!!! AL 10
U SUBFAMILY SQ WARNINGENTRY !!!! [H.sapiens]//7.2e-40:163:83//Hs.152369:AA504818
R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087
R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025
R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597
R-HEMBA1007113//Homo sapiens mRNA, clone:RES4-16//1.1e-47:427:76//Hs.121493:D25272
R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438
R-HEMBA1007147
R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818
R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674
R-nnnnnnnnnnnnn//Homo sapiens epsin 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085
R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI330
02954
R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:D86987
R-HEMBA1007206//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:AB018340
R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394
R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI1221207
- R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
R-HEMBA1007301
R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//5.5e-15:311:64//Hs.142764:AA205569
R-HEMBA1007322//Human kpni repeat mRNA (cdna clone pcn-kpni-4), 3' end//5.7e-49:383:83//Hs.139107:K00629
R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452
R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
20 R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H.sapiens]//3.3e-44:341:71//Hs.111730:AA604403
R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090
30 R-HEMBA1000018//H.sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465
40 R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928
R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954
R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802

- R-HEM BB1000050//ESTs//0.039:91:74//Hs.163189:AA236
903
- R-HEM BB1000054//ESTs//3.0e-104:550:94//Hs.152395:A
A533107
- R-HEM BB1000055//ESTs, Moderately similar to UBIQUI
NOL-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQU
IRING PROTEIN [H.sapiens]//1.1e-72:350:99//Hs.1164
90:AA659584
- R-HEM BB1000059//ESTs//1.7e-10:200:70//Hs.163954:N5
7939
- R-HEM BB1000083//Homo sapiens mRNA for GCP170, comp
lete cds//6.0e-41:337:80//Hs.4953:D63997
- R-HEM BB1000089//Human mRNA for KIAA0355 gene, comp
lete cds//3.5e-39:487:70//Hs.153014:AB002353
- R-HEM BB1000099//ESTs//5.7e-37:353:75//Hs.22910:W18
193
- R-HEM BB1000103//Homo sapiens mRNA for KIAA0640 pro
tein, partial cds//6.5e-18:298:69//Hs.153026:AB014
540
- R-HEM BB1000113//EST//8.2e-94:437:100//Hs.136893:AA
805239
- R-HEM BB1000119//Homo sapiens ASMTL gene//1.2e-84:4
28:95//Hs.6315:Y15521
- R-HEM BB1000136//ESTs//0.043:262:59//Hs.61304:AA025
692
- R-HEM BB1000141//ESTs//5.0e-38:254:79//Hs.141658:N7
7915
- R-HEM BB1000144//ESTs//9.6e-05:235:60//Hs.61700:AA0
33951
- R-HEM BB1000173//EST//9.6e-44:258:76//Hs.161917:AA4
83223
- R-HEM BB1000175//ESTs//4.8e-98:475:97//Hs.149740:AI
199558
- R-HEM BB1000198//ESTs//1.0:123:62//Hs.116602:AA6659
65
- R-HEM BB1000215//Human mRNA for KIAA0355 gene, comp
lete cds//2.2e-46:302:86//Hs.153014:AB002353
- R-HEM BB1000217//ESTs//2.2e-105:496:99//Hs.65973:AI
339364
- R-HEM BB1000218//Homo sapiens DNA fragmentation fac
tor 40 kDa subunit (DFF40) mRNA, complete cds//1.1
e-48:292:79//Hs.133089:AF064019
- R-HEM BB1000226//ESTs, Weakly similar to HYPOTHETIC
AL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.ele
gans]//5.1e-73:449:89//Hs.16803:AA843214
- R-HEM BB1000240//ESTs//1.1e-109:536:97//Hs.13528:AA
523106
- R-HEM BB1000244//Small inducible cytokine A5 (RANTE
S)//9.5e-42:323:83//Hs.155464:AF088219
- R-HEM BB1000250//EST//8.8e-12:284:64//Hs.145960:AI2
50
- 76783
- R-HEM BB1000258//EST//4.5e-14:315:66//Hs.162551:AA5
84782
- R-HEM BB1000264
- R-HEM BB1000266//ESTs, Weakly similar to similar to
the beta transducin family [C.elegans]//2.7e-102:
556:93//Hs.16079:AA083522
- R-HEM BB1000272//ESTs//4.3e-91:480:94//Hs.107467:H1
1385
- 10 R-HEM BB1000274//Homo sapiens mRNA for KIAA0557 pro
tein, partial cds//7.9e-24:198:72//Hs.101414:AB011
129
- R-HEM BB1000284//ESTs//4.8e-64:389:91//Hs.118043:N5
0458
- R-HEM BB1000307//Human mRNA for KIAA0355 gene, comp
lete cds//3.6e-43:288:87//Hs.153014:AB002353
- R-HEM BB1000312//ESTs//6.0e-23:272:73//Hs.121354:AA
758601
- R-HEM BB1000317//ESTs//7.5e-90:424:99//Hs.150042:AI
298034
- R-HEM BB1000318//Small inducible cytokine A5 (RANTE
S)//3.3e-41:318:80//Hs.155464:AF088219
- R-HEM BB1000335//ESTs//3.7e-15:324:65//Hs.85077:AA9
68576
- R-HEM BB1000336//ESTs//6.4e-76:402:95//Hs.17207:H92
480
- R-HEM BB1000337//ESTs//2.1e-80:391:97//Hs.118990:AI
378084
- R-HEM BB1000338//Small inducible cytokine A5 (RANTE
S)//4.0e-39:274:85//Hs.155464:AF088219
- R-HEM BB1000339//EST//5.8e-41:336:79//Hs.151873:AA2
05736
- R-HEM BB1000341//ESTs//3.8e-19:310:68//Hs.37573:H59
651
- R-HEM BB1000343//EST//1.1e-77:396:95//Hs.162664:AA6
05020
- R-HEM BB1000354//Human mRNA for KIAA0186 gene, comp
lete cds//1.7e-15:293:65//Hs.36232:D80008
- R-HEM BB1000369//ESTs//1.6e-21:234:73//Hs.111583:AA
463590
- R-HEM BB1000374//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0487//2.3e-56:335:77//Hs.923
81:AB007956
- R-HEM BB1000376//H.sapiens mRNA for urea transporte
r//2.7e-50:525:74//Hs.66710:X96969
- R-HEM BB1000391//ESTs//6.6e-50:316:88//Hs.142259:AA
828840
- R-HEM BB1000399//Homo sapiens mRNA for cell cycle c
heckpoint protein//3.8e-109:531:97//Hs.16184:AJ001
642

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R-HEM BB1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173
 R-HEM BB1000404//ESTs//0.088:298:59//Hs.61607:AA032026
 R-HEM BB1000420//EST//2.2e-78:376:98//Hs.160787:AI336591
 R-HEM BB1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087
 R-HEM BB1000438//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//0.30:214:63 10
 //Hs.142209:AA873303
 R-HEM BB1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990
 R-HEM BB1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221
 R-HEM BB1000455//EST//4.8e-14:421:65//Hs.68832:AA088438
 R-HEM BB1000472//ESTs//1.1e-104:505:98//Hs.132824:AI033396
 R-HEM BB1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390
 R-HEM BB1000487//EST//0.78:87:68//Hs.134601:AI081506
 R-HEM BB1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219
 R-HEM BB1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080
 R-HEM BB1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125
 R-HEM BB1000510//EST//1.4e-45:139:97//Hs.152260:AA43089703
 R-HEM BB1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087
 R-HEM BB1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080
 R-HEM BB1000530//ESTs//2.7e-73:425:90//Hs.141254:AI334099
 R-HEM BB1000550//EST//2.9e-11:113:79//Hs.161503:N68662
 R-HEM BB1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288
 R-HEM BB1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986
 R-HEM BB1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258
 R-HEM BB1000573//ESTs//1.6e-86:494:90//Hs.120979:AI160709
 R-HEM BB1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618

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R-HEM BB1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247
 R-HEM BB1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895
 R-HEM BB1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704
 R-HEM BB1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391
 R-HEM BB1000598//Human antisecretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199
 R-HEM BB1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125
 R-HEM BB1000630//ESTs//5.1e-106:538:96//Hs.13422:AI082249
 R-HEM BB1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152
 R-HEM BB1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531
 R-HEM BB1000637//Human mRNA for KIAA0080 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522
 R-HEM BB1000638//EST//2.2e-38:371:76//Hs.162236:AA551582
 R-HEM BB1000643//ESTs//0.0049:191:62//Hs.55445:W31963
 R-HEM BB1000649//ESTs, Moderately similar to hTAFII 68 [H.sapiens]//4.0e-76:399:95//Hs.124106:AA948100
 R-HEM BB1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
 R-HEM BB1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
 R-HEM BB1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
 R-HEM BB1000673//EST//0.58:46:82//Hs.142286:AA338293
 R-HEM BB1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
 R-nnnnnnnnnnnnn//Homo sapiens neuroanl mRNA, complete cds//6.5e-52:287:93//Hs.158300:AF040723
 R-HEM BB1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
 R-HEM BB1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
 R-HEM BB1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403
 R-HEM BB1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306
 R-HEM BB1000726//EST//5.3e-49:303:88//Hs.149580:AI281881
 50 R-HEM BB1000738//Homo sapiens mRNA, clone: RES4-16//

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2.5e-49:302:89//Hs.121493:D25272
 R-HEMBB1000749//ESTs//1.6e-49:331:86//Hs.152788:AA
 630925
 R-HEMBB1000763//ESTs//9.7e-104:474:95//Hs.77480:AA
 100522
 R-HEMBB1000770//EST//1.0e-75:359:99//Hs.136564:AA6
 42445
 R-HEMBB1000781//ESTs//5.3e-66:317:99//Hs.28827:AI1
 25541
 R-HEMBB1000789//ESTs//5.9e-83:394:99//Hs.120842:AA 10
 435771
 R-HEMBB1000790//PLATELET GLYCOPROTEIN V PRECURSOR/
 /1.3e-37:193:75//Hs.73734:Z23091
 R-HEMBB1000794//ESTs//7.1e-98:490:96//Hs.105743:AA
 532718
 R-HEMBB1000807//ESTs//2.6e-22:145:92//Hs.53913:AA9
 08961
 R-HEMBB1000810//Small inducible cytokine A5 (RANTE
 S)//1.8e-34:206:79//Hs.155464:AF088219
 R-HEMBB1000821//ESTs//2.4e-90:425:99//Hs.118659:AI 20
 052447
 R-HEMBB1000822//ESTs//1.7e-45:288:89//Hs.24130:R27
 124
 R-HEMBB1000826//Small inducible cytokine A5 (RANTE
 S)//2.9e-51:245:82//Hs.155464:AF088219
 R-HEMBB1000827//EST//2.8e-40:295:84//Hs.149580:AI2
 81881
 R-HEMBB1000831//ESTs//4.0e-59:291:98//Hs.62675:AA0
 44176
 R-HEMBB1000835//ESTs//7.3e-21:124:82//Hs.102671:N5 30
 2545
 R-HEMBB1000840//ATPase, Na+/K+ transporting, beta
 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
 R-HEMBB1000848//Homo sapiens mRNA for KIAA0565 pro
 tein, complete cds//9.5e-41:367:78//Hs.129740:AB01
 1137
 R-HEMBB1000852//EST//1.2e-09:188:70//Hs.127869:AA9
 68599
 R-HEMBB1000870//Cytochrome P450, 51 (lanosterol 14
 -alpha-demethylase)//1.0e-41:483:73//Hs.2379:U2394 40
 2
 R-HEMBB1000876//EST//0.0022:211:63//Hs.125552:AA88
 4141
 R-HEMBB1000883//ESTs//1.4e-65:343:95//Hs.98269:H27
 247
 R-HEMBB1000887//ESTs//4.0e-22:212:79//Hs.138965:AI
 004740
 R-HEMBB1000888//EST//8.2e-07:196:64//Hs.118276:W15
 258
 R-HEMBB1000890//ISLET AMYLOID POLYPEPTIDE PRECURSO 50

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R//1.1e-46:327:83//Hs.51048:X68830
 R-HEMBB1000893//EST//4.7e-34:242:85//Hs.149580:AI2
 81881
 R-HEMBB1000908//EST//0.95:27:100//Hs.142568:AA2850
 66
 R-HEMBB1000910//ESTs//1.9e-36:318:78//Hs.141140:AA
 715983
 R-HEMBB1000913//Human mRNA for KIAA0327 protein, c
 omplete cds//2.5e-33:367:73//Hs.149323:AB002325
 R-HEMBB1000915//ESTs//0.00018:188:61//Hs.144847:AI
 222742
 R-HEMBB1000917//Homo sapiens KIAA0414 mRNA, partia
 l cds//3.7e-41:228:84//Hs.127649:AB007874
 R-HEMBB1000927//ESTs//2.2e-62:307:98//Hs.97044:AA3
 65784
 R-HEMBB1000947//ESTs, Weakly similar to F26E4.13
 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
 R-HEMBB1000959//Human Line-1 repeat mRNA with 2 op
 en reading frames//8.1e-84:546:86//Hs.23094:M19503
 R-HEMBB1000973//ESTs//6.8e-95:445:99//Hs.105859:AI
 419354
 R-HEMBB1000975//ESTs//1.2e-39:197:100//Hs.26176:AI
 032007
 R-HEMBB1000981//EST//7.7e-58:284:98//Hs.60179:AA00
 7242
 R-HEMBB1000985//ESTs//1.2e-103:524:95//Hs.43102:AA
 131369
 R-HEMBB1000991//EST//0.99:58:72//Hs.100246:T23625
 R-HEMBB1000996//Homo sapiens LIM protein mRNA, com
 plete cds//1.3e-41:482:70//Hs.154103:AF061258
 R-HEMBB1001004//ESTs//5.7e-70:362:95//Hs.6434:W271
 12
 R-HEMBB1001008//ESTs, Weakly similar to hypothetic
 al L1 protein [H.sapiens]//2.3e-25:339:71//Hs.1299
 92:H58762
 R-HEMBB1001011//ESTs//4.0e-53:325:92//Hs.33268:AI1
 91214
 R-HEMBB1001014//ESTs//1.3e-46:323:83//Hs.163980:AA
 715814
 R-HEMBB1001020//Homo sapiens PYRIN (MEFV) mRNA, co
 mplete cds//3.0e-46:305:76//Hs.113283:AF018080
 R-HEMBB1001024//ESTs//8.5e-47:374:80//Hs.141602:N6
 3562
 R-HEMBB1001037//ESTs//2.6e-47:282:91//Hs.155384:Z7
 8385
 R-HEMBB1001047//EST//6.2e-33:232:74//Hs.160146:AI0
 49975
 R-HEMBB1001051//ESTs//3.7e-79:385:98//Hs.95290:AA0
 46107
 R-HEMBB1001056//Homo sapiens mRNA for KIAA0618 pro

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tein, complete cds//1.1e-87:497:91//Hs.15832:AB014518
 R-HEM BB1001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944
 R-HEM BB1001060//ESTs//1.9e-37:541:69//Hs.141534:N64785
 R-HEM BB1001063//ESTs//4.7e-42:269:88//Hs.55855:AA621381
 R-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803
 R-HEM BB1001096//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233:70//Hs.37181:D64108
 R-HEM BB1001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353
 R-HEM BB1001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080
 R-HEM BB1001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426
 R-HEM BB1001117//ESTs//1.1e-80:471:90//Hs.61935:T75092
 R-HEM BB1001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942
 R-HEM BB1001126
 R-HEM BB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077
 R-HEM BB1001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962
 R-HEM BB1001142//EST//6.4e-48:315:85//Hs.149580:AI281881
 R-HEM BB1001151
 R-HEM BB1001153//ESTs, Moderately similar to HLA LU SUBFAMILY J WARNINGENTRY [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197
 R-HEM BB1001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878
 R-HEM BB1001177
 R-HEM BB1001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349
 R-HEM BB1001199
 R-HEM BB1001208//ESTs//3.3e-43:216:99//Hs.121806:N71183
 R-HEM BB1001209//ESTs//6.7e-80:409:96//Hs.141185:R99549
 R-HEM BB1001210//ESTs//2.2e-46:290:88//Hs.103329:D11573
 R-HEM BB1001218//Kangai 1 (suppression of tumorigen

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icity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody 1A4))//3.1e-44:298:87//Hs.103458:X53795
 R-HEM BB1001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817
 R-HEM BB1001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Callus gallus]//3.8e-80:400:96//Hs.71873:AA148213
 R-HEM BB1001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560
 R-HEM BB1001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236
 R-HEM BB1001253//EST//0.0011:84:77//Hs.124579:AA853987
 R-HEM BB1001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268
 R-HEM BB1001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970
 R-HEM BB1001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087
 R-HEM BB1001282//EST//2.9e-78:401:96//Hs.72871:AA169412
 R-HEM BB1001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021
 R-HEM BB1001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840
 R-HEM BB1001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112
 R-HEM BB1001302
 R-HEM BB1001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154
 R-HEM BB1001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627
 R-HEM BB1001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627
 R-HEM BB1001317//Human cytochrome P450-IIB (hIIB3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873
 R-HEM BB1001326//ESTs//0.85:174:62//Hs.133487:AI393754
 R-HEM BB1001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222
 R-HEM BB1001335//EST//5.2e-80:381:99//Hs.116769:AA630365
 R-HEM BB1001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639
 R-HEM BB1001339//ESTs//2.1e-97:485:96//Hs.88357:AA2

- 62470
R-HEM BB1001346
R-HEM BB1001348//ESTs//1.1e-43:295:85//Hs.163604:R9
4354
R-HEM BB1001356//EST//6.0e-11:89:88//Hs.152366:AA48
6721
R-HEM BB1001364//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//3.0e
-12:129:79//Hs.9792:AA027055
R-HEM BB1001366//Human mRNA for KIAA0118 gene, part 10
ial cds//1.2e-50:550:72//Hs.154326:D42087
R-HEM BB1001367//ESTs//1.2e-19:165:82//Hs.146314:R9
9617
R-HEM BB1001369//Small inducible cytokine A5 (RANTE
S)//1.9e-25:217:80//Hs.155464:AF088219
R-HEM BB1001380//ESTs//4.0e-08:216:63//Hs.143763:AI
174205
R-HEM BB1001384//ESTs//6.6e-110:547:96//Hs.6671:AI3
41699
R-HEM BB1001387//ESTs//1.1e-104:497:98//Hs.87654:AA 20
853970
R-HEM BB1001394//ESTs//6.4e-73:428:89//Hs.139922:AA
281350
R-HEM BB1001410//Alcohol dehydrogenase 7 sigma subu
nit (class IV)//0.88:365:58//Hs.389:X76342
R-HEM BB1001424//ESTs//1.3e-88:466:94//Hs.42174:AA1
94644
R-HEM BB1001426//ESTs//2.2e-45:337:82//Hs.37573:H59
651
R-HEM BB1001429//EST//3.8e-59:543:76//Hs.158803:AI3 30
76846
R-HEM BB1001436//ESTs//3.7e-69:332:99//Hs.156518:AA
724317
R-HEM BB1001443//ESTs//4.8e-54:270:98//Hs.21898:AI0
88201
R-HEM BB1001449//ESTs//3.2e-43:170:84//Hs.150727:AI
292236
R-HEM BB1001454//ESTs//9.1e-46:304:86//Hs.139190:N5
5515
R-HEM BB1001458//ESTs//3.2e-98:478:97//Hs.50144:N67 40
293
R-HEM BB1001463//Homo sapiens KIAA0421 mRNA, partia
l cds//4.3e-50:440:78//Hs.41742:AB007881
R-HEM BB1001464//ESTs, Weakly similar to K01H12.1
[C.elegans]//0.25:222:61//Hs.13275:AI341468
R-HEM BB1001482//ESTs, Moderately similar to zinc f
inger protein [R.norvegicus]//0.80:53:83//Hs.2679
9:W74481
R-HEM BB1001500//EST//1.4e-13:310:67//Hs.162663:AA6
04515
- R-HEM BB1001521//Homo sapiens mRNA for KIAA0737 pro
tein, complete cds//2.5e-29:186:92//Hs.17630:AB018
280R-HEM BB1001527//ESTs, W
eakly similar to HYPOTHET
ICAL 92.1 KD PROTEIN ZK10
98.3 IN CHROMOSOME III [C
aenorhabditis elegans]//
4.7e-51:404:81//Hs.14142
9:AA631915
R-HEM BB1001531//ESTs//3.3
e-13:250:67//Hs.139158:AA
226159
R-HEM BB1001535//H. sapiens
mRNA for sigma 3B protei
n//1.9e-39:291:82//Hs.154
782:X99459
R-HEM BB1001536//Human mRN
A for KIAA0355 gene, comp
lete cds//5.0e-44:318:83/
Hs.153014:AB002353
R-HEM BB1001537//Homo sapi
ens KIAA0409 mRNA, partia
l cds//3.2e-47:318:80//H
s.5158:AB007869
R-HEM BB1001555//ESTs//2.6
e-13:182:71//Hs.112671:AI
377274
R-HEM BB1001562//ESTs//1.7
e-43:316:83//Hs.151365:AA
643962
R-HEM BB1001564//EST//1.3e
-35:141:81//Hs.162197:AA5
35216
R-HEM BB1001565//Human mRN
A for KIAA0331 gene, comp
lete cds//5.1e-18:152:85/
Hs.146395:AB002329
R-HEM BB1001585//ESTs//1.1
e-32:190:84//Hs.33354:AA1
79944
R-HEM BB1001586//ESTs//4.9
e-94:447:99//Hs.124084:AA
843219
R-HEM BB1001588//EST//8.3e
-27:363:69//Hs.141603:N66
015
R-HEM BB1001603//ESTs//1.2
e-101:482:99//Hs.12403:AI
090184
50 R-HEM BB1001618//ESTs//5.8

4035

e-35:437:70//Hs. 136868:AA
805044
R-HEMBB1001619//EST//1.7e
-38:476:70//Hs. 139093:AA1
66888
R-HEMBB1001630//Homo sapi
ens mRNA, clone:RES4-16//
5.7e-41:193:90//Hs. 12149
3:D25272
R-HEMBB1001635//ESTs//9.5
e-34:304:82//Hs. 140444:AI
002082
R-HEMBB1001637//ESTs//1.0
e-42:443:74//Hs. 21978:AA0
09633
R-HEMBB1001641//EST//2.4e
-06:67:86//Hs. 162398:AA57
2813
R-HEMBB1001653//ESTs//4.8
e-80:381:99//Hs. 140502:AA
806438
R-HEMBB1001665//ESTs//2.3
e-44:372:79//Hs. 132818:AI
038577
R-HEMBB1001668//ESTs//0.7
3:212:62//Hs. 8928:N32572
R-HEMBB1001673//Homo sapiens mRNA for KIAA0646 pro
tein, complete cds//5.9e-117:573:97//Hs.24439:AB01
4546
R-HEMBB1001684//ESTs, Moderately similar to Tbc1
[M.musculus]//5.4e-106:523:97//Hs.26939:AA804534
R-HEMBB1001685//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//1.9e
-43:292:86//Hs.96337:AA225358
R-HEMBB1001695//ESTs//7.7e-101:539:94//Hs.78289:R6
0867
R-HEMBB1001704//EST//0.96:248:57//Hs.163025:AA7030
38
R-HEMBB1001706//ESTs//1.3e-39:308:81//Hs.141318:N7
1080
R-HEMBB1001707//ESTs, Moderately similar to hypoth
etical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.1
42764:AA205569
R-HEMBB1001717//ESTs//1.6e-34:225:87//Hs.57883:AA2
18645
R-HEMBB1001735//ESTs, Highly similar to LINE-1 RE
VERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-1
1:158:71//Hs.141263:H64113
R-HEMBB1001736//ESTs//0.0035:223:60//Hs.21354:AA20
3403

4036

R-HEMBB1001747//EST//9.9e-55:293:81//Hs.112866:AA6
20488
R-HEMBB1001749//ESTs//2.5e-13:95:91//Hs.139888:N25
287
R-HEMBB1001753//ESTs//2.6e-07:141:70//Hs.144604:AI
052059
R-HEMBB1001756//EST//2.6e-06:165:64//Hs.121195:AA7
57211
R-HEMBB1001760//LOW-DENSITY LIPOPROTEIN RECEPTOR P
RECURSOR//1.3e-24:264:74//Hs.70008:L00352
R-HEMBB1001762//ESTs//2.1e-81:447:93//Hs.152766:AA
211369
R-HEMBB1001785//ESTs//0.040:390:58//Hs.116651:AA99
3406
R-HEMBB1001797//ESTs//2.1e-90:428:99//Hs.8958:AA16
9253
R-HEMBB1001802//Desmin//9.9e-95:497:93//Hs.119104:
M63391
R-HEMBB1001812//ESTs//1.2e-12:91:78//Hs.138852:AA2
84247
R-HEMBB1001816//Human Line-1 repeat mRNA with 2 op
en reading frames//5.9e-13:143:76//Hs.23094:M19503
R-HEMBB1001831//Homo sapiens PAM COOH-terminal int
eractor protein 1 (PCIP1) mRNA, complete cds//5.5e
-106:498:98//Hs.159396:AF056209
R-HEMBB1001836//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0488//9.6e-39:288:73//Hs.676
19:AB007957
R-HEMBB1001839
30 R-HEMBB1001850//EST//0.020:119:68//Hs.32767:H38125
R-HEMBB1001863//ESTs//4.5e-17:226:72//Hs.157253:AI
357539
R-HEMBB1001867//ESTs//2.3e-16:254:68//Hs.123664:AA
806106
R-HEMBB1001868//EST//9.8e-30:155:100//Hs.160572:AA
888397
R-HEMBB1001869//ESTs//2.8e-42:376:78//Hs.141973:N2
1434
R-HEMBB1001872//EST//0.85:156:64//Hs.119501:AA4879
80
40 R-HEMBB1001874//EST//0.64:107:70//Hs.147482:AI2155
72
R-HEMBB1001875//EST//0.079:199:59//Hs.121810:AA775
240
R-HEMBB1001880//Thromboxane A2 receptor//9.0e-47:2
97:88//Hs.89887:D38081R-HEMBB1001899//ESTs//6.3e-6
8:323:100//Hs.121538:AA609310
R-HEMBB1001905//ESTs//4.4e-19:227:73//Hs.146173:AA
906191
50 R-HEMBB1001906//ESTs//1.6e-90:463:95//Hs.28266:H46

- 725
 R-HEM BB1001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915
 R-HEM BB1001910//EST//6.0e-37:308:78//Hs.162197:AA535216
 R-HEM BB1001911//Homo sapiens tapasin (NCS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750
 R-HEM BB1001915//ESTs//3.1e-73:395:93//Hs.17054:AI139897
 R-HEM BB1001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390
 R-HEM BB1001922//H. sapiens mRNA for novel member of serine-arginine domain protein, SRp129//7.4e-38:531:70//Hs.153086:Y11251
 R-HEM BB1001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325
 R-HEM BB1001930//EST//1.9e-18:136:78//Hs.132635:AI032875
 R-HEM BB1001944//EST//0.034:228:57//Hs.93664:N23366
 R-HEM BB1001945//ESTs//1.8e-83:439:95//Hs.7341:N57875
 R-HEM BB1001947//ESTs//5.6e-109:533:97//Hs.48855:AA134589
 R-HEM BB1001950//ESTs//1.5e-107:583:93//Hs.8033:N94998
 R-HEM BB1001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788
 R-HEM BB1001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522
 R-HEM BB1001957//EST//4.8e-50:382:81//Hs.149580:AI23081881
 R-HEM BB1001962//ESTs//1.5e-20:143:88//Hs.11924:W26972
 R-HEM BB1001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:AB011147
 R-HEM BB1001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531
 R-HEM BB1001983//ESTs//2.6e-72:374:95//Hs.141022:H06475
 R-HEM BB1001988//ESTs//2.0e-31:204:88//Hs.142531:N91572
 R-HEM BB1001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223
 R-HEM BB1001996
 R-HEM BB1001997//ESTs//7.6e-78:380:98//Hs.32682:H37798
 R-HEM BB1002002//Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:K00627
- R-HEM BB1002005//EST//2.2e-41:339:80//Hs.160833:AI345334
 R-HEM BB1002009//EST//2.9e-44:245:94//Hs.28788:R66896
 R-HEM BB1002015//EST//0.0027:198:63//Hs.160868:AI359052
 R-HEM BB1002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900
 R-HEM BB1002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426
 R-HEM BB1002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638
 R-HEM BB1002045//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080
 R-HEM BB1002049//ESTs//3.8e-77:409:94//Hs.122624:R82638
 R-HEM BB1002050//ESTs//8.7e-45:330:82//Hs.44702:AI148840
 R-HEM BB1002068//ESTs//8.3e-70:333:99//Hs.134807:AI090671
 R-HEM BB1002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144
 R-HEM BB1002092//ESTs//6.5e-46:331:83//Hs.22910:W18193
 R-HEM BB1002094//EST//3.6e-45:280:88//Hs.149580:AI281881
 R-HEM BB1002115
 R-HEM BB1002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814
 R-HEM BB1002142//Homo sapiens haemopoietic progenitor or homeobox HPX42B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006
 R-HEM BB1002152//EST//4.3e-39:250:89//Hs.156552:AA833553
 R-HEM BB1002189//H. sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073
 R-HEM BB1002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185
 R-HEM BB1002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934
 R-HEM BB1002217//EST//6.6e-50:303:89//Hs.149580:AI281881
 R-HEM BB1002218//ESTs//2.3e-19:150:86//Hs.136031:W95841
 R-HEM BB1002232//ESTs//8.9e-47:445:77//Hs.163971:N27584
 R-HEM BB1002247//EST//6.6e-09:236:65//Hs.130578:AI004631
 R-HEM BB1002249//ESTs//5.2e-16:325:64//Hs.156253:AI

- 334807
R-HEM BB1002254//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-99:590:88//Hs.23094:M19503
R-HEM BB1002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363
R-HEM BB1002266//ESTs//4.4e-98:472:98//Hs.65366:AI189112
R-HEM BB1002280//EST//2.9e-41:247:90//Hs.161917:AA483223
R-HEM BB1002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
R-HEM BB1002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892
R-HEM BB1002327//EST//0.042:249:61//Hs.121097:AA714637
R-HEM BB1002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
R-HEM BB1002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
R-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841
R-HEM BB1002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322
R-HEM BB1002359//ESTs//2.7e-106:517:97//Hs.13634:AI051613
R-HEM BB1002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522
R-HEM BB1002371//Catalase//3.3e-22:235:77//Hs.76359:X04085
R-HEM BB1002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467
R-HEM BB1002383//ESTs//3.5e-108:520:98//Hs.45140:D80055
R-HEM BB1002387
R-HEM BB1002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.3e-23:168:77//Hs.133526:N21103
R-HEM BB1002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280
R-HEM BB1002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
R-HEM BB1002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353
R-HEM BB1002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087
R-HEM BB1002458//EST//1.8e-72:343:100//Hs.162006:AA508089
R-HEM BB1002477//ESTs//1.6e-38:215:93//Hs.18240:AA450
- 60083
R-HEM BB1002489//ESTs//1.2e-101:534:94//Hs.7981:H15176
R-HEM BB1002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
R-HEM BB1002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
R-HEM BB1002502//ESTs, Weakly similar to p40 [H.sapiens]//1.2e-68:336:98//Hs.141515:T41142
R-HEM BB1002509//ESTs//2.7e-97:459:99//Hs.127638:AI014615
R-HEM BB1002510//ESTs, Weakly similar to located at OATL1 [H.sapiens]//2.2e-48:265:95//Hs.48827:AA873278
R-HEM BB1002520//EST//7.2e-40:198:84//Hs.140493:AA804538
R-HEM BB1002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672
R-HEM BB1002531//EST//0.024:147:61//Hs.148305:AA909605
R-HEM BB1002534//EST//3.1e-22:168:84//Hs.146794:AI149478
R-HEM BB1002545//ESTs//9.2e-90:421:99//Hs.118317:AI033259
R-HEM BB1002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C.elegans]//5.1e-22:210:81//Hs.11896:T68813
R-HEM BB1002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.51048:X68830
R-HEM BB1002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
R-HEM BB1002582//ESTs//0.00036:91:76//Hs.140039:AA047045
R-HEM BB1002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
R-HEM BB1002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087
R-HEM BB1002600//EST//2.5e-17:147:84//Hs.121918:AA777424
R-HEM BB1002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
R-HEM BB1002603//EST//1.1e-47:281:90//Hs.149580:AI281881
R-HEM BB1002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
R-HEM BB1002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.2e-07:140:70//Hs.155456:AA707265
R-HEM BB1002613//Homo sapiens mRNA, chromosome 1 sp

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ecific transcript KIAA0508//8.5e-47:278:83//Hs.159
187:AB007977
R-HEM BB1002614//ESTs//3.4e-81:383:99//Hs.13012:AI0
94150
R-HEM BB1002617//Homo sapiens protease-activated re
ceptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.13
7574:AF055917
R-HEM BB1002623//ESTs//1.6e-45:288:87//Hs.138852:AA
284247
R-HEM BB1002635//Small inducible cytokine A5 (RANTE 10
S)//5.5e-39:278:81//Hs.155464:AF088219
R-HEM BB1002664//EST//8.9e-49:315:87//Hs.149580:AI2
81881
R-HEM BB1002677//ESTs//0.65:159:62//Hs.163517:AI419
775
R-HEM BB1002683//H.sapiens mRNA for delta 4-3-oxost
eroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z2
8339
R-HEM BB1002684//ESTs//3.0e-18:148:87//Hs.158270:AA
776646
R-HEM BB1002686//ESTs//6.1e-80:419:96//Hs.103002:W0
2753
R-HEM BB1002692//ESTs//3.3e-58:451:82//Hs.141254:AI
334099
R-HEM BB1002697//ESTs//6.2e-86:423:98//Hs.129812:AA
769487
R-HEM BB1002699//EST//5.6e-46:322:84//Hs.140231:AI0
54398
R-HEM BB1002702//ESTs//5.6e-36:412:72//Hs.154993:AA
142842
R-HEM BB1002705//POLYPOSIS LOCUS PROTEIN 1//0.024:4
12:58//Hs.74648:M73547R-HEM BB1002712//ESTs//9.0e-9
6:451:99//Hs.136806:AA805682
R-MAMMA1000009//ESTs//3.0e-78:392:96//Hs.163947:AA
678701
R-MAMMA1000019//Small inducible cytokine A5 (RANTE
S)//1.5e-47:247:87//Hs.155464:AF088219
R-MAMMA1000020//Zinc finger protein 2 (AI-5)//4.9e
-49:384:80//Hs.155533:X60152
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, comple 40
te cds//4.7e-11:154:71//Hs.32511:AB007901
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 pro
tein, partial cds//2.0e-58:277:84//Hs.93121:AB0183
04
R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA
287165
R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA99635
0
R-MAMMA1000057//Fucosyltransferase 1 (galactoside
2-alpha-L-fucosyltransferase, Bombay phenotype inc 50

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luded)//3.8e-77:545:83//Hs.69747:M35531
R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N3
7065
R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequ
ence//7.3e-43:313:83//Hs.46918:AF052099
R-MAMMA1000085//ESTs, Highly similar to PUTATIVE
CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosacchar
omyces pombe]//7.7e-104:546:94//Hs.7779:AA045241
R-MAMMA1000092//EST, Moderately similar to !!!! AL
U SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//4.2e-
22:287:71//Hs.136063:U51713
R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR P
RECURSOR//8.4e-49:334:86//Hs.70008:L00352
R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU S
UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-0
8:96:80//Hs.115088:AA230172
R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA5
23577
R-MAMMA1000133
20 R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA
174017
R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0501//6.3e-40:288:78//Hs.159
897:AB007970
R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI2
81881
R-MAMMA1000155//Homo sapiens apoptotic protease ac
tivating factor 1 (Apaf-1) mRNA, complete cds//1.5
e-59:562:75//Hs.77579:AF013263
30 R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA
884787
R-MAMMA1000171//Homo sapiens mRNA for putative lip
idic acid synthetase, partial//2.5e-39:173:83//Hs.5
3531:AJ224162
R-MAMMA1000173//ESTs, Highly similar to SRC SUBST
RATE P80/85 PROTEINS [Gallus gallus]//2.4e-07:63:9
0//Hs.90367:AI357069
R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI1276
11
R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA
872054
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI2
81881
R-MAMMA1000221//ESTs, Weakly similar to circadian
clock protein [M.musculus]//1.4e-41:272:90//Hs.683
98:AA421103
R-MAMMA1000227//EST//2.4e-39:388:76//Hs.144175:H70
425
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H5794
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- R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315
- R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090
- R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041
- R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238
- R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814
- R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977
- R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369
- R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694
- R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956
- R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066
- R-MAMMA1000287
- R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892
- R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067
- R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251
- R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434
- R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491
- R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998
- R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881
- R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525
- R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159
- R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomycetaceae]//0.42:172:61//Hs.11463:AA535912
- R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087
- R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA 50
- 845659
- R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
- R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
- R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
- R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AI301060
- R-MAMMA1000402//ESTs, Moderately similar to RETRO VIRUS-RELATED POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.138698:N38973
- R-MAMMA1000410//Archaeal//1.8e-40:443:74//Hs.33642:X81198
- R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958
- R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
- R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171
- R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
- R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
- R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
- R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452
- R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
- R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171
- R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
- R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
- R-MAMMA1000458
- R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
- R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
- R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
- R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886

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R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
 R-MAMMA1000500//Small inducible cytokine A5 (RANTE S)//4.7e-43:283:86//Hs.155464:AF088219
 R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
 R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
 R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
 R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
 R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
 R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
 R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
 R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:373:77//Hs.6200:AB007872
 R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
 R-MAMMA1000594//Small inducible cytokine A5 (RANTE S)//3.0e-45:225:80//Hs.155464:AF088219
 R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
 R-MAMMA1000605//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267
 R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SIS1-MRP L2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105
 R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
 R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
 R-MAMMA1000623
 R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
 R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
 R-MAMMA1000664//Homo sapiens mRNA for putative lipoidic acid synthetase, partial//3.2e-43:400:76//Hs.53531:AJ224162
 R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881
 R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TONB 3' REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065

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R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476
 R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212
 R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343
 R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644
 R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333
 R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569
 R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515
 R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329
 R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2) fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942
 R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267
 R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893
 R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:371:74//Hs.141429:AA631915
 R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1e-58:253:98//Hs.31575:AF100141
 R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs.71472:AA632288
 R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:AI224205
 R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-90:568:86//Hs.23094:M19503
 R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627
 R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131
 R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256
 R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:465:76//Hs.153014:AB002353
 R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204
 R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:H57439
 R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA74

- 7150
R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA
704163
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)/
/1.5e-45:358:76//Hs.73919:X81637
R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA
572675
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:AI2
81881
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA 10
757902
R-MAMMA1000842//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//9.4e
-44:363:79//Hs.96337:AA225358
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:A
A603097
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA
468955
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R7
6251
R-MAMMA1000855//Human mRNA for KIAA0392 gene, part
ial cds//5.7e-47:281:91//Hs.40100:AB002390
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA7
89212
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:AI41
9311
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA
098922
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequ
ence//3.0e-39:324:80//Hs.46918:AF052099
R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA
521399
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:AI0
32875
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA
621243
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H0
7128
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 pro
tein, partial cds//3.2e-40:542:68//Hs.154872:AB011
166
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:AI3
10215
R-MAMMA1000905//Human mRNA for KIAA0331 gene, comp
lete cds//9.7e-53:307:91//Hs.146395:AB002329
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA
017093
R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA7
01634
- R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA39
9989
R-MAMMA1000921//Human 53K isoform of Type II phosph
atidylinositol-4-phosphate 5-kinase (PIPK) mRNA,
complete cds//7.7e-38:269:74//Hs.108966:U48696
R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA
782335
R-MAMMA1000940//ESTs//3.3e-43:329:82//Hs.35254:AI1
33727
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA
632281
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA
650428
R-MAMMA1000943//Cytochrome P450, subfamily I (arom
atic compound-inducible), polypeptide 2//9.3e-79:5
67:80//Hs.1361:M55053
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA
536178
R-MAMMA1000957//Kangai 1 (suppression of tumorigen
icity 6, prostate; CD82 antigen (R2 leukocyte anti
gen, antigen detected by monoclonal and antibody I
A4))//7.5e-49:340:85//Hs.103458:X53795
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 pro
tein, complete cds//2.0e-48:216:85//Hs.153468:AB01
1147
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:AI2
81881
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W2
2204
30 R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 pro
tein, partial cds//8.0e-39:338:79//Hs.93121:AB0183
04
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:AI2
81881
R-MAMMA1000998//Homo sapiens apoptotic protease ac
tivating factor 1 (Apaf-1) mRNA, complete cds//3.9
e-50:445:77//Hs.77579:AF013263
R-MAMMA1001003//Sialophorin (gpL115, leukosialin,
CD43)//4.1e-51:282:82//Hs.80738:X52075
40 R-MAMMA1001008//ESTs, Weakly similar to renin [H.s
apiens]//1.9e-82:405:97//Hs.25863:AA630313
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complet
e cds//3.0e-44:309:86//Hs.153563:AF011333
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA
126814
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA
524536
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H4
7461
50 R-MAMMA1001038//Human mRNA for KIAA0392 gene, part

- ial cds//3.0e-50:298:91//Hs.40100:AB002390
 R-nnnnnnnnnnnn//ESTs//3.6e-86:445:95//Hs.122625:R68650
 R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:AI281881
 R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.musculus]//1.7e-13:273:65//Hs.98738:AI015487
 R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
 R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
 R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-38:544:68//Hs.153014:AB002353
 R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:N38944
 R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-84:556:85//Hs.23094:M19503
 R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
 R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
 R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF035587
 R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, complete cds//4.2e-27:232:76//Hs.61840:U28686
 R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:AI421576
 R-MAMMA1001126//CD4 receptor {exons 1 and 2} [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267
 R-MAMMA1001133//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.8e-59:460:81//Hs.5247:AF029750
 R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
 R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
 R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.13572:AF068179
 R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
 R-MAMMA1001161//Homo sapiens tapasin (NGS-17) mRNA, complete cds//1.1e-58:409:84//Hs.5247:AF029750
 R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-91:430:99//Hs.129982:AI420970
 R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
 R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W450
 4959
 R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
 R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by the epidermal growth factor receptor [M.musculus]//2.6e-80:358:96//Hs.163827:AA074202
 R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
 R-MAMMA1001203//Clathrin, light polypeptide (Lcb)/10 /2.8e-65:348:79//Hs.73919:X81637
 R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148
 R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
 R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
 R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
 R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
 R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
 R-MAMMA1001249//ESTs//4.2e-68:343:97//Hs.147139:AI191307
 R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
 R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
 R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.0e-21:226:75//Hs.65238:AB014561
 R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X81001
 R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30643
 R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cds//4.4e-32:188:94//Hs.14409:AB011144
 R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
 R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
 R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.2e-27:348:70//Hs.15731:AB011135
 R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
 R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.0e-43:300:85//Hs.464

68: U45984
 R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRNA, complete cds//8.8e-12:188:70//Hs.55771:AF004709
 R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
 R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
 R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285:75//Hs.32567:AF073519
 R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
 R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
 R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:N39322
 R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
 R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:AI281881
 R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831
 R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275
 R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957
 R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:AI335267
 R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:AI222168
 R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618
 R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:328:67//Hs.155174:AB007892
 R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:N57542
 R-MAMMA1001465
 R-MAMMA1001476//Homo sapiens yolk sac permease-like molecule 3 (YSPL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317
 R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:328:78//Hs.43681:AL022394
 R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065
 R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-15:220:69//Hs.74554:D38522
 R-MAMMA1001510
 R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242

R-MAMMA1001547//H.sapiens mRNA for urea transporter//2.3e-45:282:89//Hs.66710:X96969
 R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//Hs.108966:U48696
 R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140
 R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo sapiens]//1.9e-111:549:96//Hs.21635:AI417305
 R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441
 R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792
 R-MAMMA1001604
 R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sapiens]//1.9e-97:488:96//Hs.143263:AI057616
 R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//Hs.121493:D25272
 R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-49:472:76//Hs.15519:AB018315
 R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//6.8e-15:168:73//Hs.115216:AA291074
 R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377
 R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606
 R-MAMMA1001649
 R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.7e-54:272:81//Hs.129735:AF010144
 R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:89//Hs.155464:AF088219
 R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248
 R-MAMMA1001679//H.sapiens mRNA for rho GDP-dissociation Inhibitor 1//0.066:196:62//Hs.159161:X69550
 R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:AI151081
 R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
 R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-47:294:89//Hs.3094:D31884
 R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:N52088
 R-MAMMA1001715//ESTs//1.2e-73:399:93//Hs.124620:AI

- 082338
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:AI
084596
R-MAMMA1001735//ESTs, Highly similar to TUBULIN B
ETA-5 CHAIN [Gallus gallus]//3.7e-110:552:96//Hs.6
923:AI161158
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59
651
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:AI2
85666
R-MAMMA1001744
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA8
77817
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:N25
041
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA15141
3
R-MAMMA1001757//ESTs//1.0e-98:488:96//Hs.45184:C14
904
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:AI 20
142276
R-MAMMA1001764//ESTs//0.00012:434:58//Hs.120051:AA
707847
R-MAMMA1001768//Human mRNA for KIAA0327 protein, c
omplete cds//2.3e-41:299:85//Hs.149323:AB002325
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA5
72825
R-MAMMA1001771//ESTs, Moderately similar to semaph
orin B [M.musculus]//7.6e-43:257:91//Hs.7634:AA481
246
R-MAMMA1001783//Human high-affinity copper uptake
protein (hCTR1) mRNA, complete cds//5.6e-42:272:86/
/Hs.73614:U83460
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA
972238
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:AI2746
44
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA
425744
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60 40
313
R-MAMMA1001812//ESTs//2.4e-93:446:98//Hs.129034:AA
776892
R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:AI0
52659
R-MAMMA1001817//Human mRNA for KIAA0226 gene, comp
lete cds//2.1e-46:325:87//Hs.44106:D86979
R-MAMMA1001818
R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:AI2
81881
- R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete c
ds//4.3e-48:438:75//Hs.32567:AF073519
R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M7
8140
R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partia
l cds//3.8e-47:339:83//Hs.43681:AL022394
R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA
836811
R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H4
7461
R-MAMMA1001854//Small inducible cytokine A5 (RANTE
S)//2.6e-38:280:83//Hs.155464:AF088219
R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:AI1
48840
R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 pro
tein, complete cds//7.8e-31:262:77//Hs.5737:AB0079
44
R-nnnnnnnnnnnn//Homo sapiens antigen NY-CO-16 mRN
A, complete cds//9.2e-06:450:58//Hs.132206:AF03969
4
R-MAMMA1001874//Human high-affinity copper uptake
protein (hCTR1) mRNA, complete cds//4.9e-46:332:83/
/Hs.73614:U83460
R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14
-alpha-demethylase)//1.2e-46:429:78//Hs.2379:U2394
2
R-MAMMA1001880//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//7.6e
-26:230:79//Hs.106008:AA147606
30 R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA
410788
R-MAMMA1001907//Kangai 1 (suppression of tumorigen
icity 6, prostate; CD82 antigen (R2 leukocyte anti
gen, antigen detected by monoclonal and antibody I
A4))//6.7e-47:283:89//Hs.103458:X53795
R-nnnnnnnnnnnn//ESTs//0.043:134:65//Hs.145333:AI25
1374
R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA
693801
R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 pro
tein, complete cds//1.4e-18:174:77//Hs.139648:AB01
4606
R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA
828790
R-MAMMA1001969//ESTs, Weakly similar to hypothetic
al protein [H.sapiens]//6.7e-24:331:71//Hs.140506:
AA308018
R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA
211734
50 R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W2

4055

7084

R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:70//Hs.155464:AF088219

R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054

R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MART-1) mRNA//3.7e-45:370:80//Hs.154069:U06452

R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223

R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:AI206412

R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:76//Hs.32567:AF073519

R-MAMMA1002047//Homo sapiens mRNA for chemokine LE C precursor, complete cds//1.9e-37:316:74//Hs.10458:AF088219

R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:AI281881

R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA12046979

R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTEIN INQOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:78//Hs.138596:N38806

R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:AI032875

R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds//1.7e-42:314:83//Hs.10887:AB013924

R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-46:308:87//Hs.40100:AB002390

R-MAMMA1002093//EST//0.89:213:60//Hs.151201:AI125907

R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347

R-MAMMA1002118

R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:D38081

R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete

4056

cds//1.4e-58:396:78//Hs.129735:AF010144

R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//1.4e-37:422:75//Hs.128834:AF035835

R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276

10 R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:371:69//Hs.97476:AB007886

R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548

R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frames//8.7e-39:506:69//Hs.23094:M19503

R-MAMMA1002156//Homo sapiens mRNA for putative lipoid acid synthetase, partial//2.9e-44:336:82//Hs.53531:AJ224162

R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040

R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-37:370:77//Hs.29736:AB000509

R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:H52638

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956

40 R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734

R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038

R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540

R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA,

4057

complete cds//9.1e-50:330:77//Hs.108966:U48696
 R-MAMMA1002236
 R-MAMMA1002243
 R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080
 R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.6e-54:207:81//Hs.92381:AB007956
 R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283
 R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772
 R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA25141
 R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751
 R-MAMMA1002293//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982
 R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881
 R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454
 R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153
 R-MAMMA1002299//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359
 R-MAMMA1002308
 R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452
 R-MAMMA1002311//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503
 R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094
 R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280
 R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183
 R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084
 R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658
 R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317
 R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897
 R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W5

4058

7618
 R-MAMMA1002347//ESTs//1.5e-44:326:83//Hs.111723:H57439
 R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127
 R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228
 R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390
 R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367
 R-MAMMA1002356//Clathrin, light polypeptide (Lcb)/4.9e-31:217:88//Hs.73919:X81637
 R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080
 R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475
 R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2(XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587
 R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236
 R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542
 R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219
 R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061
 R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845
 R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294
 R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488
 R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:N22588
 R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477
 R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475
 R-MAMMA1002434//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348
 R-MAMMA1002446//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996
 R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.891

- 21: AB007954
 R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:A
 A147076
 R-MAMMA1002470//ESTs, Highly similar to HYPOTHETI
 CAL 80.7 KD PROTEIN INERG7-NMD2 INTERGENIC REGION
 [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94
 570: AI192106
 R-MAMMA1002475//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-3
 1:263:79//Hs.38687:AA744496
 R-MAMMA1002480//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-3
 4:159:79//Hs.133526:N21103
 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-
 2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:
 AF055460
 R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N7
 0293
 R-MAMMA1002498//Human novel homeobox mRNA for a DN
 A binding protein//0.0043:331:58//Hs.37035:U07664
 R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA8
 06277
 R-MAMMA1002530//Homo sapiens cytosolic phospholipa
 se A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e
 -103:529:95//Hs.18858:AF065214
 R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 pro
 tein, complete cds//9.5e-50:317:88//Hs.153468:AB01
 1147
 R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA
 218851
 R-MAMMA1002556//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-1
 2:280:65//Hs.12725:T65058
 R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA7
 05681
 R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA
 595693
 R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R7
 4433
 R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49
 371
 R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419
 258
 R-MAMMA1002597//Cytochrome P450, subfamily IIB (ph
 enobarbital-inducible), polypeptide 6//2.9e-21:17
 7:75//Hs.1360:M29874
 R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA
 573737
 R-MAMMA1002603//Thiopurine S-methyltransferase//7.
 6e-35:225:80//Hs.51124:AF019369
- R-MAMMA1002612//Cytochrome P450, subfamily I (arom
 atic compound-inducible), polypeptide 2//4.2e-46:4
 24:75//Hs.1361:M55053
 R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27
 389
 R-MAMMA1002618//Landsteiner-Wiener blood group gly
 coprotein//1.3e-27:185:73//Hs.108287:L27670
 R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA5
 26306
 10 R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:2
 98:87//Hs.89887:D38081
 R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI2
 81881
 R-MAMMA1002625//ESTs, Moderately similar to ovaria
 n-specific protein [R.norvegicus]//2.3e-35:308:79/
 Hs.93332:AA811920
 R-MAMMA1002629//Homo sapiens mRNA for small GTP-bi
 nding protein, complete cds//9.7e-57:283:86//Hs.11
 5325:D84488
 20 R-MAMMA1002636//Human mRNA for KIAA0392 gene, part
 ial cds//1.2e-49:303:89//Hs.40100:AB002390
 R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI1
 44421
 R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N6
 9915
 R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W6
 3776
 R-MAMMA1002655
 R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, comple
 te cds//2.2e-46:462:75//Hs.97476:AB007886
 30 R-MAMMA1002665//Human mRNA for KIAA0118 gene, part
 ial cds//9.1e-51:376:82//Hs.154326:D42087
 R-MAMMA1002671//ESTs, Weakly similar to coded for
 by C. elegans cDNA yk52e10.5 [C.elegans]//5.3e-10
 8:544:96//Hs.16464:W19606
 R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA6
 68213
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 pro
 tein, complete cds//4.6e-109:544:96//Hs.3363:D8698
 7
 R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA6
 01385
 R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA
 652675
 R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F
 22510
 R-MAMMA1002701//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-7
 0:353:96//Hs.138404:R70986
 50 R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69

4061

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R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858

R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:273:89//Hs.153563:AF011333

R-MAMMA1002727//ESTs//2.9e-84:395:100//Hs.162826:AA679571

R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219

R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757 10

R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907

R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452

R-MAMMA1002754//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776

R-MAMMA1002758

R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281

R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651

R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272

R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750

R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145

R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812

R-MAMMA1002807//Archaeal//1.4e-39:315:80//Hs.33642:X81198

R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260

R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:AI248319

R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:AI281881

R-MAMMA1002835

R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723

R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395

R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238

R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081

R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e- 50

4062

101:361:91//Hs.85155:X79067

R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941

R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:AI243592

R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194

R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:AI365871

R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219

R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811

R-MAMMA1002890//ESTs, Weakly similar to coded for by C. elegans cDNA CEESB82F [C.elegans]//4.2e-92:438:99//Hs.155871:AA533783

R-MAMMA1002892//Homo sapiens EVI5 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915

R-MAMMA1002895//ESTs//2.7e-32:330:76//Hs.139132:AA211087 20

R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179

R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002

R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:AI281881

R-MAMMA1002938

R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frames//1.1e-83:556:85//Hs.23094:M19503

30 R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243

R-MAMMA1002964//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353

R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081

R-MAMMA1002972//ESTs, Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630

R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835

40 R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279

R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019

R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179

R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:AI127857

R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617

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R-MAMMA1003011//ESTs, Highly similar to HISTONE H
ACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//H
s.92023:AI022248
R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA
573189
R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA
251268
R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA8
97315
R-MAMMA1003031//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//3.5e
-27:257:77//Hs.96337:AA225358
R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA6
03321
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA5521
60
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55
940
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:AI0
02941
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12
862
R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60/
/Hs.2510:X57348
R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:AI2
81881
R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:AI0385
59
R-MAMMA1003057//ESTs, Highly similar to hypothetic
al protein MD6 [M.musculus]//1.1e-102:545:93//Hs.1
3755:AA878911
R-MAMMA1003066//H.sapiens mRNA for urea transporte
r//8.1e-45:322:83//Hs.66710:X96969
R-MAMMA1003089//ESTs, Weakly similar to !!!! ALU S
UBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.4e-3
4:421:70//Hs.161959:AA493652
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59
651
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T512
83
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA8
15366
R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA
410788
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA
863125
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:AI
149537
R-MAMMA1003146//Wingless-type MMTV integration sit
e 5A, human homolog//0.020:413:61//Hs.152213:L2086

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1
R-nnnnnnnnnnnnn
R-MAMMA1003166//ESTs, Moderately similar to PEANU
T PROTEIN [Drosophilamelanogaster]//2.0e-87:524:89
//Hs.6884:W30736
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequ
ence//1.6e-111:587:94//Hs.108112:AF070640
R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59
312
R-NT2RM4000027
R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03
663
R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:AI
186169
R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z7
8379
R-NT2RM4000085//Homo sapiens clone 24700 unknown m
RNA, partial cds//4.0e-113:549:97//Hs.95665:AF0706
39
20 R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA8
77817
R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H1
9708
R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:AI0
52312
R-NT2RM4000155//ESTs, Moderately similar to THREON
YL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-
99:536:92//Hs.127810:AI246301
R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA6763
97
R-nnnnnnnnnnnnn//ESTs//1.0:214:61//Hs.119370:W52962
R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:AI
382160
R-NT2RM4000191//ESTs, Weakly similar to P68 PROTEI
N [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113
R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA
156723
R-NT2RM4000199//ESTs//0.020:95:65//Hs.146203:AI254
528
40 R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:A
A931876
R-NT2RM4000202//Small inducible cytokine A5 (RANTE
S)//4.3e-37:330:77//Hs.155464:AF088219
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 pro
tein, complete cds//1.7e-103:546:94//Hs.111138:AB0
18255
R-NT2RM4000215
R-nnnnnnnnnnnnn//ESTs//7.1e-92:457:97//Hs.162074:AA
477760
50 R-NT2RM4000233//Fms-related tyrosine kinase 1 (vas

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cular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602
 R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031
 R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974
 R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:AI378742
 R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128
 R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673
 R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219
 R-NT2RM4000344//Clathrin, light polypeptide (Lcb)/8.6e-60:452:84//Hs.73919:X81637
 R-NT2RM4000349//ESTs, Weakly similar to KIAA0005 [H. sapiens]//2.5e-117:579:96//Hs.5216:AA534881
 R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:AI224479
 R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418063
 R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542
 R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:M78140
 R-NT2RM4000386//ESTs, Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879
 R-NT2RM4000395//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN INSAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977
 R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285
 R-NT2RM4000421//ESTs, Weakly similar to No definition line found [C.elegans]//5.4e-75:470:90//Hs.69235:AA192359
 R-NT2RM4000425//H. sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173
 R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:AI150687
 R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA75865
 R-NT2RM4000471//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492:96//Hs.21090:AA418587

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R-NT2RM4000486//ESTs, Moderately similar to unnamed protein product [H. sapiens]//2.2e-102:493:97//Hs.111279:W84558
 R-NT2RM4000496
 R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:AI358465
 R-NT2RM4000514//ESTs//1.7e-112:552:96//Hs.6686:AA205496
 R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN INCPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879
 R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731
 R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461
 R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777
 R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198
 R-NT2RM4000585//EST//0.28:63:77//Hs.150024:AI291981
 R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437
 R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891
 R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589
 R-nnnnnnnnnnnn//ESTs//1.5e-89:431:97//Hs.26117:W16697
 R-NT2RM4000616//ESTs, Highly similar to ACETYL-CO ENZYME A SYNTHETASE [Escherichia coli]//1.4e-102:519:96//Hs.14779:N64822
 R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144
 R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C. elegans]//2.9e-115:550:98//Hs.11820:AA205531
 R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510
 R-nnnnnnnnnnnn
 R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128
 R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103:519:95//Hs.6823:W18181
 R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA65311
 R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:AB018303

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R-NT2RM4000741//ESTs//0.99:266:58//Hs.142718:AA034046
 R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988
 R-NT2RM4000764
 R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174
 R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:AB007920
 R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.154069:U06452
 R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:AI417008
 R-NT2RM4000795//Human mRNA for KIAA0067 gene, complete cds//1.0:203:63//Hs.20991:D31891
 R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:AI003520
 R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:M21868
 R-NT2RM4000813
 R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:AI219667
 R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031
 R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864
 R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:AI309597
 R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:AI283343
 R-ntnnnnnnnnnnnn
 R-NT2RM4000895//ESTs, Moderately similar to !!!! A LU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514
 R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262
 R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA27887
 R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647
 R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126
 R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272

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R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539
 R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352
 R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132
 R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300
 R-ntnnnnnnnnnnnn//ESTs//3.4e-91:439:99//Hs.103177:W72798
 R-NT2RM4001092//ESTs//1.4e-86:517:89//Hs.132969:Z78324
 R-NT2RM4001116//EST//5.2e-57:275:100//Hs.131115:AI016962
 R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276
 R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311
 R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848
 R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:AI209085
 R-NT2RM4001187//ESTs, Moderately similar to !!!! A LU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174
 R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//3.1e-32:274:70//Hs.2379:U23942
 R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849
 R-NT2RM4001203
 R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307
 R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410
 R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677
 R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184
 R-NT2RM4001309
 R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857
 R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:AI128899
 R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:AI042352
 R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//H

S. 18442: AI129307
R-NT2RM4001344//EST//1.1e-90: 436: 99//Hs. 95900: AA160339
R-NT2RM4001347//EST//0.17: 186: 61//Hs. 16751: T90476
R-NT2RM4001371//EST//0.0069: 270: 62//Hs. 99239: AA450211
R-NT2RM4001382
R-NT2RM4001384//ESTs//9.6e-91: 445: 98//Hs. 55000: AA805507
R-NT2RM4001410//EST//0.13: 50: 82//Hs. 157675: AI358790
R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adaptor protein Lnk [M.musculus]//4.0e-102: 539: 94//Hs. 15744: AI055859
R-NT2RM4001412
R-NT2RM4001414//ESTs//6.5e-35: 226: 88//Hs. 121727: AA775895
R-NT2RM4001437//EST//0.017: 169: 67//Hs. 13207: F10054
R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108: 544: 94//Hs. 7558: AA526812
R-NT2RM4001454//ESTs//4.7e-108: 517: 98//Hs. 32295: N32277
R-NT2RM4001455//EST//9.6e-81: 395: 97//Hs. 127978: AA969739
R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58: 324: 85//Hs. 22271: D26067
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104: 547: 93//Hs. 153121: AB014585
R-NT2RM4001519//Histatin 1//0.53: 340: 59//Hs. 119101: M26664
R-NT2RM4001522//Small inducible cytokine A5 (RANTE S)//8.4e-55: 306: 80//Hs. 155464: AF088219
R-NT2RM4001557//ESTs, Weakly similar to F11A10.4 [C.elegans]//6.1e-21: 165: 83//Hs. 29134: H43072
R-NT2RM4001565//ESTs//2.0e-103: 483: 99//Hs. 121273: A A758027
R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha -Trypsin Inhibitor Heavy Chain LIKE gene, alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains EST s, STSs and genomic marker DXS8032//2.7e-43: 446: 72//Hs. 4943: Z98046
R-NT2RM4001569//ESTs//3.6e-37: 186: 100//Hs. 86959: AA888009
R-NT2RM4001582//ESTs//1.2e-96: 459: 98//Hs. 114432: N52946
R-NT2RM4001594//ESTs//1.6e-83: 404: 98//Hs. 134740: AA282171
R-NT2RM4001597//ESTs//6.9e-111: 558: 96//Hs. 11408: AI358871
R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112: 565: 95//Hs. 23255: AB018334
R-NT2RM4001611//EST//5.9e-74: 353: 99//Hs. 125318: AA37079
R-NT2RM4001629//ESTs//6.1e-95: 453: 99//Hs. 115765: AA485957
R-NT2RM4001650
R-NT2RM4001662
R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36: 230: 70//Hs. 7764: AB007938
R-NT2RM4001682//EST//4.3e-68: 393: 90//Hs. 157362: AI367496
R-NT2RM4001710//ESTs//4.3e-48: 235: 99//Hs. 7299: AA203440
R-NT2RM4001714//ESTs//0.0014: 568: 58//Hs. 50458: AA868686
R-NT2RM4001731//ESTs, Weakly similar to No definit ion line found [C.elegans]//3.1e-108: 563: 94//Hs. 18510: AA522887
R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083: 124: 68//Hs. 120980: S83390
R-NT2RM4001746//ESTs//6.1e-90: 420: 100//Hs. 139003: A A948200
R-NT2RM4001754//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//5.4e-59: 504: 78//Hs. 139107: K00629
R-NT2RM4001758//ESTs//8.9e-27: 140: 100//Hs. 149973: A I290740
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24: 236: 80//Hs. 39871: AB018270
R-NT2RM4001783//ESTs//9.9e-30: 156: 99//Hs. 115260: AA314956
R-NT2RM4001810//ESTs//1.3e-65: 346: 95//Hs. 131915: W22567
R-NT2RM4001813//ESTs//5.7e-102: 473: 100//Hs. 87574: A I089920
R-NT2RM4001823//ESTs//3.8e-62: 324: 95//Hs. 124109: AA888839
R-NT2RM4001828//ESTs//1.3e-119: 563: 98//Hs. 102397: A

- A706551
R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA51070
R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
R-NT2RM4001842//ESTs, Weakly similar to !!!! ALU S UBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652
R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000
R-ntnnnnnnnnnn//ESTs//6.2e-104:495:98//Hs.118686:AA682280
R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711
R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149
R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
R-NT2RM4001922//ESTs, Weakly similar to !!!! ALU S UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
R-NT2RM4001930//ESTs//4.1e-84:425:96//Hs.80042:N63143
R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:AI205893
R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162
R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
R-NT2RM4001965//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
R-ntnnnnnnnnnn//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097
R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265
R-NT2RM4001984
R-NT2RM4001987
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528
R-NT2RM4002018
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087
R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435
R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226
R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887
R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179
R-ntnnnnnnnnnn//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309
R-NT2RM4002067//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end//2.3e-43:468:73//Hs.139107:K00629
R-NT2RM4002073//ESTs, Weakly similar to very-long-chain acyl-CoA synthetase [H.sapiens]//6.8e-57:290:96//Hs.109274:AA193416
R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655
R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528
R-ntnnnnnnnnnn//ESTs//1.0:95:69//Hs.25897:W65409
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620
R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712
R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987
R-NT2RM4002146//ESTs//1.9e-93:439:99//Hs.119295:AA442090
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258
R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678
R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079
R-NT2RM4002226//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984
R-NT2RM4002251//ESTs, Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C.elegans]//1.1e-100:544:93//Hs.27567:W72190
R-NT2RM4002256//Small inducible cytokine A5 (RANTE S)//1.0e-44:341:81//Hs.155464:AF088219

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- R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864
- R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263
- R-NT2RM4002281//ESTs//4.9e-20:187:80//Hs.141203:H52638
- R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:N52461
- R-NT2RM4002294
- R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164
- R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498
- R-ntnnnnnnnnnn//ESTs//5.0e-59:283:100//Hs.125048:AA682913
- R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:M77198
- R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549
- R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594
- R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884
- R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328
- R-NT2RM4002409//ESTs, Weakly similar to coded for by *C. elegans* cDNA yk52e10.5 [*C. elegans*]//1.3e-97:473:98//Hs.16464:W19606
- R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677
- R-NT2RM4002446
- R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142
- R-NT2RM4002457
- R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890
- R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, completecds//1.6e-103:507:97//Hs.8765:AF083255
- R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:AB014591
- R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884
- R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029
- R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA64464
- R-ntnnnnnnnnnn//ESTs, Weakly similar to peroxisome targeting signal 2 receptor [*H. sapiens*]//1.4e-73:360:91//Hs.31030:H50467
- R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788
- R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057
- R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312
- R-NT2RM4002571//ESTs, Highly similar to POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE [*Bos taurus*]//2.3e-89:435:97//Hs.15830:AA165698
- R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569
- R-NT2RM4002623//ESTs, Weakly similar to ASPARTYL-TRNA SYNTHETASE [*Thermus aquaticus thermophilus*]//9.6e-28:194:87//Hs.59346:AI126802
- R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096
- R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:D38081
- R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115
- R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713
- R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290
- R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749
- R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
- R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910
- R-NT2RP2000067//ESTs, Weakly similar to tenascin-like protein [*D. melanogaster*]//2.3e-35:199:94//Hs.41793:AA775879
- R-NT2RP2000070//ESTs, Weakly similar to proto-cadherin 3 [*R. norvegicus*]//1.4e-78:383:98//Hs.58254:W72881
- R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097
- R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.54877:AF050078
- R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.102576:AJ010230
- R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB0183

38	R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064	ERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-5
	R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757	9:298:96//Hs.16085:AI261382
	R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827	R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635
	R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419	R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865
	R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17706:AB018356	R-NT2RP2000289
	R-NT2RP2000120//ESTs, Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//1.9e-19:153:86//Hs.5268:W22670	R-NT2RP2000297//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249
	R-nnnnnnnnnnnn//ESTs//1.0e-55:293:95//Hs.14570:AI422099	R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712
	R-nnnnnnnnnnnn//ESTs//0.24:354:59//Hs.157564:AI356513	R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381
	R-NT2RP2000147//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:AI208601	R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GS
	R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548	Ss//2.9e-71:342:98//Hs.87684:AL022398
	R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820	R-NT2RP2000329//ESTs, Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441
	R-NT2RP2000161//ESTs//1.6e-99:492:97//Hs.21738:AI188190	R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062
	R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741	R-NT2RP2000346//Homo sapiens apoptosis associated protein (GADD34) mRNA, complete cds//1.1e-47:262:94
	R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:N51373	//Hs.76556:U83981
	R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510	R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103
	R-NT2RP2000205//ESTs, Moderately similar to !!!! A LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//1.4e-80:415:95//Hs.11807:T86897	R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//8.4e-09:93:83//Hs.808:L28010
	R-NT2RP2000224//RNA polymerase II, polypeptide C (33kd)//1.1e-57:306:94//Hs.79402:AC004382	R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324
	R-NT2RP2000232	R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265
	R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683	R-NT2RP2000438//ESTs, Weakly similar to misato [D.melanogaster]//1.3e-65:362:93//Hs.22197:AI151425
	R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379	R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROTEIN INPAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-75:435:92//Hs.21938:W81045
	R-NT2RP2000248//ESTs, Weakly similar to O-linked GlcNAc transferase [H.sapiens]//1.3e-95:454:99//Hs.102057:AA649005	R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013
	R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840	R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078
	R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649	R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI
	R-NT2RP2000270//ESTs, Weakly similar to LINE-1 REV	

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290215
 R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455:58//Hs.110:AB007896
 R-nnnnnnnnnnnnn//ESTs//9.9e-63:376:89//Hs.47546:AA181348
 R-NT2RP2000523
 R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//3.5e-30:167:97//Hs.14409:AB011144
 R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72 10
 446
 R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//8.1e-66:335:96//Hs.7314:AB014514
 R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222
 R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA15275
 R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396
 R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R1 20
 6767
 R-NT2RP2000678//ESTs//2.6e-53:271:96//Hs.23790:N99347
 R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368
 R-NT2RP2000715//EST//1.2e-87:418:99//Hs.139425:AA429279
 R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965
 R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642 30
 R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419
 R-NT2RP2000809
 R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745
 R-nnnnnnnnnnnnn//ESTs//6.3e-87:433:97//Hs.145479:AA969404
 R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918
 R-NT2RP2000819
 R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511
 R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR//4.6e-10:247:66//Hs.29352:W31165
 R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552
 R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345
 R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 pro 50

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tein, complete cds//2.8e-43:277:89//Hs.3615:AB018284
 R-NT2RP2000892//ESTs//2.8e-50:258:96//Hs.119238:AA476267
 R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266
 R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTEIN ZK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:199:95//Hs.112318:AA186477
 R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//9.8e-98:494:96//Hs.19822:AB018298
 R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021
 R-NT2RP2000970//EST//8.7e-06:255:62//Hs.149202:AI246481
 R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN INSIS2-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95//Hs.12124:AA522537
 R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521
 R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643
 R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA53660
 R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108
 R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665
 R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068
 R-NT2RP2001119
 R-NT2RP2001127//Homo sapiens mRNA for HRI HFB2060, partial cds//1.5e-56:304:94//Hs.146282:AB015348
 R-NT2RP2001137
 R-NT2RP2001149//ESTs//5.1e-66:324:97//Hs.27475:AA704512
 R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145
 R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//1.5e-96:490:96//Hs.26247:AB007949
 R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287
 R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510
 R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402
 R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358
 R-NT2RP2001233//ESTs, Highly similar to ZINC FING

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ER PROTEIN ZFP-36 [Homo sapiens]//3.7e-65:538:80//
Hs.44014:AA632298
R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92
996
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 pro
tein, partial cds//1.5e-112:544:97//Hs.7531:AB0183
53
R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA9
08229
R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA0
44775
R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA
412665
R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA40
1205
R-NT2RP2001327//ESTs, Moderately similar to tumor
necrosis factor-alpha-induced protein B12 [H.sapie
ns]//2.3e-43:238:93//Hs.106632:N25679
R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI3
41138
R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA11
4178
R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50
028
R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA
444038
R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDR
IAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]//3.
9e-74:411:93//Hs.47305:AA195153
R-NT2RP2001394//ESTs//9.5e-54:305:93//Hs.70256:R07
875
R-NT2RP2001397//ESTs, Highly similar to G2/MITOTI
C-SPECIFIC CYCLIN B2 [Mesocricetus auratus]//5.2e-
97:469:97//Hs.20483:AA522505
R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N3
2030
R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R3
5431
R-NT2RP2001427//EST//1.7e-11:107:84//Hs.148584:AI2
01728
R-NT2RP2001436//ESTs, Weakly similar to F02D8.3
[C.elegans]//2.9e-114:558:97//Hs.7627:AI341556
R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI0613
94
R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:A
A501453
R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI
076765
R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI0
79539

4080

R-NT2RP2001467//Small inducible cytokine A5 (RANTE
S)//1.2e-34:255:83//Hs.155464:AF088219
R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T235
13
R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA2
51146
R-NT2RP2001520//Homo sapiens mRNA for mitochondria
l carrier protein ARALAR1//6.7e-106:545:95//Hs.427
7:Y14494
R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF03
9240
R-NT2RP2001536//Homo sapiens X-ray repair cross-co
mplementing protein 3(XRCC3) mRNA, complete cds//
1.9e-15:99:95//Hs.99742:AF035586
R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA7
32816
R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 sp
ecific transcript KIAA0488//2.0e-76:387:96//Hs.676
19:AB007957
20 R-NT2RP2001576//Human mRNA for KIAA0105 gene, comp
lete cds//0.17:193:60//Hs.119:D14661
R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T5
8884
R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI3
69995
R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI
393767
R-NT2RP2001613
R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294
30 R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56
090
R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI
370845
R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI2013
36
R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI12
5323
R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA
290579
40 R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:A
A987538
R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI
147100
R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA
828840
R-NT2RP2001762//Homo sapiens exonuclease 1a (EX01
a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:A
F091754
R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44
50 037

4081

R-NT2RP2001861
 R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI0
 02941
 R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA5
 33088
 R-NT2RP2001883//ESTs, Weakly similar to No definit
 ion line found [C.elegans]//6.9e-110:556:95//Hs.23
 159:AA113849
 R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA
 171724
 R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA
 188423
 R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI0
 97268
 R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T6
 6087
 R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI0
 32180
 R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72
 594
 R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72
 588
 R-NT2RP2001969
 R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA
 902745
 R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACT
 IVATING PROTEIN SPA-1[M.musculus]//8.3e-15:118:89/
 /Hs.18760:AA166678
 R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI
 378233
 R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA8
 13332
 R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA1
 02627
 R-NT2RP2002041
 R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:A
 A825938
 R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA
 629895
 R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA2
 58068
 R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA
 846091
 R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T9
 2265
 R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequ
 ence//1.7e-26:178:87//Hs.11039:AF052183
 R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI
 350524
 R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-as

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sociated protein//1.5e-60:376:89//Hs.155218:AJ0075
 09
 R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI1
 23000
 R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA
 525134
 R-NT2RP2002137//Deoxycytidine kinase//0.29:183:62/
 /Hs.709:M60527
 R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA5
 23268
 R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI33449
 5
 R-NT2RP2002185//ESTs, Weakly similar to F15C11.2
 [C.elegans]//1.4e-54:269:98//Hs.107201:W52859
 R-NT2RP2002192//ESTs, Moderately similar to !!!! A
 LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//3.9e
 -15:245:71//Hs.87578:AI125363
 R-NT2RP2002193//ESTs//3.5e-79:453:90//Hs.76578:AI2
 90672
 R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI
 003946
 R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287
 499
 R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA6
 42341
 R-ntnnnnnnnnnnnn//ESTs, Highly similar to co-repress
 or protein [M.musculus]//5.4e-48:238:99//Hs.22583:
 AA188168
 R-NT2RP2002256//Homo sapiens retinoic acid hydroxy
 lase mRNA, complete cds//1.6e-15:131:83//Hs.15059
 5:AF005418
 R-NT2RP2002259//Human L-myc protein gene, complete
 cds//5.3e-99:548:91//Hs.92137:M19720
 R-NT2RP2002270//ESTs, Weakly similar to AF-9 PROTE
 IN [H.sapiens]//4.8e-100:550:91//Hs.4029:Z78373
 R-NT2RP2002292//ESTs, Weakly similar to F13B12.1
 [C.elegans]//3.2e-92:482:93//Hs.5570:AI377863
 R-NT2RP2002312//Homo sapiens CDP-diacylglycerol sy
 nthase 2 (CDS2) mRNA, partial cds//4.1e-103:527:94/
 /Hs.24812:AF069532
 R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI3
 68015
 R-NT2RP2002325//Homo sapiens peroxisomal biogenesi
 s factor (PEX11a) mRNA, complete cds//1.2e-112:56
 7:95//Hs.31034:AB015594
 R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA
 767372
 R-NT2RP2002385//Homo sapiens synaptic glycoprotein
 SC2 spliced variant mRNA, complete cds//1.2e-103:
 600:89//Hs.109051:AF038958

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R-NT2RP2002394//ESTs//0.11:158:65//Hs.68792:AI3434
67
R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W228
15
R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 pro
tein, complete cds//1.7e-33:285:80//Hs.15731:AB011
135
R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA4
64020
R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97
521
R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI
362230
R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W272
33
R-ntnnnnnnnnnnnn//Homo sapiens mRNA for ABC transpor
ter 7 protein, complete cds//9.9e-115:605:92//Hs.1
25856:AB005289
R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N7
3180
R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60
838
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 pro
tein, complete cds//8.5e-107:583:91//Hs.23255:AB01
8334
R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA2
05305
R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:A
A533090
R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-cha
t region mRNA//2.6e-109:570:93//Hs.49476:AF009314
R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:
86//Hs.80961:U60325
R-NT2RP2002591//ESTs, Weakly similar to ZINC FINGE
R PROTEIN 84 [H. sapiens]//7.5e-118:564:97//Hs.9454
9:AA149547
R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA9
94783
R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40
170
R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI1
84220
R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541
615
R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI2
81881
R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA1
79944
R-NT2RP2002672
R-NT2RP2002701//N-acetylglucosaminidase, alpha- (S

anfilippo disease IIIB//0.99:184:63//Hs.50727:U43572

R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA83223

R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210

R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626

R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA93300

R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108

R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352

R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131

R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042

R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124

R-NT2RP2002769//ESTs//1.3e-59:376:88//Hs.4046:H03587

R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:341:94//Hs.17481:AF070537

R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124

R-NT2RP2002839//ESTs, Moderately similar to !!!!! ALU SUBFAMILY J WARNINGENTRY !!!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578

R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031

R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870

R-NT2RP2002880

R-NT2RP2002891

R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894

R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143

R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096

R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771

R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:N57480

R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060

R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213

R-NT2RP2002986//ESTs, Highly similar to RING CANA

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L PROTEIN [Drosophilamelanogaster]//3.1e-119:578:97//Hs.106290:AI125291
 R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:78:74//Hs.146395:AB002329
 R-NT2RP2002993//ESTs, Weakly similar to DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.86337:AA149311
 R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
 R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:HI 10 2594
 R-NT2RP2003073//Human transporter protein (gl7) mRNA, complete cds//0.95:259:61//Hs.76460:U49082
 R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:D38081
 R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
 R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-49:336:86//Hs.101996:AB002345
 R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA 20 133355
 R-NT2RP2003125
 R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
 R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506
 R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
 R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067
 R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
 R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
 R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
 R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
 R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
 R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
 R-NT2RP2003243//ESTs//3.6e-53:300:92//Hs.118793:AA192438
 R-NT2RP2003265//ESTs, Highly similar to protein NC D5 [M.musculus]//3.3e-110:557:96//Hs.24994:AA236937
 R-NT2RP2003272//ESTs, Weakly similar to F15C11.2 [C.elegans]//1.2e-34:228:89//Hs.107201:W52859
 R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 pro 50

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tein, partial cds//1.4e-111:565:95//Hs.154919:AB014525
 R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
 R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
 R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-44:458:74//Hs.154326:D42087
 R-NT2RP2003295//Protein serine/threonine kinase sk2//0.31:321:57//Hs.1087:L20321
 R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
 R-NT2RP2003308//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126
 R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
 R-NT2RP2003339//ESTs//1.3e-85:441:96//Hs.24115:N32618
 R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825
 R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014
 R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476
 R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
 R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249
 R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683
 R-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.131840:AI016073
 R-NT2RP2003445//ESTs, Moderately similar to LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360
 R-NT2RP2003446//ESTs, Weakly similar to C27H6.4 [C.elegans]//6.0e-105:529:96//Hs.8055:W60903
 R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332
 R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121
 R-NT2RP2003499//ESTs, Weakly similar to elastin like protein [D.melanogaster]//7.0e-71:365:95//Hs.101056:R52777
 R-NT2RP2003506//ESTs, Weakly similar to ORF YPL207 w [S.cerevisiae]//2.3e-115:577:96//Hs.16277:N36831
 R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733

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R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-108:566:94//Hs.78482:Y16270
 R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (simiansarcoma viral (v-sis) oncogene homolog)//4.9e-62:518:79//Hs.1976:W12783
 R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170
 R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101
 R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684
 R-NT2RP2003559//ESTs, Moderately similar to LU SUBFAMILY J WARNINGENTRY LU [H.sapiens]//1.8e-58:316:94//Hs.28891:W72439
 R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696
 R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719
 R-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//4.7e-101:495:98//Hs.34627:AA126463
 R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067
 R-NT2RP2003629//EST//0.032:440:59//Hs.135297:AI038981
 R-NT2RP2003643//ESTs, Weakly similar to HYPOTHETICAL 14.1 KD PROTEIN IN MURZ-RPON INTERGENIC REGION [E.coli]//9.1e-62:359:92//Hs.12492:AA203188R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951
 R-NT2RP2003687//EST//5.9e-05:196:65//Hs.139064:AA135523
 R-NT2RP2003691//ESTs, Weakly similar to F59C6.9 [C.elegans]//1.0:202:62//Hs.65539:AI148540
 R-NT2RP2003702//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//4.3e-99:492:96//Hs.93332:AA811920
 R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246
 R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.4e-47:265:93//Hs.78494:AB011097
 R-NT2RP2003713//EST//0.81:210:59//Hs.14551:T79401
 R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:AI365003
 R-NNNNNNNNNN//Human 19.8 kDa protein mRNA, complete cds//0.84:221:60//Hs.2384:U18914
 R-NT2RP2003737//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W74577
 R-NT2RP2003751

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R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808
 R-NT2RP2003764//ESTs//8.2e-25:134:98//Hs.64036:AA127709
 R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606
 R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds//6.0e-106:531:96//Hs.90436:AF047437
 R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:AI381811
 R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836
 R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955
 R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077
 R-NT2RP2003857//H.sapiens mRNA for G9a//2.8e-23:351:65//Hs.75196:X69838
 R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124
 R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167
 R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341
 R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:AI094611
 R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//0.90:190:60//Hs.75875:U49278
 R-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//7.6e-116:568:97//Hs.35086:AB014458
 R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//3.6e-109:540:97//Hs.7302:AB007916
 R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//2.5e-115:568:96//Hs.7316:AB018347
 R-NT2RP2003984
 R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087
 R-NT2RP2003988//ESTs, Weakly similar to reverse transcriptase [H.sapiens]//3.2e-110:519:99//Hs.36093:AI149968
 R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:AI417478
 R-NT2RP2004041
 R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706

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R-nnnnnnnnnnnnn/ESTs//1.4e-110:559:96//Hs.71916:AA
219699
R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA
977204
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R414
61
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23
036
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:AI1
47500
R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:AI
342241
R-NT2RP2004165//ESTs, Highly similar to DYNEIN BE
TA CHAIN, CILIARY [Anthocidaris crassispina]//1.0e
-118:583:97//Hs.16520:AI224533
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:AI
348544
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:A
A033974
R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26
589
R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA
203167
R-NT2RP2004196
R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA
604756
R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26
972
R-NT2RP2004232//ESTs, Highly similar to protein ki
nase C mu [H. sapiens]//5.2e-105:499:98//Hs.143460: 30
AA483305
R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA2
03116
R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-C
O-1) mRNA, complete cds//3.4e-103:530:93//Hs.5490
0:AF039687
R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA
211483
R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA
035744
R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187
R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA
905056
R-NT2RP2004316//Homo sapiens EXT-like protein 2 (E
XTL2) mRNA, complete cds//4.7e-110:544:96//Hs.6115
2:AF000416
R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA
044788
R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA4
83223

4090

R-NT2RP2004347
R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:AI
268173
R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:AI129
310
R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:AI
218624
R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32
192
10 R-NT2RP2004389//ESTs, Highly similar to HYPOTHETI
CAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Cae
norhabditis elegans]//1.4e-11:108:82//Hs.30490:AA1
46916
R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA58
1646
R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92
473
R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900
R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:A
A602921
R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA
403121
R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:AI1
68124
R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N296
95
R-NT2RP2004490//Homo sapiens 3-phosphoinositide de
pendent protein kinase-1 (PDK1) mRNA, complete cds
//8.6e-34:143:98//Hs.154729:AF017995
30 R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:AI
270700
R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61
320
R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:2
79:89//Hs.89887:D38081R-NT2RP2004551//ESTs//0.47:1
47:66//Hs.131519:AI024347
R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA
195470
R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:AI
221661
40 R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA
781126
R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA9
54666
R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69
862
R-NT2RP2004602//ESTs, Weakly similar to !!!! ALU S
UBFAMILY J WARNING ENTRY !!!! [H. sapiens]//4.5e-0
7:149:76//Hs.12845:N28835
50 R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N5

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R-NT2RP2005227//Homo sapiens LIM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258
 R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587
 R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503
 R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596
 R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA16272
 R-NT2RP2005287//ESTs//1.7e-109:565:94//Hs.61976:AI279001
 R-NT2RP2005288//Homo sapiens RCC1-like G exchangein g factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219
 R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein //4.9e-112:545:96//Hs.44766:AJ007590
 R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:AI341261
 R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338
 R-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, completecds//2.5e-45:272:91//Hs.1569:U11701
 R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699
 R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445
 R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:H14544
 R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247
 R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304
 R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697
 R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//8.1e-96:491:95//Hs.7194:AI185631
 R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068
 R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:H14423
 R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096

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R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307
 R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:AI378936
 R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:AI222019
 R-NT2RP2005476//ESTs//5.1e-40:205:98//Hs.101577:AI168526
 R-NT2RP2005490//ESTs//1.3e-70:364:96//Hs.134382:AA083573
 R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455
 R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540
 R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426
 R-NT2RP2005498//ESTs, Highly similar to PROTEIN P HOSPHATASE PP2A, 55 KDREGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:AI138993
 R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:AI141755
 R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:570:94//Hs.119023:AF092563
 R-NT2RP2005525//ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//1.3e-84:433:95//Hs.36942:AA524535
 R-NT2RP2005531//EST//0.98:64:70//Hs.146573:AI139856
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//8.8e-108:560:94//Hs.159597:AJ012449
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:AB007963
 R-NT2RP2005549//EST//0.61:111:62//Hs.147482:AI215572
 R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:AI357567
 R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169
 R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:HO3240
 R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733

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R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060
 R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:AI376788
 R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
 R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:AI418211
 R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
 R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173
 R-NT2RP2005651//ESTs, Highly similar to XFIN PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:AA868470
 R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302
 R-NT2RP2005669//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//5.8e-91:434:98//Hs.25664:AF089814
 R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229
 R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:AI292236
 R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:AI273643
 R-NT2RP2005701//ESTs, Highly similar to BUTYROPHILIN PRECURSOR [Bos taurus]//2.8e-68:376:93//Hs.9095:AA532630
 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:AB018342
 R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H. sapiens]//5.4e-105:500:98//Hs.14298:AI417523
 R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA23982
 R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455
 R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:AI223153
 R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258
 R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96/

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/Hs.159651:AF068868
 R-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.26285:AF082516
 R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:AI362163
 R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463
 R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-112:559:96//Hs.14214:AI189379
 R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.22151:AI214321
 R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664
 R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724
 R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398
 R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:AI298746
 R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981
 R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122
 R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
 R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:AI076062
 R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:AI338462
 R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
 R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:AI284133
 R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
 R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:AI125268
 R-NT2RP2005908//ESTs, Weakly similar to weakly similar to gastrula zincfinger protein [C. elegans]//2.4e-73:397:94//Hs.16667:T92427
 R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R. norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
 R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:AI1338419
 R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988

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R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
 R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
 R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C.elegans]//1.2e-50:278:94//Hs.7194:AI185631
 R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
 R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA522714
 R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
 R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918
 R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//Hs.46440:U21943
 R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
 R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
 R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-17:255:72//Hs.154103:AF061258
 R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435
 R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds//6.1e-110:553:95//Hs.109299:AB014554
 R-NT2RP2006196//Human clone 23960 mRNA sequence//0.0037:48:100//Hs.151293:U79276
 R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398
 R-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//1.2e-94:532:90//Hs.153910:X96484
 R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:AI341312
 R-NT2RP2006238//ESTs, Highly similar to rA8 [R.norvegicus]//1.5e-29:183:91//Hs.4048:AA404253
 R-NT2RP2006258//ESTs//3.2e-87:462:94//Hs.141556:N49928
 R-NT2RP2006261//ESTs//3.4e-57:326:92//Hs.22523:W02999
 R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7e-96:481:97//Hs.3404:AF035262
 R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015
 R-NT2RP2006321//ESTs, Moderately similar to karyopherin beta 3 [H.sapiens]//1.9e-89:460:96//Hs.21889:N78664

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R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.61697:AI081771
 R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412
 R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:AI282321
 R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411
 R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053
 R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.4e-27:155:76//Hs.115325:D84488
 R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092
 R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:AI341146
 R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595
 R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//2.1e-109:524:97//Hs.72160:AJ006266
 R-NT2RP2006467//EST//0.99:140:61//Hs.146958:AI174478
 R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679
 R-NT2RP2006534//ESTs//1.2e-83:394:99//Hs.162116:AA524947
 R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474
 R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:AI299886
 R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622
 R-nnnnnnnnnnnn//ESTs//2.0e-112:533:98//Hs.18685:AI393829
 R-NT2RP2006598//ESTs, Weakly similar to retinoid X receptor interacting protein [M.musculus]//4.1e-109:542:97//Hs.7889:AI337112
 R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:AI301598
 R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-116:560:97//Hs.6764:AJ011972
 R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:85//Hs.155464:AF088219
 R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213
 R-NT2RP3000050//ESTs, Weakly similar to putative p150 [H.sapiens]//3.1e-41:249:90//Hs.156155:AI22220

- 2
R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:AI2
55095
R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49
574
R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA
424029
R-NT2RP3000085//ESTs//4.5e-101:482:98//Hs.47649:AA
838715
R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:AI3 10
42241
R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA
884000
R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 pro
tein, partial cds//1.2e-116:578:96//Hs.13273:AB011
164
R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N934
18
R-NT2RP3000186
R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R5 20
1882
R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA
933091
R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R6
1306
R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N648
17
R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:AI0328
19
R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA9 30
69239
R-NT2RP3000251
R-NT2RP3000252//ESTs, Weakly similar to Lpg15p [S.
cerevisiae]//2.0e-108:532:97//Hs.111086:AI379177
R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA74307
3
R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA
534446
R-NT2RP3000299//ESTs, Weakly similar to enhancer o
f filamentation 1 [H.sapiens]//3.6e-103:516:96//Hs. 40
4894:AI191323
R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:AI
094117
R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA
192438
R-NT2RP3000324
R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:A
A476267
R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA7776
89
R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:AI2
76225
R-NT2RP3000350//ESTs, Weakly similar to Lpg15p [S.
cerevisiae]//3.1e-110:556:96//Hs.111086:AI379177
R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA9
13741
R-NT2RP3000361//ESTs, Weakly similar to PRE-mRNA S
PLICING FACTOR PRP6 [S.cerevisiae]//4.8e-91:439:97
//Hs.31334:AI144423
R-NT2RP3000366//EST//0.20:392:57//Hs.149652:AI2833
03
R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA8
55106
R-NT2RP3000403//Homo sapiens formin binding protei
n 21 mRNA, complete cds//4.2e-111:529:98//Hs.2830
7:AF071185
R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA6
82947
R-NT2RP3000433
R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26
340
R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA
421254
R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:AI3
79102
R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA74
8492
R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chrom
osome 4p16.3 DNA fragment//1.8e-23:347:70//Hs.1149
63:L34408
R-NT2RP3000484//Heparin cofactor II//0.98:166:62//
Hs.1478:M58600
R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885
141
R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.4
9931:X16667
R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA1
87151
R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:A
I078161
R-NT2RP3000531//ESTs, Weakly similar to TH1 protei
n [D.melanogaster]//0.95:85:71//Hs.5184:AA709151
R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30
180
R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:AI1
98036
R-NT2RP3000562//Human mRNA for KIAA0233 gene, comp
lete cds//0.97:141:68//Hs.79077:D87071
R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA7
79447

4101

R-NT2RP3000582//ESTs//2.1e-25:131:80//Hs.152465:AA
 563785
 R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:AI
 241511
 R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:A
 A953817
 R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:AI
 190916
 R-nnnnnnnnnnnn//Human mRNA for KIAA0314 gene, part
 ial cds//1.5e-09:447:58//Hs.155045:AB002312
 R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA8
 29880
 R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA
 422049
 R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:AI
 127394
 R-NT2RP3000624//ESTs, Weakly similar to KIAA0256
 [H.sapiens]//5.4e-115:545:98//Hs.4857:AI090739
 R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 pro
 tein, complete cds//4.3e-49:397:80//Hs.15519:AB018
 315
 R-NT2RP3000632//ESTs, Moderately similar to cyclin
 -selective ubiquitin carrier protein [H.sapiens]//
 6.3e-92:434:99//Hs.152517:AA719022
 R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W2
 7084
 R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W7
 6185
 R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81
 185
 R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R608
 73
 R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.146589:AI
 085578
 R-NT2RP3000736
 R-NT2RP3000742//ESTs, Highly similar to 1-PHOSPHA
 TIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE D
 ELTA 1 [Rattus norvegicus]//1.8e-07:114:75//Hs.136
 065:W21960
 R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:A
 1310447
 R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA
 207243
 R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:AI
 378583
 R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N2081
 0
 R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA5
 51582
 R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:AI

4102

151081
 R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98
 082
 R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA81
 3022
 R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:AI
 051657
 R-NT2RP3000850
 R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.7943
 2:U03272
 R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA57
 6895
 R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA5
 05741
 R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N7
 0837
 R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:AI0
 14673
 R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84/
 /Hs.75138:M88468
 R-NT2RP3000901//ESTs//2.1e-95:466:97//Hs.10647:AA4
 28217
 R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA
 479385
 R-NT2RP3000917//ESTs, Highly similar to mouse Dhml
 protein [M.musculus]//9.5e-113:566:96//Hs.5900:AA
 035728
 R-NT2RP3000919
 R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.5e-2
 5:375:71//Hs.2953:X84407
 R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA11
 4178
 R-NT2RP3000994//ESTs//3.5e-111:537:97//Hs.21146:AA
 683542
 R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87
 405
 R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:AI
 088029
 R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA86
 3044
 R-NT2RP3001057//ESTs, Highly similar to ZINC FING
 ER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//H
 s.145956:AA007349
 R-NT2RP3001081//Retinal pigment epithelium-specifi
 c protein (65kD)//0.0012:447:58//Hs.2133:U18991
 R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W8
 7874
 R-NT2RP3001096//ESTs//1.1e-110:540:96//Hs.42824:AA
 873182
 R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA

- 287832
R-nnnnnnnnnnnn/DNA polymerase gamma//0.0014:50:10
0//Hs.80961:U60325
R-NT2RP3001111//ESTs, Weakly similar to Trf-proxim
al protein [D.melanogaster]//3.2e-104:543:95//Hs.9
3796:C06063
R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA
401575
R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67/
/Hs.2820:X64878
R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74
779
R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA2
03180
R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI
190166
R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78
188
R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA
573761
R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 pro
tein, partial cds//2.6e-115:549:97//Hs.5378:AB0183
05
R-NT2RP3001147//ESTs, Highly similar to GTPASE AC
TIVATING PROTEIN ROTUND [Drosophila melanogaster]/
/9.6e-113:552:97//Hs.23900:U82984
R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA7
60717
R-NT2RP3001155//Homo sapiens mRNA for AND-1 protei
n//9.4e-118:563:98//Hs.72160:AJ006266
R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI
074460
R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA
573139
R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI2
54963
R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221
196
R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA
778399
R-NT2RP3001236//ESTs, Highly similar to KIAA0377
[H.sapiens]//2.8e-89:462:95//Hs.116793:AA779588
R-NT2RP3001239//ESTs, Moderately similar to NEURA
XIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:
AA524416
R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI4176
31
R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI
222997
R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA9321
- 35
R-NT2RP3001268//Human Aac11 (aac11) mRNA, complete
cds//0.12:494:59//Hs.151031:U83857
R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI
383965
R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.113184:N2
5651
R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI2
47332
10 R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA8686
91
R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H9
2571
R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H9
8989
R-NT2RP3001338//Human protein tyrosine phosphatase
sigma mRNA, completecds//0.22:199:63//Hs.159534:U
35234
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 pro
tein, complete cds//3.9e-114:566:96//Hs.18586:AB00
7920
R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81
653
R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA
776798
R-NT2RP3001374//ESTs//2.7e-82:395:98//Hs.117102:AA
993090
R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA
169778
30 R-NT2RP3001384//ESTs, Weakly similar to A-kinase a
nchor protein 95, AKAP95 [R.norvegicus]//5.7e-92:5
22:90//Hs.96200:AA218942
R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:A
A907375
R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA
152232
R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI
276628
R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI04
1186
40 R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA
496898
R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA8
77817
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequ
ence//3.6e-106:550:94//Hs.6957:AF052158
R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H056
92
R-nnnnnnnnnnnn//Neurotrophic tyrosine kinase, rece
ptor, type 1//4.7e-96:533:91//Hs.85844:X66397
- 50

4105

R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:A
1041374
R-NT2RP3001447//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//5.1e
-101:482:98//Hs.124135:AA910560
R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N459
94
R-NT2RP3001453//Small inducible cytokine A5 (RANTE
S)//8.1e-45:295:85//Hs.155464:AF088219
R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA 10
644658
R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA
167280
R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N3
7009
R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA21
1783
R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA
A, complete cds//1.4e-61:338:93//Hs.519:U13395
R-NT2RP3001497//Homo sapiens multiple membrane spa 20
nning receptor TRC8 (TRC8) mRNA, complete cds//6.8
e-112:549:97//Hs.28285:AF064801
R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:A
A631047
R-NT2RP3001529//Homo sapiens tapasin (NGS-17) mRNA
A, complete cds//7.9e-59:427:83//Hs.5247:AF029750
R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA20
9463
R-NT2RP3001554//ESTs, Moderately similar to NEURA
XIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048: 30
AA524416
R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:N49
477
R-NT2RP3001587//Homa sapiens mRNA for HRIHFB2115,
partial cds//1.8e-09:86:88//Hs.4311:AB015337
R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA6
05194
R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA74
8328
R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:A 40
1279798
R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI
193598
R-NT2RP3001629
R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, c
omplete cds//2.7e-109:541:96//Hs.9899:AF099149
R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA9
15989
R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA1
27709

4106

R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA4
57030
R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI3
82189
R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N6
7648
R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI
268225
R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI2
22558
R-NT2RP3001688//Human mRNA for KIAA0392 gene, part
ial cds//8.6e-46:301:87//Hs.40100:AB002390
R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI
341312
R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA8
68618
R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29
669
R-NT2RP3001716//ESTs, Highly similar to BONE MORP
HOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//4.1e
-80:444:91//Hs.6823:W18181
R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI
422099
R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA
669923
R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27
810
R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA74
0440
R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA
912968
R-NT2RP3001764//ESTs, Weakly similar to protein-ty
rosine phosphatase [H.sapiens]//1.2e-87:450:96//H
s.20281:N92517
R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:HO
6725
R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 pro
tein, partial cds//4.2e-113:549:97//Hs.28169:AB007
928
R-NT2RP3001792//ESTs, Weakly similar to F35C12.2
[C.elegans]//1.1e-21:119:99//Hs.44268:AA455900
R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:
374:79//Hs.129780:X75962
R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI2
91292
R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N5011
7
R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52
900
50 R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81

4107

792
 R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73
 642
 R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA52
 1180
 R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA9
 54666
 R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYS
 IN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.2470
 9:AI123300
 R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA6
 82781
 R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA5
 34737
 R-NT2RP3001938//ESTs, Highly similar to SPORULATI
 ON-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]//
 1.3e-95:483:96//Hs.5771:W74591
 R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA
 160990
 R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI
 291325
 R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025
 889
 R-NT2RP3001989//ESTs, Weakly similar to C01A2.4
 [C.elegans]//8.9e-64:310:99//Hs.11449:AI201540
 R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA89
 7088
 R-NT2RP3002004//H.sapiens mRNA for FAST kinase//1.
 6e-42:335:82//Hs.75087:X86779
 R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA8467
 29
 R-NT2RP3002014//Small inducible cytokine A5 (RANTE
 S)//6.8e-47:291:89//Hs.155464:AF088219
 R-NT2RP3002033
 R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W2
 9081
 R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426
 R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI3
 65221
 R-NT2RP3002057//Human mRNA for KIAA0152 gene, comp
 lete cds//0.69:127:66//Hs.90438:D63486
 R-NT2RP3002062
 R-ntnnnnnnnnnnnn//ESTs//2.1e-113:552:97//Hs.9591:AA0
 69657
 R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:A
 A969139
 R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N591
 48
 R-NT2RP3002102
 R-NT2RP3002108

4108

R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA6
 25385
 R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:AI2
 49703
 R-NT2RP3002151//ESTs, Highly similar to G1 TO S P
 HASE TRANSITION PROTEIN 1 HOMOLOG [Homo sapiens]//
 6.2e-107:534:96//Hs.59523:AA602837
 R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA
 412293
 10 R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:AI0
 74024
 R-NT2RP3002166//ESTs//1.0:261:59//Hs.132817:AA5937
 13
 R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07
 120
 R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:AI1
 93598
 R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W7244
 6
 20 R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA13
 0588
 R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA43
 1672
 R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA7
 44743
 R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA7
 78171
 R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA
 836898
 30 R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA4
 18500
 R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PH
 ASE TRANSITION PROTEIN1 HOMOLOG [H.sapiens]//1.8e-
 19:136:87//Hs.106928:AI041737
 R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W256
 67
 R-NT2RP3002351//Homo sapiens 9G8 splicing factor m
 RNA, complete cds//0.0048:221:64//Hs.556:L41887
 R-NT2RP3002352//Homo sapiens mRNA for protein enco
 ded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.648
 3:Y16355
 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 pro
 tein, partial cds//1.5e-103:524:95//Hs.12707:AB014
 578
 R-NT2RP3002484//Human APRT gene for adenine phosph
 oribosyltransferase//0.54:108:71//Hs.28914:Y00486
 R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:N74
 185
 50 R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETIC
 AL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.ele

4109

gans]//3.2e-90:526:90//Hs.8083:AA521436
 R-NT2RP3002529//ESTs, Highly similar to PUTATIVE
 VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.
 O3C [Schizosaccharomyces pombe]//3.8e-101:497:96//
 Hs.6650:AA843246
 R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 pro
 tein, partial cds//1.1e-83:438:94//Hs.19542:AB0182
 72
 R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA19
 1673
 R-NT2RP3002566//Homo sapiens calcium-activated pot
 assium channel (KCNH3)mRNA, complete cds//0.14:18
 4:63//Hs.89230:AF031815
 R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, comple
 te cds//2.0e-18:138:78//Hs.129883:AB007880
 R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:AI
 243850
 R-NT2RP3002602//Homo sapiens stannin mRNA, complet
 e cds//5.5e-06:58:100//Hs.76691:AF070673
 R-NT2RP3002603
 R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA1
 92514
 R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA
 401365
 R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA
 708573
 R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA5
 25172
 R-NT2RP3002671//ESTs, Highly similar to ELONGATIO
 N FACTOR 2 [Drosophilamelanogaster]//5.9e-109:537:
 97//Hs.19348:AA151678
 R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA1
 15502
 R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA
 910871
 R-NT2RP3002688//ESTs, Weakly similar to !!!! ALU S
 UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-10
 1:524:95//Hs.32580:AI123601
 R-NT2RP3002701//EST//0.87:131:63//Hs.161916:AA4831
 69
 R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA
 160945
 R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA
 809159
 R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA52
 6973
 R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:AI
 376958
 R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71
 377

4110

R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA7752
 40
 R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:AI
 348080
 R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA9
 09678
 R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA0
 19641
 R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA6
 87262
 R-NT2RP3002877//Homo sapiens X-ray repair cross-co
 mplementing protein 2(XRCC2) mRNA, complete cds//
 8.1e-14:146:72//Hs.129727:AF035587
 R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 pro
 tein, partial cds//1.5e-110:570:95//Hs.6162:AB0183
 14
 R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:AI
 206286
 R-NT2RP3002948//EST//1.0:102:65//Hs.144730:AI19197
 20 5
 R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:A
 I201698
 R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0492//0.23:563:56//Hs.12733
 8:AB007961
 R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN
 -FATTY-ACID--COA LI GASE 1 [Saccharomyces cerevisia
 e]//2.0e-56:387:86//Hs.144597:W20143
 R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA47
 30 6850
 R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:A
 A252116
 R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:AI3
 60553
 R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA52
 4423
 R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS
 -RELATED POL POLYPROTEIN [Mus musculus]//3.0e-100:
 528:94//Hs.90353:N98551
 R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W0
 5355
 R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:AI1
 41912
 R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C.e
 legans]//5.9e-83:392:99//Hs.101364:AA534439
 R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA
 180809
 R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:AI35
 9466
 R-NT2RP3003101//EST//0.032:235:60//Hs.147920:AI202
 50

- 441
R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:AI03520
R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982
R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535:96//Hs.27437:AA004208
R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:AI271632
R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774
R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007
R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:AI131226
R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944
R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796
R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:AI422634
R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573
R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:N26107
R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229:93//Hs.17377:AI078151
R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:AI290343
R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628
R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960
R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061
R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983
R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:AI384035
R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055
R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818
R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:AI341261
R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:CO5931
R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AI4959
- A625445
R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:AI125289
R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993
R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102
R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:AI246155
R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567
R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272
R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721
R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H. sapiens]//2.2e-24:418:67//Hs.139488:AI124095
R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372
R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041
R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023
R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156
R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828
R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268
R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C. elegans]//4.0e-106:549:94//Hs.7886:AI057529
R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556
R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTC)n repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952
R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:AI123430
R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681
R-NT2RP3003564
R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:N48721
R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944
R-NT2RP3003589//EST//0.58:242:59//Hs.130804:AA894759

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R-NT2RP3003625//ESTs//7.6e-41:349:80//Hs.140608:N53448
 R-NT2RP3003656//Human LIM protein (LPP) mRNA, partial cds//0.26:222:60//Hs.17217:U49957
 R-NT2RP3003659//ESTs//2.0e-113:547:97//Hs.23389:AA769310
 R-NT2RP3003665//ESTs//1.6e-80:415:95//Hs.141084:H11714
 R-NT2RP3003672
 R-NT2RP3003686//ESTs//6.8e-114:552:97//Hs.43299:N2103036
 R-NT2RP3003701//ESTs//2.1e-16:282:66//Hs.115512:AI208768
 R-NT2RP3003716//ESTs//2.1e-45:195:91//Hs.41296:N71923
 R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds//5.6e-103:492:97//Hs.48513:AB018300
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:AI050863
 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:AI089747
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913
 R-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446
 R-NT2RP3003809//ESTs, Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:AI285198
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:W57627
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761
 R-NT2RP3003828//ESTs, Weakly similar to unknown [H. sapiens]//9.6e-98:511:95//Hs.26955:AI333224
 R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611
 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:AI332962
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170

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R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726
 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593
 R-NT2RP3004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142
 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714
 R-NT2RP3004041
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820
 R-NT2RP3004070//ESTs//5.5e-108:552:95//Hs.23392:AI310139
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W45387
 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:AI262104
 R-NT2RP3004095//ESTs//0.00013:93:78//Hs.36567:AA262045
 R-NT2RP3004110//ESTs, Weakly similar to similar to oxysterol-binding proteins: partial CDS [C. elegans]//3.5e-76:402:95//Hs.55847:W31092
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696
 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:AI183425
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:AI279093
 R-NT2RP3004206//ESTs, Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126
 R-NT2RP3004207//ESTs, Weakly similar to gene SEZ-6 [M. musculus]//1.1e-41:266:89//Hs.6314:AA522619
 R-NT2RP3004209//ESTs, Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:AI346680
 R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794
 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:N46252
 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA88

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00295
 R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N
 66569
 R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807
 257
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 pro
 tein, partial cds//1.5e-100:505:96//Hs.13999:AB014
 600
 R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA08
 1788
 R-NT2RP4000214//Human mRNA for KIAA0392 gene, part
 ial cds//6.2e-43:272:90//Hs.40100:AB002390
 R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA
 978185
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-as
 sociated protein (CASP)//2.9e-70:354:96//Hs.15548
 1:AJ006470
 R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA5
 02757
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRN
 A, complete sequence//9.3e-79:379:99//Hs.43728:AF0
 91092
 R-NT2RP4000263
 R-nnnnnnnnnnnn//ESTs, Weakly similar to similar to
 Achlya ambisexualis antheridiol steroid receptor
 [C.elegans]//4.7e-104:525:96//Hs.152069:AA548972
 R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:AI2
 71631
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequ
 ence//1.3e-109:513:99//Hs.13410:AF070524
 R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA
 192760
 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N8
 0390
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 pro
 tein, complete cds//7.6e-111:520:99//Hs.107479:AB0
 18281
 R-NT2RP4000367//Homo sapiens IkappaB kinase comple
 x associated protein (IKAP) mRNA, complete cds//2.
 8e-110:527:98//Hs.31323:AF044195
 R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:AI3
 01130
 R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA6
 04498
 R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W273
 76
 R-NT2RP4000415//ESTs, Weakly similar to coded for
 by C. elegans cDNA yk30b3.5 [C.elegans]//3.9e-87:4
 99:91//Hs.26156:AA630975
 R-NT2RP4000417//ESTs, Moderately similar to HYPOT

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HETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC R
 EGION [Saccharomyces cerevisiae]//8.9e-95:468:96//
 Hs.93871:AI191318
 R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:AI1
 89011
 R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60
 955
 R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:AI0
 37953
 10 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate
 receptor 2D subunit precursor (NMDAR2D) mRNA, comp
 lete cds//0.35:153:63//Hs.113286:U77783
 R-nnnnnnnnnnnn//ESTs//4.5e-89:455:96//Hs.62638:AA1
 27740
 R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:AI
 204167
 R-nnnnnnnnnnnn
 R-NT2RP4000500//ESTs, Weakly similar to HYPOTHETIC
 AL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME III [C.el
 egans]//1.2e-40:125:97//Hs.56124:AI424792
 R-NT2RP4000515//EST//6.7e-30:183:90//Hs.150710:AI1
 22713
 R-NT2RP4000517//Aldehyde dehydrogenase 7//7.5e-28:
 183:76//Hs.83155:U10868
 R-NT2RP4000518//EST//0.091:178:58//Hs.133031:AI049
 874
 R-NT2RP4000519
 R-NT2RP4000524//ESTs, Highly similar to rsec8 [R.n
 orvegicus]//3.4e-93:496:93//Hs.107394:H07126
 30 R-NT2RP4000528//EST//0.84:130:66//Hs.140208:AA7022
 13
 R-NT2RP4000541//EST//5.2e-63:337:94//Hs.156337:AI3
 37328
 R-NT2RP4000556//ESTs, Highly similar to 60S RIBOSO
 MAL PROTEIN L11 [R.norvegicus]//8.2e-92:448:98//H
 s.25597:H93026
 R-NT2RP4000588//ESTs//3.8e-94:445:98//Hs.44077:N28
 840
 R-NT2RP4000614//ESTs//6.5e-18:159:83//Hs.24549:N57
 263
 R-NT2RP4000638//ESTs//2.5e-46:296:87//Hs.132722:AA
 618531
 R-NT2RP4000648//ESTs//2.6e-103:559:93//Hs.23794:W8
 0393
 R-NT2RP4000657//ESTs//1.0:189:60//Hs.87073:AA97270
 4
 R-NT2RP4000704//ESTs//2.8e-101:509:96//Hs.84824:AA
 935651
 R-NT2RP4000724//ESTs//1.5e-83:442:94//Hs.142114:AA
 205615
 50

4119

R-NT2RP4000728//ESTs//0.84:61:75//Hs.145334:AI2513
 99
 R-NT2RP4000739//ESTs//8.8e-80:418:94//Hs.42959:N21
 211
 R-NT2RP4000781//ESTs//1.4e-79:376:99//Hs.135458:AI
 081312
 R-NT2RP4000817//Homo sapiens mRNA for KIAA0470 pro
 tein, complete cds//3.1e-106:550:94//Hs.25132:AB00
 7939
 R-NT2RP4000833//ESTs//5.8e-46:309:85//Hs.163979:AA 10
 828834
 R-NT2RP4000837//ESTs//1.7e-112:539:97//Hs.97718:AI
 334028
 R-NT2RP4000855//ESTs//1.1e-95:486:95//Hs.5345:AA98
 8104
 R-NT2RP4000865//EST//6.2e-68:412:89//Hs.142196:AA2
 58356
 R-NT2RP4000878//ESTs//1.9e-80:417:95//Hs.104716:AI
 023185
 R-NT2RP4000879//ESTs//1.8e-42:211:99//Hs.89991:AI 3 20
 74617
 R-nnnnnnnnnnnn//ESTs//1.2e-89:453:97//Hs.100182:N9
 2594
 R-nnnnnnnnnnnn//EST//9.4e-06:197:63//Hs.145970:AI2
 77106
 R-NT2RP4000925//ESTs, Weakly similar to KIAA0405
 [H. sapiens]//5.9e-17:134:85//Hs.14146:W92235
 R-nnnnnnnnnnnn//ESTs//4.3e-14:84:100//Hs.155360:AA
 984683
 R-NT2RP4000928//Homo sapiens CDP-diacylglycerol sy 30
 nthase 2 (CDS2) mRNA, partial cds//8.2e-108:548:95/
 /Hs.24812:AF069532
 R-NT2RP4000929//ESTs//1.3e-119:567:98//Hs.62717:AA
 044905
 R-NT2RP4000955//ESTs//3.5e-10:119:78//Hs.42946:N21
 111
 R-NT2RP4000973//ESTs//2.8e-05:93:69//Hs.155126:AA5
 63986
 R-NT2RP4000975//ESTs//4.4e-58:324:95//Hs.126070:AA
 045179
 R-NT2RP4000979//ESTs//3.5e-42:468:73//Hs.106210:AI
 193017
 R-NT2RP4000984//Homo sapiens clone 23770 mRNA sequ
 ence//8.7e-120:570:98//Hs.12457:AF052123
 R-NT2RP4000989//ESTs//1.3e-122:581:98//Hs.10499:AA
 528018
 R-NT2RP4000996//ESTs//9.2e-113:579:94//Hs.23762:N2
 6620
 R-NT2RP4000997//Homo sapiens neuronal thread prote
 in AD7c-NTP mRNA, complete cds//1.1e-28:439:68//H 50

4120

s.129735:AF010144
 R-NT2RP4001004//ESTs//3.6e-78:389:98//Hs.156290:AI
 016769
 R-NT2RP4001006//ESTs, Moderately similar to ORF2:
 function unknown [H. sapiens]//6.6e-124:574:99//Hs.
 47393:AA218858
 R-NT2RP4001010//EST//2.8e-31:194:90//Hs.161186:AI4
 18635
 R-NT2RP4001029//ESTs//4.4e-111:523:99//Hs.28423:AI
 336292
 R-NT2RP4001041//ESTs, Highly similar to LEUCYL-TR
 NA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisi
 ae]//3.6e-114:569:96//Hs.6762:AA088424
 R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partia
 l cds//2.0e-51:282:94//Hs.100955:AB007859
 R-NT2RP4001064//ESTs, Weakly similar to protein B
 [H. sapiens]//2.1e-103:485:99//Hs.10114:AI345945
 R-NT2RP4001078
 R-NT2RP4001079//Homo sapiens mRNA for putative Ca2
 +-transporting ATPase, partial//1.7e-119:569:98//H
 s.106778:AJ010953
 R-NT2RP4001080//ESTs//7.6e-10:65:100//Hs.131694:AA
 927668
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0592 pro
 tein, partial cds//5.9e-121:548:95//Hs.13273:AB011
 164
 R-NT2RP4001095//ESTs//1.5e-113:563:96//Hs.118732:A
 I344055
 R-NT2RP4001100//ESTs//2.0e-46:413:79//Hs.146314:R9
 9617
 R-NT2RP4001117//EST//7.4e-51:294:92//Hs.7260:T2373
 7
 R-NT2RP4001122//ESTs//5.4e-109:509:99//Hs.16390:AI
 052357
 R-NT2RP4001126//EST//0.97:169:61//Hs.148107:AA6934
 76
 R-NT2RP4001138//ESTs//3.0e-110:543:97//Hs.57655:AI
 056890
 R-NT2RP4001143//ESTs, Highly similar to HYPOTHETI
 CAL 52.9 KD PROTEIN INSAP155-YMR31 INTERGENIC REGI
 ON [Saccharomyces cerevisiae]//5.4e-113:573:96//H
 s.5249:U55977
 R-NT2RP4001148//ESTs//3.1e-103:490:98//Hs.121282:A
 I091453
 R-NT2RP4001149//EST//1.7e-50:281:93//Hs.101727:H16
 171
 R-NT2RP4001150//ESTs//1.9e-90:422:100//Hs.125490:A
 I138884
 R-NT2RP4001159
 R-NT2RP4001174//ESTs//2.5e-110:526:98//Hs.116555:A

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A639278
 R-nnnnnnnnnnnn/ESTs//1.1e-25:140:97//Hs.83756:AI0
 02822
 R-NT2RP4001207//ESTs//4.4e-70:432:89//Hs.13109:AA1
 92514
 R-NT2RP4001210//ESTs//1.4e-108:509:99//Hs.27021:AI
 359495
 R-NT2RP4001213//ESTs, Highly similar to ZINC FING
 ER PROTEIN 8 [Homo sapiens]//4.4e-123:624:95//Hs.2
 2744:AI379892
 R-NT2RP4001219//ESTs//0.0043:142:65//Hs.6733:AI160
 750
 R-NT2RP4001228//ESTs//4.9e-101:482:98//Hs.62684:AA
 806103
 R-NT2RP4001235//ESTs//3.7e-105:571:93//Hs.37706:AA
 005120
 R-NT2RP4001256//ESTs//1.1e-12:189:74//Hs.20621:W28
 255
 R-NT2RP4001260//EST//6.9e-05:313:61//Hs.116438:AA6
 48430
 R-NT2RP4001274//EST//0.0020:246:63//Hs.149955:AI28
 9933
 R-nnnnnnnnnnnn/ESTs//2.9e-34:213:91//Hs.43100:AA1
 86588
 R-NT2RP4001313
 R-NT2RP4001315//EST//6.1e-38:217:93//Hs.97832:AA40
 0892
 R-NT2RP4001339//ESTs//3.8e-91:430:99//Hs.34840:AI2
 79612
 R-NT2RP4001345//ESTs//5.3e-89:443:96//Hs.6770:AA97
 2732
 R-NT2RP4001351//ESTs//6.0e-78:394:97//Hs.102796:N7
 0837
 R-NT2RP4001353//ESTs//4.8e-06:90:82//Hs.7778:AA195
 616
 R-NT2RP4001372
 R-NT2RP4001373//ESTs, Weakly similar to HYPOTHETI
 CAL 48.8 KD PROTEIN INTRK2-MRS4 INTERGENIC REGION
 [Saccharomyces cerevisiae]//1.7e-108:546:96//Hs.32
 271:AA203680
 R-NT2RP4001375//ESTs//2.4e-19:155:87//Hs.62119:AA0
 43299
 R-NT2RP4001379//EST//4.4e-29:288:72//Hs.157848:AI3
 62501
 R-NT2RP4001389//ESTs, Highly similar to HYPOTHEI
 CAL 51.6 KD PROTEIN INPAP1-MRPL13 INTERGENIC REGIO
 N [Saccharomyces cerevisiae]//3.8e-79:438:93//Hs.2
 1938:W81045
 R-NT2RP4001407//ESTs//8.3e-112:541:97//Hs.22587:AA
 743132

4122

R-NT2RP4001414//ESTs//8.6e-18:117:90//Hs.90789:W27
 649
 R-NT2RP4001433//ESTs, Moderately similar to PROHB
 ITIN [H. sapiens]//1.6e-102:498:97//Hs.62386:AA5129
 48
 R-NT2RP4001442//ESTs//8.8e-104:489:99//Hs.101619:A
 I339433
 R-NT2RP4001447
 R-NT2RP4001474
 10 R-NT2RP4001483//ESTs//2.1e-100:528:92//Hs.17860:AA
 706655
 R-NT2RP4001498//ESTs//1.1e-97:470:98//Hs.95744:AI3
 92846
 R-NT2RP4001502//ESTs//6.7e-73:382:96//Hs.11874:N93
 511
 R-NT2RP4001507//ESTs//2.6e-57:302:96//Hs.65328:AA6
 25385
 R-NT2RP4001524//ESTs, Weakly similar to F13B12.1
 [C. elegans]//2.9e-107:546:96//Hs.5570:AI377863
 20 R-NT2RP4001529//ESTs//3.3e-112:524:99//Hs.28423:AI
 336292
 R-NT2RP4001547//ESTs, Weakly similar to NADH-UBIQU
 INONE OXIDOREDUCTASE CHAIN 5 [Paramecium tetraurel
 ia]//2.8e-120:566:98//Hs.108530:AA523928
 R-nnnnnnnnnnnn/ESTs, Weakly similar to CELL DIVIS
 ION CONTROL PROTEIN 68[S. cerevisiae]//1.4e-26:184:
 88//Hs.136189:AA133224
 R-NT2RP4001555//ESTs//1.1e-95:445:100//Hs.134403:A
 A677552
 30 R-NT2RP4001567//ESTs//2.8e-106:506:98//Hs.102708:A
 A292285
 R-NT2RP4001568//ESTs//6.4e-55:300:94//Hs.57442:N63
 437
 R-NT2RP4001571//ESTs//1.3e-114:556:97//Hs.30340:AA
 521251
 R-NT2RP4001574//ESTs//0.0035:120:67//Hs.96339:AA22
 5906
 R-NT2RP4001575
 R-NT2RP4001592//ESTs, Weakly similar to ISOLEUCYL-
 TRNA SYNTHETASE, MITOCHONDRIAL [S. cerevisiae]//8.7
 e-112:557:97//Hs.7558:AA526812
 R-NT2RP4001610//ESTs//6.2e-77:382:96//Hs.21543:AA1
 66776
 R-NT2RP4001614//ESTs//2.8e-117:565:98//Hs.9591:AA0
 69657
 R-NT2RP4001634//ESTs//2.0e-39:213:96//Hs.32360:AA5
 34737
 R-NT2RP4001638//Homo sapiens clone 23967 unknown m
 RNA, partial cds//1.7e-116:559:97//Hs.5332:AF00715

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R-NT2RP4001644//ESTs, Moderately similar to MNK1 [H. sapiens]//5.3e-36:192:97//Hs.5662:AA868361
 R-NT2RP4001656//ESTs, Highly similar to HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOME II [Caenorhabditis elegans]//1.1e-104:525:96//Hs.20472:W28734
 R-NT2RP4001677//ESTs//1.8e-106:522:97//Hs.106390:AA156805
 R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence//5.7e-118:583:96//Hs.15562:U96629
 R-NT2RP4001725//ESTs//2.0e-11:141:74//Hs.117589:N25941
 R-nnnnnnnnnnnn//ESTs, Weakly similar to UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D. melanogaster]//3.4e-73:362:97//Hs.152332:AI141922
 R-NT2RP4001739//ESTs//6.6e-59:340:91//Hs.122293:AA843692
 R-NT2RP4001753//Zinc finger protein 3 (A8-51)//5.6e-113:552:96//Hs.2481:X78926
 R-NT2RP4001760//ESTs//2.5e-94:453:98//Hs.122579:AA766315
 R-NT2RP4001790//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H. sapiens]//2.0e-62:326:94//Hs.110839:W28098
 R-NT2RP4001803
 R-NT2RP4001822//ESTs//4.4e-98:526:92//Hs.96908:AI161133
 R-NT2RP4001823//ESTs//1.7e-72:357:97//Hs.144900:AI218434
 R-NT2RP4001828//ESTs//3.3e-101:536:92//Hs.18851:AA857826
 R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663
 R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-34:212:88//Hs.154326:D42087
 R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79602
 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:AI345528
 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:AI018606
 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:AI417099
 R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848
 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436

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R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:AI341793
 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)/2.3e-62:310:82//Hs.73919:X81637
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D. melanogaster]//8.3e-87:457:94//Hs.41793:AA775879
 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252
 R-NT2RP4002018
 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA [Pseudomonas fluorescens]//4.7e-09:90:86//Hs.41127:AA555184
 R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738
 R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106
 R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:AI284198
 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [Homo sapiens]//1.6e-61:464:82//Hs.144228:N99507
 R-nnnnnnnnnnnn//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME II [C. elegans]//2.3e-56:271:100//Hs.6185:AA428565
 R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407
 R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592
 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555
 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPEPTIDE [Avian spleen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272
 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds//2.8e-115:605:94//Hs.108258:AB007934
 R-OVARC1000004
 R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:AI126929
 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273
 R-OVARC1000017
 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:AI07

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 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//3.8e-46:331:83//Hs.96247:X95073
 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367
 R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R67871
 R-OVARC1000085//Proteasome component C5//8.6e-67:31066:92//Hs.75748:AL031259
 R-nnnnnnnnnnnn//ESTs//1.0e-111:526:98//Hs.129020:AL380703
 R-OVARC1000091//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sapiens]//3.9e-112:596:94//Hs.20597:W58370
 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:AI289942
 R-OVARC1000106
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250
 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7e-45:489:74//Hs.101238:Y11312
 R-OVARC1000133//EST//0.0028:284:61//Hs.30547:H05482
 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:AI333214
 R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090
 R-OVARC1000151
 R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023
 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629
 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-44:339:81//Hs.154103:AF061258
 R-OVARC1000209//ESTs, Mod 50

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erately similar to ZINC FINGER PROTEIN 93 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864
 R-OVARC1000212//EST//0.20:178:61//Hs.133031:AI049874
 R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958
 R-OVARC1000241//EST//0.0018:115:68//Hs.150728:AI123130
 R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROTEIN INCDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.3e-74:403:93//Hs.108117:AI097079
 R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476
 R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROTEIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:AI027777
 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449
 R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743
 R-OVARC1000326//ESTs, Moderately similar to lamina associated polypeptide 1 C [R.norvegicus]//1.3e-98:488:96//Hs.125749:AI377682
 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:AI050863
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA03423
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:CO5928
 R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219

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|---|---|
| R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-27:211:79//Hs.108287:L27670 | R-OVARC1000605 |
| R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237 | R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.4e-47:417:77//Hs.159897:AB007970 |
| R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034 | R-OVARC1000640//H.sapiens mRNA for translin associated protein X//1.9e-28:366:72//Hs.96247:X95073 |
| R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:AI123426 | R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//5.1e-31:162:100//Hs.111862:AB011162 |
| R-OVARC1000437 | R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480 |
| R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:AI018671 | R-nnnnnnnnnnnnn//ESTs//0.94:416:59//Hs.130754:AA279522 |
| R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.3e-45:320:84//Hs.73614:U83460 | R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:AI032875 |
| R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds//3.6e-79:418:94//Hs.12334:AB014583 | R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.053:160:64//Hs.108447:AJ000517 |
| R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582 | R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:141:73//Hs.32511:AB007901 |
| R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576 | R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:BA7461 |
| R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:AI421211 | R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:AI141736 |
| R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926 | R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918 |
| R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1e-102:514:96//Hs.11833:AI299947 | R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//4.6e-28:430:69//Hs.42457:AA523306 |
| R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983 | R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016 |
| R-OVARC1000496 | R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793 |
| R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484 | R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659 |
| R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:87//Hs.155464:AF088219 | R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-19:119:95//Hs.3069:L11066 |
| R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]//8.5e-48:264:92//Hs.49860:AA702248 | R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:AI419764 |
| R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021 | R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC//1.2e-106:536:95//Hs.61628:Y17711 |
| R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:202:85//Hs.90859:X85106 | R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87//Hs.73919:X81637 |
| R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:AI244285 | R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:579:96//Hs.18910:AF045584 |
| R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:AI141587 | R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096 |
| R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627 | R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:AI150674 |
| R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:84//Hs.155464:AF088219 | |
| R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053 | |

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R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:AI336292
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTASE INROCC-PTA INTERGENIC REGION [Bacillus subtilis]//7.9e-98:525:93//Hs.10366:W21953
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401
 R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA10873350
 R-OVARC1000912
 R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814
 R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127
 R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696
 R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215
 R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794
 R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971
 R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219
 R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394
 R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909
 R-OVARC1000984//ESTs, Weakly similar to No definition line found [C.elegans]//3.5e-68:346:96//Hs.25544:AA532784
 R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811
 R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874
 R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:N53448
 R-OVARC1001004//Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629
 R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270
 R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117
 R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630
 R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1 50

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e-09:137:74//Hs.77579:AF013263
 R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149
 R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046
 R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:N94384
 R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962
 R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:H99231
 R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:N98652
 R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:AF082657
 R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844
 R-OVARC1001074
 20 R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029
 R-OVARC1001092//Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897
 R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:AF051782
 R-OVARC1001117//Human G protein-coupled receptor (STR122) mRNA, complete cds//3.9e-37:283:84//Hs.46468:U45984
 R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548
 R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312
 R-OVARC1001161//ESTs, Moderately similar to !!!! A LU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//2.2e-66:346:95//Hs.53263:AA173226
 R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223
 R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727
 R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200
 R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219
 R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223
 R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:80

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//Hs. 97203: U83171
 R-OVARC1001188//ESTs//4.1e-18: 296: 69//Hs. 139197: AA
 228343
 R-OVARC1001200//ESTs//2.0e-28: 207: 85//Hs. 35121: AA8
 77826
 R-OVARC1001232//ESTs//3.2e-61: 358: 91//Hs. 6449: W950
 25
 R-OVARC1001240//ESTs//6.7e-45: 316: 85//Hs. 121675: AA
 629668
 R-OVARC1001243//ESTs//2.3e-86: 409: 99//Hs. 163091: AA 10
 742361
 R-OVARC1001261//ESTs//0.63: 125: 64//Hs. 155743: AI 344
 166
 R-OVARC1001268//ESTs//8.1e-20: 113: 98//Hs. 109477: AA
 477929
 R-OVARC1001270//ESTs//1.5e-107: 530: 97//Hs. 62905: AA
 460708
 R-OVARC1001271//ESTs//4.5e-36: 401: 72//Hs. 20190: AA5
 25532
 R-OVARC1001282//EST//4.0e-91: 428: 99//Hs. 145599: AI 2 20
 63113
 R-OVARC1001296//ESTs//2.6e-63: 301: 100//Hs. 125753: A
 A740885
 R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0518 pro
 tein, partial cds//3.8e-70: 334: 100//Hs. 23763: AB011
 090
 R-OVARC1001329//Clathrin, light polypeptide (Lcb)/
 /1.3e-68: 304: 83//Hs. 73919: X81637
 R-OVARC1001330//Proline arginine-rich end leucine-
 rich repeat protein//1.0: 147: 63//Hs. 76494: U41344
 R-OVARC1001339//Small inducible cytokine A5 (RANTE
 S)//5.0e-48: 452: 76//Hs. 155464: AF088219
 R-OVARC1001341//ESTs, Moderately similar to !!!! A
 LU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]//6.
 9e-85: 464: 93//Hs. 23651: AA650356
 R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-11
 0: 568: 95//Hs. 118690: X67247
 R-OVARC1001344//EST//3.6e-44: 341: 81//Hs. 162197: AA5
 35216
 R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-
 44: 250: 93//Hs. 3337: M90657
 R-OVARC1001360//ESTs//5.2e-110: 534: 98//Hs. 24743: AA
 843844
 R-OVARC1001369//ESTs//1.7e-98: 478: 97//Hs. 7729: AA83
 0777
 R-OVARC1001372//ESTs//2.6e-97: 456: 99//Hs. 153648: AI
 341415
 R-OVARC1001376//Homo sapiens mRNA for KIAA0575 pro
 tein, complete cds//1.1e-53: 344: 72//Hs. 153468: AB01
 1147

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R-OVARC1001381//ESTs//5.1e-19: 200: 66//Hs. 114031: AA
 700958
 R-OVARC1001391
 R-nnnnnnnnnnnn//ESTs//0.0039: 48: 95//Hs. 117964: N209
 13
 R-OVARC1001417//Homo sapiens EXLW1 mRNA, complete
 cds//3.2e-111: 561: 95//Hs. 21586: AB006651
 R-OVARC1001419
 R-OVARC1001425//EST//5.7e-20: 395: 66//Hs. 159707: AI 3
 93136
 R-OVARC1001436//ESTs//9.6e-90: 427: 99//Hs. 6982: AA62
 2427
 R-OVARC1001442//ESTs//1.1e-66: 317: 100//Hs. 18437: AI
 206345
 R-OVARC1001453//ESTs//2.0e-20: 163: 84//Hs. 133503: AA
 628592
 R-OVARC1001476//EST//0.23: 125: 66//Hs. 71444: AA13170
 0
 R-OVARC1001480//ESTs//3.1e-56: 181: 97//Hs. 40109: AA9
 28694
 R-OVARC1001489//ESTs//1.0: 297: 58//Hs. 86723: AA39308
 9
 R-OVARC1001496//Homo sapiens C-terminal binding pr
 otein 2 mRNA, complete cds//3.0e-117: 585: 96//Hs. 653
 4: AF016507
 R-OVARC1001506//Small inducible cytokine A5 (RANTE
 S)//1.8e-48: 283: 90//Hs. 155464: AF088219
 R-OVARC1001525//EST//0.80: 170: 60//Hs. 157398: AI 3645
 39
 R-OVARC1001542//Homo sapiens hJTB mRNA, complete c
 ds//1.6e-111: 566: 95//Hs. 6396: AB016492
 R-OVARC1001547//ESTs//5.7e-105: 564: 93//Hs. 68835: AA
 088388
 R-OVARC1001577//Homo sapiens SRp46 splicing factor
 retropseudogene mRNA//4.4e-20: 150: 89//Hs. 155160: A
 F031166
 R-OVARC1001600//Human mRNA for KIAA0118 gene, part
 ial cds//8.6e-21: 282: 72//Hs. 154326: D42087
 R-OVARC1001610//ESTs//4.6e-108: 555: 95//Hs. 44295: N3
 2019
 R-OVARC1001611//ESTs//0.0021: 117: 71//Hs. 135568: AA9
 72965
 R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partia
 l cds//9.2e-19: 114: 78//Hs. 5158: AB007869
 R-OVARC1001668//ESTs//1.0: 127: 69//Hs. 153290: AI 0226
 59
 R-OVARC1001702//ESTs//4.8e-44: 225: 97//Hs. 96855: AA3
 46854
 R-OVARC1001703//ESTs//2.3e-89: 426: 99//Hs. 27099: W60
 50 080

4133

R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784
 R-OVARC1001726//ESTs, Highly similar to APICAL PR
 OTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:AA
 A046954
 R-OVARC1001731//Tropomyosin 4 (fibroblast)//7.9e-7
 4:422:90//Hs.102824:X05276
 R-OVARC1001745//Human mRNA for tryptophan hydroxyl
 ase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:AF05
 7280
 R-nnnnnnnnnnnnn//ESTs, Weakly similar to N-TERMINAL
 ACETYLTRANSFERASE 1 [S.cerevisiae]//6.8e-100:540:
 92//Hs.117741:AA903456
 R-OVARC1001766//Homo sapiens eukaryotic translatio
 n initiation factor eIF3, p35 subunit mRNA, comple
 te cds//1.1e-109:567:94//Hs.155377:U97670
 R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0675 pro
 tein, complete cds//2.0e-109:529:97//Hs.15869:AB01
 4575
 R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H6
 6127
 R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA1
 60604
 R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA1
 56978
 R-OVARC1001802//Homo sapiens DEC-205 mRNA, complet
 e cds//4.8e-36:276:81//Hs.153563:AF011333
 R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI
 374688
 R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA6
 04831
 R-OVARC1001813//Homo sapiens mRNA for KIAA0538 pro
 tein, partial cds//2.1e-15:519:63//Hs.25639:AB0111
 10
 R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:W5
 2705
 R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI3746
 21
 R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242
 160
 R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:N31
 809
 R-OVARC1001873//Homo sapiens clones 24718 and 2482
 5 mRNA sequence//1.9e-105:571:91//Hs.25300:AF07061
 1
 R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA6
 30476
 R-OVARC1001880//Homo sapiens mRNA for KIAA0575 pro
 tein, complete cds//2.2e-49:302:90//Hs.153468:AB01
 1147

4134

R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA
 447310
 R-OVARC1001900//Homo sapiens tumorous imaginal dis
 cs protein Tid56 homolog (TID1) mRNA, complete cds
 //1.6e-87:346:90//Hs.6216:AF061749
 R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA
 904435
 R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73
 855
 10 R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97
 842
 R-OVARC1001928
 R-OVARC1001942//ESTs, Weakly similar to N-TERMINAL
 ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:8
 8//Hs.117741:AA903456
 R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W3
 8637
 R-OVARC1001949//ESTs, Highly similar to ZINC FING
 ER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22
 744:AI379892
 20 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:AI0
 32875
 R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:AI1
 83729
 R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA
 935887
 R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA
 618531
 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 pro
 tein, partial cds//4.4e-109:542:96//Hs.108258:AB00
 7934
 R-OVARC1002066//ESTs//8.5e-97:455:99//Hs.135477:AI
 088556
 R-OVARC1002082//Homo sapiens mRNA for KIAA0772 pro
 tein, complete cds//8.1e-47:340:82//Hs.15519:AB018
 315
 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:A
 A629860
 R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:AI
 347130
 40 R-OVARC1002138//ESTs, Weakly similar to HYPOTHETIC
 AL 54.7 KD PROTEIN C07A9.1 IN CHROMOSOME III [Caen
 orhabditis elegans]//1.7e-102:485:98//Hs.137516:AA
 805691
 R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W2
 6825
 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA4
 78923
 R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA9
 08631
 50

4136

[illegible]

4137

binding protein 1, interferon-inducible, 67kD//6.1e-79:542:82//Hs. 62661:M55542

R-PLACE1000596//ESTs//0.0
028:364:59//Hs. 106090:AA4
57030

R-PLACE1000599//Human mRNA
A for KIAA0118 gene, partial cds//4.3e-49:295:90//
Hs.154326:D42087

```
R-PLACE1000610//ESTs//0.0
010:104:74//Hs.17413:N453
01
```

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R-PLACE1000636//ESTs//1.8
e-64:340:95//Hs.100895:AA
479308
```

R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265

R-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))//1.4e-102:559:92//Hs.29595:AJ005896

R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1)mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353

R-PLACE1000712//ESTs//7.8
e-60:317:95//Hs.8245:AA11
5485

R-PLACE1000716

R-PLACE1000748//ESTs//8.9
c-87:466:93//Hs. 25245:AA1
76701

R-PLACE1000749//EST//0.01
9:186:61//Hs.135443:A1077
396

R-PLACE1000755//ESTs, Weakly similar to HYPOTHETICAL HELICASE K12H4.8 INCHROMOSOME III [C. elegans]//3.9e-40:224:94//Hs.87889:

4138

AA262008

R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:531:66//Hs.133342:AF070536

R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds//8.5e-103:513:96//Hs.31921:AB014548

R-PLACE1000786//ESTs//5.2
e-93:449:97//Hs. 58389:W74
482

R-nnnnnnnnnnnnnnn//H. sapiens
mRNA for chemokine HCC-1
//0.88:201:60//Hs.20144:A
F088219

R-PLACE1000798//ESTs//1.1
e-97:508:94//Hs.139119:N3
2189

R-PLACE1000841//ESTs, Highly similar to guanine nucleotide regulatory protein [H.sapiens]//7.7e-31:20:86/Hs.117576:R33135

R-nnnnnnnnnnnn//ESTs//1.8e-87:459:94//Es.43100:AA1
86588

R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:AI2
75039

R-PLACE1000863//ESTs, Highly similar to PUTATIVE
40S RIBOSOMAL PROTEIN YHR148W [Saccharomyces cerevi
siae]/2.2e-92; 467: 95/Hs.6118:AI141558

R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:AI3
92846

R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:AI0
97091

R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA60
8697

R-PLACE1000972//EST//3. 3e-24; 264: 74//Hs. 130321: AI 0
02941

R-PLACE1000977//EST//0.085:153:65//Hs.131646:AI025
689

R-PLACE1000979

R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA
810725

R-PLACE1001007//ESTs. Moderately similar to MNK1 [H. sapiens]//5.2e-63;343:93//Hs.5662:AA868361

R-PLACE1001010//EST//0.96:53:71//Es.96973:AA351146
R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71/

/Hs. 2820: X64878

R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA40
4736

4139

R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:AI025762
 R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120
 R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124
 R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580
 R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.035:259:59//Hs.31575:AF100141
 R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268
 R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610
 R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594
 R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834
 R-PLACE1001171//ESTs, Highly similar to CYTOCHROME B-245 LIGHT CHAIN [H.sapiens]//0.91:77:71//Hs.115211:AA287527
 R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297
 R-PLACE1001238//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//1.9e-99:512:94//Hs.24884:AA176812
 R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:AI073464
 R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
 R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
 R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
 R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:AI334460
 R-PLACE1001294//ESTs, Moderately similar to GAMETO GENESIS EXPRESSED PROTEIN GEG-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548
 R-PLACE1001304//ESTs, Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:W27601
 R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:AI339056
 R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mRNA, complete cds//5.5e-44:215:86//Hs.50984:U01160
 R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:AI097077
 R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219

4140

R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615
 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030
 R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419
 R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:AI298280
 R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555
 R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087
 R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800
 R-PLACE1001440
 R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115
 R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:AI017547
 R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:AI248625
 R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617
 R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361
 R-PLACE1001517//Homo sapiens hCAA1 mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969
 R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:AI042153
 R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265
 R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431
 R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249
 R-PLACE1001602//EST//0.33:297:57//Hs.149839:AI287601
 R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904
 R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174
 R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.1

- 14547:AA167095
R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:AI16
8526
R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61
640
R-PLACE1001672//ESTs, Moderately similar to !!!! A
LU SUBFAMILY J WARNINGENTRY !!!! [H.sapiens]//0.9
8:141:62//Hs.153060:AA195804
R-PLACE1001691//Homo sapiens okadaic acid-inducibl
e phosphoprotein (OA48-18) mRNA, complete cds//4.7 10
e-113:545:97//Hs.3688:AF069250
R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA6
79124
R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:AI3
74903
R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA9836
67
R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA0
10993
R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA 20
282171
R-PLACE1001739//ESTs, Weakly similar to P68 PROTEI
N [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113
R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA6
44266
R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA
236479
R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:AI
423937
R-PLACE1001748//Homo sapiens metalloprotease 1 (MP 30
1) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF0
61243
R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N6466
2
R-PLACE1001761
R-PLACE1001771//ESTs//0.92:165:62//Hs.47387:N51980
R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA0
81236
R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA8
07352
R-PLACE1001817//Homo sapiens ATP-specific succinyl
-CoA synthetase beta subunit (SCS) mRNA, partial c
ds//1.3e-93:463:95//Hs.40820:AF058953
R-PLACE1001821//Small inducible cytokine A5 (RANTE
S)//2.7e-35:328:75//Hs.155464:AF088219
R-PLACE1001845
R-PLACE1001869//EST//1.0:207:62//Hs.137298:W32868
R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H500
09
R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA 50
- 789098
R-PLACE1001920//Homo sapiens TNF-induced protein G
G2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:
AF099936
R-PLACE1001928//Homo sapiens mRNA for KIAA0623 pro
tein, complete cds//0.85:130:66//Hs.151406:AB01452
3
R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA
007313
R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA
171941
R-PLACE1002046
R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N325
95
R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA
543094
R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809
619
R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:AI0
28552
R-PLACE1002090//ESTs//6.3e-73:361:96//Hs.134469:AA
731632
R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R2
3311
R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA5
21293
R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W9
1937
R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:AI16
7614
R-PLACE1002157//EST, Weakly similar to LINE-1 REVE
RSE TRANSCRIPTASE HOMOLOG [H.sapiens]//3.6e-39:40
0:76//Hs.162172:AA534189
R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:AI
185965
R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA1
43745
R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48
793
R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA
410788
R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N498
92
R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:AI0
04257
R-PLACE1002259//Human Line-1 repeat mRNA with 2 op
en reading frames//5.8e-67:501:81//Hs.23094:M19503
R-PLACE1002319//ESTs//1.4e-28:178:92//Hs.7353:AA20
9308
R-PLACE1002342//Homo sapiens mRNA for KIAA0728 pro

- tein, partial cds//1.6e-95:501:93//Hs.18277:AB018271
 R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291
 R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381
 R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959
 R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110
 R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804
 R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333
 R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320
 R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263
 R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132
 R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273
 R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429
 R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869
 R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:AI140609
 R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256
 R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1//2.7e-19:116:93//Hs.99348:AC004774
 R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491
 R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437
 R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131
 R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:AI339738
 R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778
 R-PLACE1002598//ESTs, Highly similar to PROTEIN H11715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208
 R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA 50
 632147
 R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749
 R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130
 R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180
 10 R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:H19830
 R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586
 R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:H12865
 R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:AI334099
 R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:AI20149014
 R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
 R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
 R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:AI304392
 R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
 R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094
 R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
 R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:AI096756
 R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
 R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:AI066762
 40 R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:AI249332
 R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
 R-PLACE1002962
 R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
 R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
 R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-8

4145

6: 502: 89//Hs. 32232: AA604268
 R-PLACE1002996//ESTs//1.9e-44: 218: 100//Hs. 63657: AI
 144268
 R-PLACE1003025//ESTs//8.4e-104: 517: 96//Hs. 10711: AI
 151499
 R-PLACE1003027//Human mRNA for KIAA0238 gene, part
 ial cds//0.97: 156: 60//Hs. 82042: D87075
 R-PLACE1003044//Human onconeural ventral antigen-1
 (Nova-1) mRNA, complete cds//1.0: 200: 63//Hs. 214: U
 04840
 R-PLACE1003092//ESTs//0.0046: 267: 60//Hs. 133095: AA9
 27777
 R-PLACE1003100//ESTs, Highly similar to NODULATIO
 N PROTEIN C [Rhizobiummeliloti]//9.5e-94: 491: 93//H
 s. 6318: AI131178
 R-PLACE1003108//ESTs//0.00065: 184: 66//Hs. 154366: AA
 527359
 R-PLACE1003136//Signal recognition particle 54 kD
 protein//0.057: 317: 59//Hs. 49346: U51920
 R-PLACE1003145//ESTs//1.9e-98: 534: 92//Hs. 61929: AA0
 44757
 R-PLACE1003153//ESTs//5.8e-76: 367: 98//Hs. 105196: AA
 483467
 R-PLACE1003174//ESTs//1.7e-44: 226: 98//Hs. 59688: AA4
 53924
 R-PLACE1003176
 R-PLACE1003190//ESTs//1.6e-74: 356: 99//Hs. 121282: AI
 091453
 R-PLACE1003200//ESTs//4.6e-93: 461: 96//Hs. 24321: AA9
 71017
 R-PLACE1003205//ESTs//0.037: 171: 61//Hs. 157077: H448
 02
 R-PLACE1003238//ESTs, Weakly similar to KIAA0001
 [H. sapiens]//2.5e-82: 436: 94//Hs. 58561: W79123
 R-PLACE1003249//Human high-affinity copper uptake
 protein (hCTR1) mRNA, complete cds//7.9e-44: 313: 84/
 /Hs. 73614: U83460
 R-PLACE1003256//EST//9.6e-46: 284: 88//Hs. 162404: AA5
 73131
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU S 40
 UBFAMILY J WARNING ENTRY !!!! [H. sapiens]//8.3e-10
 2: 551: 92//Hs. 52431: AA625326
 R-PLACE1003296//ESTs//1.9e-88: 451: 96//Hs. 57749: W92
 986
 R-PLACE1003302//ESTs, Highly similar to ZINC FING
 ER PROTEIN 43 [Homo sapiens]//8.2e-93: 458: 96//Hs. 2
 9147: AA883993
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU C
 LASS B WARNING ENTRY !!!! [H. sapiens]//3.3e-94: 46
 3: 97//Hs. 155050: AA908765

4146

R-PLACE1003342//ESTs//6.0e-88: 447: 96//Hs. 107527: R6
 6438
 R-PLACE1003343//EST//0.0087: 412: 58//Hs. 159963: AA97
 7701
 R-PLACE1003353//Homo sapiens breast cancer antiest
 rogen resistance 3 protein (BCAR3) mRNA, complete
 cds//1.1e-99: 469: 98//Hs. 6564: U92715
 R-PLACE1003361//ESTs//3.5e-64: 332: 95//Hs. 163861: AI
 199636
 10 R-PLACE1003366//ESTs//1.0e-87: 492: 92//Hs. 72222: AA1
 58234
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4
 [C. elegans]//3.5e-18: 109: 95//Hs. 27670: AI051591
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 pro
 tein, partial cds//2.6e-54: 279: 80//Hs. 6874: AB00794
 1
 R-PLACE1003375//ESTs//1.7e-88: 431: 97//Hs. 41327: AI0
 39909
 R-PLACE1003383//ESTs//0.00084: 177: 64//Hs. 120695: AI
 377755
 R-PLACE1003401//ESTs//1.1e-16: 147: 80//Hs. 132187: AI
 039020
 R-PLACE1003420//ESTs//1.4e-93: 481: 94//Hs. 122565: AI
 126840
 R-PLACE1003454//ESTs//4.0e-57: 310: 93//Hs. 121688: AA
 743697
 R-PLACE1003478//EST//1.0: 162: 63//Hs. 147003: AI18467
 1
 R-PLACE1003493//ESTs//1.2e-73: 383: 95//Hs. 28852: R64
 270
 30 R-PLACE1003516//ESTs//3.2e-23: 206: 80//Hs. 138632: H9
 7952
 R-PLACE1003519//H. sapiens hnRNP-E1 mRNA//1.7e-22: 2
 36: 79//Hs. 2853: Z29505
 R-PLACE1003521//ESTs//5.8e-74: 371: 96//Hs. 30818: AA1
 94980
 R-PLACE1003528//ESTs//1.1e-40: 219: 82//Hs. 138856: H4
 7461
 R-PLACE1003537//ESTs, Weakly similar to multispann
 ing membrane protein [H. sapiens]//7.4e-69: 338: 98//
 Hs. 110439: N93209
 R-PLACE1003553//ESTs//2.2e-87: 438: 97//Hs. 132022: AI
 040321
 R-PLACE1003566//ESTs//1.2e-62: 298: 92//Hs. 30799: AI0
 52591
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 sp
 ecific transcript KIAA0487//2.4e-22: 145: 80//Hs. 923
 81: AB007956
 R-PLACE1003583//ESTs, Weakly similar to hypothetic
 al L1 protein [H. sapiens]//1.5e-14: 264: 65//Hs. 1582

- 53: R86178
 R-PLACE1003584
 R-PLACE1003592//ESTs//1.3e-15: 213: 69//Hs. 139507: T7
 7542
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene
 product [H. sapiens]//5.8e-75: 459: 89//Hs. 23884: AI37
 7106
 R-PLACE1003596//ESTs//0.011: 273: 61//Hs. 71719: AA142
 875
 R-PLACE1003602//Homo sapiens mRNA expressed in pla 10
 centa//7.8e-97: 576: 88//Hs. 56851: D83200
 R-PLACE1003605//ESTs//3.7e-86: 407: 99//Hs. 136057: AA
 988299
 R-nnnnnnnnnnnnn//ESTs//1.0: 78: 71//Hs. 101248: T26446
 R-PLACE1003618//ESTs//6.8e-30: 281: 79//Hs. 114455: AA
 411943
 R-PLACE1003625//ESTs//7.2e-78: 377: 98//Hs. 102708: AA
 292285
 R-PLACE1003638//ESTs//6.7e-38: 274: 82//Hs. 138852: AA
 284247
 R-PLACE1003669//ESTs//9.7e-83: 418: 95//Hs. 4842: AI34
 2607
 R-PLACE1003704//ESTs//3.0e-13: 99: 89//Hs. 81648: W265
 21
 R-PLACE1003709//ESTs//0.019: 178: 60//Hs. 32100: N5986
 6
 R-PLACE1003711//ESTs//0.99: 126: 63//Hs. 47005: N98639
 R-PLACE1003723//ESTs//1.7e-89: 448: 96//Hs. 157222: AA
 766987
 R-PLACE1003738//ESTs//2.5e-36: 182: 100//Hs. 122162: A 30
 I057087
 R-PLACE1003760//Human globin gene//1.9e-98: 538: 91/
 /Hs. 100090: W69023
 R-PLACE1003762//EST//2.9e-15: 125: 85//Hs. 162083: AA4
 87512
 R-PLACE1003768//Human P042 gene, complete cds//3.1
 e-18: 300: 69//Hs. 158302: U88965
 R-PLACE1003771//ESTs//1.2e-09: 64: 100//Hs. 23799: AI0
 03798
 R-PLACE1003783//ESTs, Weakly similar to D2085.5 40
 [C. elegans]//3.8e-38: 199: 97//Hs. 115197: AA215757
 R-PLACE1003784//ESTs//3.7e-87: 428: 97//Hs. 157985: AI
 366909
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 pro
 tein, complete cds//3.2e-36: 236: 88//Hs. 153468: AB01
 1147
 R-PLACE1003833//ESTs, Moderately similar to !!!! A
 LU SUBFAMILY SC WARNING ENTRY !!!! [H. sapiens]//8.
 5e-62: 313: 96//Hs. 121020: AA526092
 R-PLACE1003850//ESTs//4.0e-67: 351: 96//Hs. 159303: T9 50
- 1059
 R-PLACE1003858//ESTs//0.96: 87: 66//Hs. 107112: AA6790
 58
 R-nnnnnnnnnnnnn
 R-PLACE1003870//EST//2.9e-34: 281: 79//Hs. 160895: AI3
 65871
 R-nnnnnnnnnnnnn
 R-PLACE1003886//ESTs//6.7e-85: 410: 97//Hs. 25129: W93
 595
 R-PLACE1003888//ESTs//0.0085: 165: 64//Hs. 96739: AA44
 1915
 R-PLACE1003900//EST//2.4e-05: 129: 69//Hs. 127931: AA9
 69259
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTH
 ASE [Homo sapiens]//1.5e-54: 282: 96//Hs. 58553: AA100
 804
 R-PLACE1003915//EST//0.87: 55: 76//Hs. 145930: AI27576
 0
 R-PLACE1003923//ESTs//1.7e-89: 456: 95//Hs. 14125: AA1
 56236
 R-PLACE1003932//ESTs//3.0e-50: 340: 84//Hs. 151208: AI
 126110
 R-PLACE1003936//EST//1.8e-08: 208: 65//Hs. 162656: AA6
 03567
 R-PLACE1003968//ESTs//7.4e-49: 301: 90//Hs. 93850: AA1
 15330
 R-PLACE1004104//ESTs//1.9e-46: 254: 94//Hs. 96802: AA4
 43231
 R-PLACE1004114//ESTs//1.2e-64: 322: 97//Hs. 28928: AI0
 52052
 R-PLACE1004118//ESTs//1.0e-83: 404: 98//Hs. 112764: AA
 609770
 R-PLACE1004128//ESTs//5.3e-80: 415: 95//Hs. 11835: AA0
 40244
 R-PLACE1004149//ESTs//7.2e-25: 331: 72//Hs. 141084: H1
 1714
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, co
 mplete cds//2.0e-56: 491: 76//Hs. 113283: AF018080
 R-PLACE1004161//ESTs//2.0e-59: 355: 88//Hs. 13830: AA9
 18601
 R-PLACE1004183//Homo sapiens cytochrome c oxidase
 assembly protein COX11(COX11) mRNA, complete cds//
 4.7e-78: 434: 91//Hs. 153504: AF044321
 R-PLACE1004197
 R-PLACE1004203//Homo sapiens GPI-anchored membrane
 protein CDw108 precursor, mRNA, complete cds//1.5
 e-105: 501: 98//Hs. 24640: AF069493
 R-PLACE1004242//ESTs//1.0e-71: 364: 87//Hs. 138632: H9
 7952
 R-PLACE1004256//EST//0.0011: 347: 61//Hs. 131385: AI02

2630
R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA39820
9
R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//
0.72:180:63//Hs.117729:J00124
R-PLACE1004270//ESTs//0.011:264:59//Hs.110044:AA18
1800
R-PLACE1004274//Human retinoic acid receptor-beta
associated open reading frame, complete sequence//
0.28:121:66//Hs.1938:S82362
R-PLACE1004277//Homo sapiens two pore domain K+ ch
annel (TASK-2) mRNA, complete cds//1.4e-107:581:91
//Hs.127007:AF084830
R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92
114
R-PLACE1004289//ESTs, Weakly similar to !!!! ALU S
UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-2
8:279:77//Hs.38687:AA744496
R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTE
IN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.
71435:AI253099
R-PLACE1004316//H.sapiens mRNA for apoptosis speci
fic protein//6.0e-115:590:94//Hs.11171:Y11588
R-PLACE1004336//Cytochrome P450, subfamily I (arom
atic compound-inducible), polypeptide 2//6.7e-69:5
72:77//Hs.1361:M55053
R-PLACE1004358//Homo sapiens connector enhancer of
KSR-like protein CNK1mRNA, complete cds//7.7e-72:
379:93//Hs.16232:AF100153
R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056
309
R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556
R-PLACE1004388//ESTs, Weakly similar to contains s
imilarity to ATP/GTP-binding site motif [C.elegan
s]//1.3e-98:572:90//Hs.14202:N46000
R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI3
43467
R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53
665
R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA
704101
R-PLACE1004437//Human NAD+-specific isocitrate deh
ydrogenase beta subunit precursor, mRNA, nuclear g
ene encoding mitochondrial protein, completecds//
9.4e-90:516:88//Hs.155410:U49283
R-PLACE1004451
R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA6
62980
R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W527
21

R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46
578
R-PLACE1004473//ESTs, Weakly similar to F20D1.2
[C.elegans]//3.8e-101:510:95//Hs.16986:W89194
R-PLACE1004491//Human mitochondrial 1,25-dihydroxy
vitamin D3 24-hydroxylase mRNA, complete cds//0.2
3:278:61//Hs.89663:L13286
R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI0
57117
10 R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:AI4
20493
R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA45
3164
R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA4
36553
R-PLACE1004548//Homo sapiens mRNA for small GTP-bi
nding protein, complete cds//1.8e-40:332:72//Hs.11
5325:D84488
R-PLACE1004550
20 R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA5
64742
R-PLACE1004629//ESTs, Weakly similar to OS-9 precu
rator [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181
R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA7
01903
R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N2
9734
R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA1
01113
30 R-XXXXXXXXXXXX//Homo sapiens mRNA for KIAA0714 pro
tein, partial cds//7.8e-23:129:99//Hs.123129:AB018
257
R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:AI
144254
R-PLACE1004674//Homo sapiens calcium binding prote
in (ALG-2) mRNA, complete cds//1.8e-90:510:91//Hs.
80019:AF035606
R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA46
1482
40 R-PLACE1004686
R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA0
21552
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:AI25
1374
R-PLACE1004716//ESTs, Weakly similar to No definit
ion line found [C.elegans]//3.4e-80:413:94//Hs.235
28:AI279571
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997
R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N63
50 911

4151

R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA4166
19
R-nnnnnnnnnnnn//EST//0.45:94:69//Hs.147174:AI19219
5
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:AI2
23374
R-PLACE1004773//Homo sapiens inversin protein mRNA
A, complete cds//2.7e-89:437:96//Hs.104715:AF08436
7
R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA3
98548
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA
398619
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0606 pro
tein, partial cds//1.9e-99:580:88//Hs.38176:AB0111
78
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA5
35856
R-PLACE1004814//Homo sapiens okadaic acid-inducibl
e phosphoprotein (OA48-18) mRNA, complete cds//1.1
e-108:358:99//Hs.3688:AF069250
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA2
58356
R-PLACE1004824//Protein kinase, interferon-inducib
le double stranded RNAdependent//4.8e-46:450:76//H
s.73821:M35663
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA
342185
R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA1
95299
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995
901
R-PLACE1004840//ESTs, Highly similar to TRANSCRIP
TIONAL ACTIVATOR GCN5[Saccharomyces cerevisiae]//
6.5e-71:381:93//Hs.8383:AA013272
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA
479308
R-PLACE1004885//Homo sapiens protein phosphatase w
ith EF-hands-2 long form (PPEF-2) mRNA, complete c
ds//1.8e-37:330:78//Hs.113259:AF023456
R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:AI2
81881
R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//H
s.2996:X63597
R-nnnnnnnnnnnn//ESTs//4.5e-75:375:96//Hs.91115:AI2
21563
R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:A
1424948
R-PLACE1004930//Homo sapiens TNF-induced protein G
C2-1 mRNA, complete cds//6.6e-102:532:93//Hs.1783

4152

9:AF099936
R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478
980
R-PLACE1004937//ESTs, Weakly similar to F55B12.3
[C.elegans]//6.4e-80:409:95//Hs.31945:AA702166
R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N7
8013
R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29
106
R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA7
08789
R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:AI
291776
R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:AI
420335
R-PLACE1005026
R-PLACE1005027//ESTs, Weakly similar to N-methyl-D
-aspartate receptor glutamate-binding chain [R.nor
vegicus]//0.72:145:66//Hs.11215:N56719
R-PLACE1005046//Homo sapiens mRNA for KIAA0575 pro
tein, complete cds//5.3e-66:297:88//Hs.153468:AB01
1147
R-PLACE1005052//ESTs, Weakly similar to weak simil
arity to rat cytosolicacyl coenzyme A thioester hy
drolase [C.elegans]//1.2e-106:543:95//Hs.18625:AI0
74605
R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA8
06103
R-PLACE1005077//Human triadin mRNA, complete cds//
30.1.8e-05:121:69//Hs.68731:U18985
R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, co
mplete cds//6.6e-49:314:74//Hs.113283:AF018080
R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA
584364
R-PLACE1005101//Homo sapiens (clone zap128) mRNA,
3' end of cds//8.0e-99:531:92//Hs.75437:L40401
R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:AI2
01336
R-PLACE1005108//Human DNA fragmentation factor-45
40 mRNA, complete cds//9.2e-40:232:82//Hs.155344:U919
85
R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA4
93225
R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA2
03423
R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA7
77349
R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI0
89013
R-nnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA4

- 54227
R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589
R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830
R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211
R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937
R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960
R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343
R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975
R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394
R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978
R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304
R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423
R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503
R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046
R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875
R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185
R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325
R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470
R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325
R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927
R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555
R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261
R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835
R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612
R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023
R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927
R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964
R-PLACE1005630
R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255
R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2(XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587
R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355
R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332
R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259
R-PLACE1005739//ESTs, Moderately similar to unknown

n intracellular protein [M.musculus]//1.3e-42:236:
94//Hs.23889:AI341137
R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA
524070
R-PLACE1005763//Human mRNA for KIAA0118 gene, part
ial cds//3.3e-47:268:87//Hs.154326:D42087
R-PLACE1005799//ESTs, Highly similar to HYPOTHETI
CAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Cae
norhabditis elegans]//7.7e-15:88:98//Hs.109857:AA0
88385
R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W309
41
R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA1
31327
R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:AI2
87693
R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N5
0058
R-PLACE1005834//Retinoblastoma 1 (including osteos
arcoma)//0.040:435:58//Hs.75770:L41870
R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:AI0
50965
R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:AI20
3471
R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98
305
R-PLACE1005876//ESTs//0.48:296:57//Hs.39140:AI0418
42
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA5
70558
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:AI
339981
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA8
85501
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:AI
341793
R-PLACE1005925//Human Line-1 repeat mRNA with 2 op
en reading frames//2.8e-27:382:70//Hs.23094:M19503
R-PLACE1005932//ESTs, Moderately similar to MNK1
[H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA9
22142
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:N62
913
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:AI1
83729
R-PLACE1005953
R-PLACE1005955//ESTs, Highly similar to HYPOTHETI
CAL 54.2 KD PROTEIN INDC12-ORC6 INTERGENIC REGION
[Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.10

8117: AI097079
 R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510: AI016239
 R-PLACE1005968//EST//0.26:103:66//Hs.161300: AI420897
 R-PLACE1005990
 R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014: AB002353
 R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROTEIN INAPE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449: AI192946
 R-PLACE1006011//ESTs, Moderately similar to NAD(+) ADP-RIBOSYLTRANSFERASE [D.melanogaster]//5.7e-100:596:88//Hs.24284: AA595596
 R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350: AI056276
 R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C.elegans]//4.1e-102:491:98//Hs.61164: AI096332
 R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680: N93765
 R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007: H74314
 R-PLACE1006119//ESTs//0.14:257:61//Hs.113149: AA908904
 R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827: W68002
 R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROTEIN INSAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249: U55977
 R-PLACE1006143//Amyl o-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463:59//Hs.904: U84010
 R-PLACE1006157//ESTs//0.014:341:58//Hs.121773: AI357886
 R-PLACE1006159//EST//0.00036:247:61//Hs.140054: AA668925
 R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024: H07128
 R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894: AC005239
 R-nnnnnnnnnnnnn//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121: AI125280
 R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464: AF091433
 R-PLACE1006195//ESTs, Weakly similar to !!!! ALU S

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UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-9
 4:532:91//Hs.105216:AI361807
 R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99
 507
 R-PLACE1006205//EST//1.7e-89:448:96//Hs.116665:AA6
 69114
 R-PLACE1006223//Human RNaseP protein p38 (RPP38) m
 RNA, complete cds//0.90:304:58//Hs.94986:U77664
 R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:AI0
 79555
 R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:AI3
 41472
 R-nnnnnnnnnnnnn/Homo sapiens BAC clone RG118D07 fr
 om 7q31//3.2e-99:497:95//Hs.3781:AC004142
 R-PLACE1006246//ESTs, Weakly similar to CMP-sialic
 acid transporter [M.musculus]//1.3e-104:532:95//H
 s.41151:AI301961
 R-PLACE1006248//Homo sapiens mRNA for KIAA0648 pro
 tein, partial cds//3.0e-97:499:95//Hs.31921:AB0145
 48
 R-PLACE1006262//ESTs, Moderately similar to !!!! A
 LU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.
 6e-07:321:62//Hs.53057:W67839
 R-PLACE1006288//Voltage-dependent anion channel 1/
 /3.8e-100:605:88//Hs.2060:L06132
 R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA0
 05265
 R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:A
 I246503
 R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R7
 0900
 R-PLACE1006357//EST//6.5e-09:309:62//Hs.132493:AA9
 23168
 R-PLACE1006360//Human mRNA for KIAA0090 gene, part
 ial cds//0.0097:381:58//Hs.154797:D42044
 R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:AI
 079284
 R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W6
 1053
 R-PLACE1006382
 R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA
 515748
 R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:AI2
 81881
 R-PLACE1006414//Homo sapiens LIM protein mRNA, com
 plete cds//4.1e-43:551:69//Hs.154103:AF061258
 R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:AI2
 78629
 R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA5
 73139

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R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA9
 36961
 R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA9382
 97
 R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47
 418
 R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA82
 7722
 R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:AI25
 1374
 R-PLACE1006521//Human mRNA for KIAA0013 gene, comp
 lete cds//2.1e-15:415:63//Hs.48824:D87717
 R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA
 453723
 R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W4
 6368
 R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:HO
 2532
 R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA7652
 14
 R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:AI
 128443
 R-PLACE1006615//Homo sapiens eukaryotic translatio
 n initiation factor eIF3, p35 subunit mRNA, comple
 te cds//9.3e-118:590:95//Hs.155377:U97670
 R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA
 205322
 R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA54161
 5
 R-PLACE1006629//Human mRNA for KIAA0386 gene, comp
 lete cds//5.3e-33:315:78//Hs.101359:AB002384
 R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W1
 6522
 R-PLACE1006673//Interleukin 10//8.4e-47:330:83//H
 s.2180:W57627
 R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:D877
 36
 R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12
 214
 R-PLACE1006731//Homo sapiens clone 23923 mRNA sequ
 ence//1.9e-102:486:98//Hs.12472:AF038172
 R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T838
 61
 R-PLACE1006760//Homo sapiens clone 24800 mRNA sequ
 ence//3.8e-73:394:93//Hs.7252:AF070622
 R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA
 262658
 R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33
 234
 R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N5

- 5515
R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335
R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989
R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847
R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159
R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-87:481:92//Hs.141263:H64113
R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933
R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA828359
R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:N35008
R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536
R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131
R-nnnnnnnnnnnn//ESTs//3.0e-95:496:94//Hs.47546:AA181348
R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168
R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:AI379514
R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
R-nnnnnnnnnnnn//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:D86956
R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:X52520
R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:AI275982
R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:AI017636
R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971
R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames//6.6e-83:584:82//Hs.23094:M19503
R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:AI20
- 2575
R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:N91027
R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:N74202
R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646
R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417
R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948
R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794
R-PLACE1007178//EST//0.68:85:65//Hs.147010:AI184765
R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998
R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619
20 R-PLACE1007239//Human mRNA for transcription elongation factor S-II, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495
R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450
R-PLACE1007243//ESTs, Weakly similar to transporter protein [H.sapiens]//3.7e-73:357:98//Hs.18272:N78499
R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909
30 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:AI275071
R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419
R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AA100812
R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087
R-PLACE1007301
R-PLACE1007317
40 R-PLACE1007342
R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870
R-PLACE1007367//ESTs, Weakly similar to !!!! ALU S UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594
R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614
R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945
50

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R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877
 R-PLACE1007409//Homo sapiens mitoxantrone resistance protein 1 mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771
 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H. sapiens]//3.8e-115:579:95//Hs.72165:AI243857
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80 10 //Hs.97203:U83171
 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230
 R-PLACE1007478
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, 20 DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533
 R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14[Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657
 R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087
 R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612
 R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404
 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840
 R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:554:93//Hs.21838:AF038179
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176
 R-PLACE1007632
 R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106
 R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946

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R-PLACE1007677//ESTs, Moderately similar to !!!! A LU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//9.0e-37:190:97//Hs.23437:AA707331
 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944
 R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]//3.4e-61:384:89//Hs.92918:AA133274
 R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.91251:U66685
 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:AF061243
 R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:AA476815
 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein; complete cds//6.7e-94:556:89//Hs.153121:AB014585
 R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322
 R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778
 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903
 R-PLACE1007791//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//8.6e-27:143:98//Hs.144194:AA706337
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frames//9.9e-45:428:76//Hs.23094:M19503
 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044
 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050
 R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-95:525:91//Hs.23094:M19503
 R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:AB018309
 50 R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01

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R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832
R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060
R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.92381:AB007956
R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510
R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966
R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.5671:AF084530
R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds//7.2e-89:465:93//Hs.78106:AF079529
R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:99//Hs.44268:AA455900
R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATOR [Drosophila melanogaster]//3.8e-97:493:95//Hs.6141:U69564
R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835
R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612
R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]//2.0e-115:575:95//Hs.92395:AA779854
R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269
R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI30934
R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
R-PLACE1008209//ESTs//1.2e-72:366:96//Hs.92308:AI052701
R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R80871
R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
R-nnnnnnnnnnnn
R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705
R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//Hs.146477:AI128445
R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
R-PLACE1008392//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//2.0e-41:448:72//Hs.139007:H74314
R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
R-PLACE1008401//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.2e-81:536:87//Hs.7570:W31010
R-nnnnnnnnnnnn//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651757
R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA0

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R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
R-PLACE1008532
R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223
R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:AA778649
R-xxxxxxxxxxxx
R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972
R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512
R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:AI279612
R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.147967:AF044333
R-PLACE1008693//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830
R-PLACE1008696//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//1.7e-51:316:76//Hs.1361:M55053
R-PLACE1008715//EST//0.63:114:64//Hs.121353:AA758600
R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303
R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408
R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:AI28650
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R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930
R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217
R-PLACE1008808//Homo sapiens putative checkpoint control protein HRAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905
R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans cDNA cm10e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810
R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:AI378428
R-xxxxxxxxxxxx
R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:AI093502
R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878
R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:AI246893
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308
R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018
R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653
R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680
R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:AI376573
R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419
R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112
R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520
R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195
R-PLACE1009048//ESTs//2.7e-17:403:63//Hs.149343:AI249139
R-PLACE1009050//ESTs//2.0e-88:475:92//Hs.122925:AA909008
R-PLACE1009060//ESTs, Highly similar to HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-112:555:96//Hs.9663:AA527142
R-PLACE1009090//ESTs//5.0e-13:175:75//Hs.140608:N53448

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- R-PLACE1009094//Human splicing factor SRp30c mRNA, complete cds//0.98:161:63//Hs.77608:AL021546
- R-PLACE1009099//ESTs, Highly similar to MKR2 PROT E1N [Mus musculus]//0.037:63:84//Hs.39943:AA203136
- R-PLACE1009110//EST//5.8e-17:307:65//Hs.117264:AA682549
- R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983
- R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945
- R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747
- R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920
- R-PLACE1009158//ESTs//0.30:149:65//Hs.155796:R80005
- R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322
- R-PLACE1009172//EST//8.9e-21:364:67//Hs.142557:AA64948
- R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707
- R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717
- R-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396
- R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701
- R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248
- R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680
- R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018
- R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423
- R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279
- R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frames//7.3e-82:578:82//Hs.23094:M19503
- R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:AI004397
- R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:AI015782
- R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760
- R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA1
- 61260
- R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:AI188883
- R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:AI243186
- R-nnnnnnnnnnnnn//ESTs//3.6e-94:452:98//Hs.103177:W72798
- R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255
- R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632
- R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:AI361269
- R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872
- R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:AI161427
- R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1//1.3e-42:266:89//Hs.155049:AC004531
- R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925
- R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596
- R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767698
- R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:AI262131
- R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263
- R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326
- R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.sapiens]//0.0012:56:91//Hs.12151:AA001818
- R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:AB014535
- R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:AI1374735
- R-PLACE1009607//ESTs//0.0093:107:70//Hs.70932:AA126482
- R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680
- R-PLACE1009621//EST//0.99:261:60//Hs.149030:AI243

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R-PLACE1009622//ESTs//8.0e-93:508:92//Hs. 20967:A1422858

R-PLACE1009637//EST//8.7e-90:442:97//Hs. 121372:AA758701

R-PLACE1009639//EST//8.5e-49:279:93//Hs. 117447:R27213

R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs. 21862:AB011159

R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H. sapiens]//9.9e-62:483:79//Hs. 140416:AA778649

R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs. 109590:AF062534

R-PLACE1009708//ESTs//3.0e-94:471:96//Hs. 40091:N48582

R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S. cerevisiae]//4.2e-98:529:92//Hs. 3945:AA004210

R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M. musculus]//6.8e-85:489:89//Hs. 26194:AA033989

R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs. 154320:AF046024

R-PLACE1009794//ESTs//7.9e-102:529:95//Hs. 42927:N20989

R-nnnnnnnnnnnnnnnnn//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.

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6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogene s, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GS Ss//1.1e-113:549:97//Hs. 16411:AL030996

R-PLACE1009845//ESTs//9.5e-106:560:93//Hs. 117751:AI056868

R-PLACE1009879//ESTs//1.8e-61:399:86//Hs. 141012:R68748

R-PLACE1009886//EST//0.54:153:64//Hs. 144281:AA081328

R-PLACE1009888//ESTs//2.7e-105:520:97//Hs. 108646:AA613031

R-nnnnnnnnnnnnnnnnn//ESTs, Weakly similar to similar to mouse MMR1 [C. elegans]//1.6e-114:594:94//Hs. 67466:AI219740

R-PLACE1009921//ESTs//7.6e-05:291:60//Hs. 124786:AA825563

R-PLACE1009924//EST//1.2e-42:216:98//Hs. 31742:H20276

R-PLACE1009925//ESTs//5.4e-30:154:100//Hs. 114605:AI304317

R-PLACE1009935//ESTs//1.4e-83:417:97//Hs. 131755:AA496543

R-PLACE1009947//Keratin 9//1.0:273:61//Hs. 2783:Z29074

R-PLACE1009971//ESTs//1.5e-87:424:98//Hs. 13781:AI160540

R-PLACE1009992//ESTs//1.3e-87:531:87//Hs. 55044:AA60698

R-PLACE1009995//ESTs//1.3e-103:575:91//Hs. 71218:C75347

R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs. 155464:AF088219

R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C. elegans]//1.7e-17:137:86//Hs. 7049:AI141736

R-PLACE1010031//ESTs//0.22:191:62//Hs. 127787:AA832204

R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M. musculus]//7.6e-104:546:94//Hs. 8215:AA521150

R-PLACE1010069//ESTs//0.99:173:59//Hs. 21415:AI1509

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R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564

R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189

R-PLACE1010743

R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250

R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:AI074024

R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN IB [Acanthamoeba castellanii]//7.6e-111:575:94//Hs.10260:AI126627

R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558

R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:AI091203

R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896

R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472

R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048

R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917

R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090

R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182

R-PLACE1010891

R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983

R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023

R-PLACE1010916//Plasminogen activator inhibitor, type II (arginine-serpin)//0.25:190:61//Hs.75716:Y00630

R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093

R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:AI125479

R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126

R-nnnnnnnnnnnn//Homo sapiens intersectin short form mRNA, complete cds//8.9e-82:441:93//Hs.66392:AF064244

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R-PLACE1010944

R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519

R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219

R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437

R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580

R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:AI199846

R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:AI147867

R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA923249

R-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153

20 R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135

R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219

R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537

R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094

R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:AI149478

R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587

R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:93//Hs.31257:AA875998

R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795

R-PLACE1011160//Homo sapiens mRNA for HRI HFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333

40 R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:AI374673

R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.4e-85:442:95//Hs.136910:AA810782

R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA088438

R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:AI138671

R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA2503299

4175

R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:AI
027693
R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W7
9602
R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA76
6772
R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:AI3
76913
R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:AI3
76849
R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71
807
R-PLACE1011325//Human clone 23721 mRNA sequence//
0.0012:486:58//Hs.83572:U79291
R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R6
0578
R-PLACE1011340//ESTs, Weakly similar to TEICHOIC A
CID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.
4e-92:452:97//Hs.144194:AA706337
R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H1
1376
R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA
001194
R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA16
7337
R-nnnnnnnnnnnnn//Homo sapiens mRNA for KIAA0530 pro
tein, partial cds//4.8e-114:600:94//Hs.10801:AB011
102
R-PLACE1011452//Homo sapiens mRNA for KIAA0707 pro
tein, partial cds//3.7e-32:310:76//Hs.138488:AB014
607
R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R7
0887
R-PLACE1011472//Homo sapiens mRNA for KIAA0712 pro
tein, complete cds//2.6e-104:515:96//Hs.111138:AB0
18255
R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA
639278
R-PLACE1011503//Homo sapiens clone 23597 mRNA sequ
ence//1.0:193:60//Hs.28197:AF035294
R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA9
68576
R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA2
06421
R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:AI
285985
R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF1
O)//4.7e-55:267:81//Hs.8597:L11672
R-PLACE1011586//Myosin, heavy polypeptide 11, smoo
th muscle//0.98:168:61//Hs.78344:AF001548

4176

R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA
780067
R-PLACE1011641//ESTs//2.5e-71:338:100//Hs.153085:A
A993965
R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:AI3
61900
R-PLACE1011649//Homo sapiens clone 24432 mRNA sequ
ence//2.5e-73:414:91//Hs.78019:AF070535
R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA8
46036
R-PLACE1011664//Restin (Reed-Steinberg cell-expres
sed intermediate filament-associated protein)//0.5
0:178:62//Hs.31638:X64838
R-PLACE1011675
R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:AI3
12025
R-PLACE1011719//Human Line-1 repeat mRNA with 2 op
en reading frames//8.5e-57:410:83//Hs.23094:M19503
R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA
251392
R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA
443426
R-PLACE1011749//Myelin oligodendrocyte glycoprotei
n {alternative products}//7.3e-40:361:77//Hs.5321
7:Z48051
R-PLACE1011762//Human kpni repeat mrna (cdna clone
pcd-kpni-8), 3' end//3.0e-60:319:76//Hs.103948:K0
0627
R-PLACE1011778//ESTs//8.0e-70:372:94//Hs.46765:AA5
21080
R-PLACE1011783//Calcium modulating ligand//8.4e-4
1:279:85//Hs.13572:AF068179
R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11
563
R-PLACE1011874//Human mRNA for KIAA0033 gene, part
ial cds//1.2e-53:439:80//Hs.22271:D26067
R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA9
87648
R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA7
25913
R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:AI
275497
R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA1
64268
R-PLACE1011923//Homo sapiens serum-inducible kinas
e mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF05
9617
R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:AI
031969
R-PLACE1011964//ESTs, Weakly similar to LINE-1 REV

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ERSE TRANSCRIPTASE HOMOLOG [H. sapiens]//2.6e-06:284:63//Hs.124102:AA701285
 R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890
 R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256
 R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069
 R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080
 R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211
 R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:AI049504
 R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:AI302868
 R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452
 R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013
 R-PLACE2000039//H. sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073
 R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622
 R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147
 R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390
 R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219
 R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179
 R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:AI292236
 R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941
 R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00043:127:71/

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/Hs.42400:AF022789
 R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662
 R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988
 R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558
 R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134
 R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:AI052357
 R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219
 R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:AI379778
 R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:AI360292
 R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067
 R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:AI382378
 R-PLACE2000223//ESTs//0.49:171:60//Hs.86154:AA207191
 R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717
 R-PLACE2000246//NAD(P)H:menadione oxidoreductase//4.0e-44:331:82//Hs.80706:M81600
 R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363
 R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H. sapiens]//1.9e-87:422:98//Hs.9740:AI004779
 R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664
 R-PLACE2000305//ESTs//2.6e-43:413:75//Hs.118732:AI344055
 R-PLACE2000317//ESTs//2.8e-92:501:92//Hs.28432:R83380
 R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058
 R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789
 R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:AI347618
 R-PLACE2000359//Zinc finger protein 139 (clone pHZ-37)//5.5e-42:288:86//Hs.140090:U09848
 R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:3

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92: 82//Hs. 89887: D38081R-PLACE2000371//ESTs//3. 6e-8
 1: 409: 97//Hs. 155138: AA158731
 R-PLACE2000373//Homo sapiens mRNA for KIAA0734 pro
 tein, partial cds//0. 89: 186: 62//Hs. 101516: AB018277
 R-PLACE2000379//ESTs//3. 4e-10: 228: 64//Hs. 57842: W63
 781
 R-PLACE2000394//ESTs//6. 7e-41: 462: 74//Hs. 107657: AA
 126814
 R-PLACE2000398//ESTs//4. 2e-33: 373: 74//Hs. 155184: AA
 573189
 R-PLACE2000399
 R-PLACE2000404//ESTs, Highly similar to LEUCYL-TR
 NA SYNTHETASE, CYTOPLASMIC [Saccharomyces cerevisi
 ae]//4. 2e-109: 540: 96//Hs. 6762: AA088424
 R-PLACE2000411//ESTs//1. 6e-89: 459: 95//Hs. 117589: N2
 5941
 R-PLACE2000419//ESTs, Weakly similar to F25H9. 6
 [C. elegans]//1. 6e-97: 436: 95//Hs. 24647: W19739
 R-PLACE2000425//Homo sapiens DEC-205 mRNA, complet
 e cds//2. 2e-44: 287: 88//Hs. 153563: AF011333
 R-PLACE2000427//ESTs, Weakly similar to coded for
 by C. elegans cDNA CEESI42F [C. elegans]//3. 0e-113:
 543: 97//Hs. 16933: AA976002
 R-PLACE2000433//ESTs//1. 8e-46: 311: 85//Hs. 145032: AA
 343523
 R-PLACE2000435//ESTs//2. 9e-33: 243: 87//Hs. 90964: AA3
 93986
 R-PLACE2000438//ESTs//2. 8e-09: 66: 96//Hs. 59548: AI27
 9887
 R-PLACE2000450//Human mRNA for KIAA0392 gene, part
 ial cds//3. 3e-39: 394: 74//Hs. 40100: AB002390
 R-PLACE2000455//ESTs//1. 2e-62: 301: 99//Hs. 151708: AA
 554714
 R-PLACE2000458//ESTs//6. 8e-92: 473: 96//Hs. 115897: AA
 156638
 R-PLACE2000465//ESTs//1. 3e-45: 435: 76//Hs. 141635: N7
 9228
 R-PLACE2000477//ESTs//2. 6e-100: 536: 94//Hs. 77822: AA
 532642
 R-PLACE3000004//ESTs//9. 1e-114: 558: 97//Hs. 13035: AA
 151838
 R-PLACE3000029//Homo sapiens mRNA for KIAA0575 pro
 tein, complete cds//6. 3e-64: 350: 86//Hs. 153468: AB01
 1147
 R-PLACE3000059//EST//0. 028: 175: 61//Hs. 159873: R9276
 3
 R-PLACE3000070//ESTs//3. 8e-16: 200: 74//Hs. 138771: N7
 0979
 R-PLACE3000103//ISLET AMYLOID POLYPEPTIDE PRECURSO
 R//3. 7e-48: 468: 75//Hs. 51048: X68830

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R-PLACE3000119//ESTs//1. 2e-45: 330: 83//Hs. 35254: AI1
 33727
 R-PLACE3000124//EST//3. 1e-75: 391: 96//Hs. 161515: N71
 739
 R-PLACE3000136//ESTs//8. 3e-18: 152: 84//Hs. 10043: D81
 792
 R-PLACE3000142//ESTs//0. 047: 183: 62//Hs. 43102: AA131
 369
 R-PLACE3000147//ESTs//6. 6e-53: 310: 90//Hs. 8230: W071
 42
 R-PLACE3000148//EST//1. 9e-16: 184: 76//Hs. 146570: AI1
 39815
 R-PLACE3000155//ESTs//1. 2e-19: 192: 79//Hs. 131350: AA
 805223
 R-PLACE3000156//ESTs, Highly similar to ENV POLYP
 ROTEIN [Avian spleen necrosis virus]//4. 8e-36: 262:
 88//Hs. 31532: H18272
 R-PLACE3000157
 R-PLACE3000158//Small inducible cytokine A5 (RANTE
 S)//8. 2e-39: 296: 81//Hs. 155464: AF088219
 R-PLACE3000160
 R-PLACE3000169//ESTs//1. 5e-64: 329: 97//Hs. 129864: R2
 0798
 R-PLACE3000194
 R-PLACE3000197//ESTs//1. 4e-38: 197: 98//Hs. 146341: AI
 269930
 R-PLACE3000199//ESTs, Highly similar to APOLIPOR
 TEIN E PRECURSOR [Susicrofa]//0. 018: 261: 61//Hs. 13
 1370: AA927516
 R-PLACE3000207//EST//1. 3e-15: 154: 78//Hs. 136617: AA6
 30476
 R-PLACE3000208//ESTs//1. 6e-18: 151: 82//Hs. 155498: W2
 7084
 R-PLACE3000218//ESTs//1. 8e-85: 463: 93//Hs. 7849: AI12
 9964
 R-PLACE3000220//ESTs//6. 4e-44: 308: 84//Hs. 136839: H9
 3717
 R-PLACE3000226//ESTs//1. 3e-49: 269: 95//Hs. 9059: AI35
 9014
 R-PLACE3000230//EST//2. 3e-34: 258: 83//Hs. 4382: T0287
 8
 R-PLACE3000242//Human trophinin mRNA, complete cds
 //1. 1e-63: 546: 78//Hs. 76313: U04811
 R-PLACE3000244//ESTs, Highly similar to NEGATIVE
 REGULATOR OF MITOSIS [Emmericella nidulans]//7. 5e-1
 10: 549: 95//Hs. 13692: AA632002
 R-PLACE3000254//Human mRNA for KIAA0309 gene, part
 ial cds//2. 4e-29: 174: 94//Hs. 87908: AB002307
 R-PLACE3000271//Human macrophage-derived chemokine
 precursor (MDC) mRNA, complete cds//2. 3e-62: 287: 82

- //Hs. 97203: U83171
 R-PLACE3000276//ESTs//7.5e-07: 187: 64//Hs. 80720: AA031782
 R-PLACE3000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//4.0e-59: 456: 80//Hs. 108966: U48696
 R-PLACE3000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45: 302: 86//Hs. 51048: X68830
 R-PLACE3000320//Interleukin 10//9.6e-42: 288: 85//Hs. 2180: M57627
 R-PLACE3000322//ESTs, Highly similar to ARGININOS UCCINATE LYASE [Homo sapiens]//5.8e-34: 190: 95//Hs. 114531: N74103
 R-PLACE3000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32: 239: 84//Hs. 15519: AB018315
 R-PLACE3000339//ESTs//1.3e-109: 548: 96//Hs. 7871: AI041837
 R-PLACE3000341//EST//1.1e-11: 231: 68//Hs. 131328: AA922688
 R-PLACE3000350//Human mRNA for adipogenesis inhibitory factor//8.0e-40: 291: 76//Hs. 1721: X58377
 R-PLACE3000352//EST//1.8e-72: 343: 100//Hs. 144871: AI202380
 R-PLACE3000353//ESTs//2.0e-75: 395: 95//Hs. 107260: W52683
 R-PLACE3000362//EST//2.8e-80: 381: 99//Hs. 136233: AA261888
 R-PLACE3000363
 R-PLACE3000365//EST//4.8e-50: 307: 88//Hs. 149580: AI281881
 R-PLACE3000373//ESTs//5.8e-60: 422: 83//Hs. 142826: W87430
 R-PLACE3000388//ESTs, Moderately similar to !!!! A LU SUBFAMILY J WARNINGENTRY !!!! [H. sapiens]//1.0e-35: 427: 73//Hs. 138795: R98534
 R-PLACE3000399//ESTs//6.5e-05: 162: 66//Hs. 149440: AI274570
 R-PLACE3000400//ESTs//8.3e-05: 310: 63//Hs. 17697: AA287528
 R-PLACE3000401//ESTs//4.6e-60: 326: 80//Hs. 139555: N48230
 R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50: 227: 62//Hs. 142570: AF052160
 R-PLACE3000405//Human HsLIM15 mRNA for HsLIM15, complete cds//5.3e-43: 315: 82//Hs. 37181: D64108
 R-PLACE3000406//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//4.4e-47: 302: 87//Hs. 73614: U83460
 R-PLACE3000413//ESTs//1.6e-116: 571: 97//Hs. 10235: H93077
 R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41: 300: 85//Hs. 155464: AF088219
 R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46: 307: 85//Hs. 32567: AF073519
 R-PLACE3000455//ESTs//1.0: 160: 64//Hs. 156045: AA884461
 R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds//6.1e-84: 440: 92//Hs. 153487: U43899
 R-PLACE3000477//ESTs//2.4e-113: 568: 96//Hs. 24557: AA142980
 R-PLACE4000009//ESTs//1.5e-72: 361: 96//Hs. 10119: AA700227
 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//8.8e-85: 433: 95//Hs. 105399: AB018352
 R-PLACE4000034//ESTs//7.0e-110: 550: 96//Hs. 76607: AA156240
 R-PLACE4000049//EST//0.028: 87: 75//Hs. 89303: AA284031
 R-PLACE4000052//ESTs//5.6e-116: 553: 98//Hs. 19067: AA521292
 R-PLACE4000063//ESTs//5.0e-80: 388: 98//Hs. 135028: AI096444
 R-PLACE4000089//ESTs//2.3e-97: 479: 97//Hs. 102425: AA807547
 R-PLACE4000093//ESTs//1.5e-82: 391: 99//Hs. 160730: AI142739
 R-PLACE4000100
 R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.7e-98: 419: 91//Hs. 129937: AB007931
 R-PLACE4000128//ESTs, Moderately similar to !!!! A LU SUBFAMILY J WARNINGENTRY !!!! [H. sapiens]//3.8e-11: 184: 71//Hs. 154278: N45985
 R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//5.2e-21: 118: 100//Hs. 118164: AB007969
 R-PLACE4000147//EST//1.6e-23: 175: 79//Hs. 162236: AA551582
 R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.0e-47: 306: 88//Hs. 153468: AB011147
 R-PLACE4000192//ESTs, Weakly similar to similar to Human zinc finger protein(ZNF142) [H. sapiens]//6.7e-31: 232: 82//Hs. 16493: T92186
 R-PLACE4000222//ESTs//2.2e-53: 195: 85//Hs. 141575: AA211734
 R-PLACE4000233//ESTs//2.9e-81: 456: 93//Hs. 124964: R850

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R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5e-72:307:85//Hs.113283:AF018080
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:83//Hs.155464:AF088219
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216
R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586
R-PLACE4000270//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263
R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA780782
R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131
R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454
R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460
R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414
R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478
R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656
R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425
R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ WARNINGENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818
R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//2.3e-70:482:83//Hs.140416:AA778649
R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:AI273502
R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780
R-PLACE4000445//ESTs, Weakly similar to C05D9.6 gene product [C.elegans]//2.6e-111:530:98//Hs.12003:AA643063
R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//8.5e-58:409:72//Hs.1361:M55053
R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:AI380932
R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:AI334210
- R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290
R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527
R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185
R-THYR01000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532
R-THYR01000034//ESTs//2.1e-43:214:100//Hs.153018:AI243524
R-THYR01000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249
R-THYR01000040//ESTs//1.7e-94:459:98//Hs.48712:AI027889
R-THYR01000070//ESTs//6.7e-43:283:86//Hs.37573:H59651
R-THYR01000072//ESTs//1.3e-57:313:96//Hs.127827:H13438
20 R-THYR01000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435
R-THYR01000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-41:344:79//Hs.153014:AB002353
R-THYR01000107//Interleukin 10//2.8e-43:292:84//Hs.2180:M57627
R-THYR01000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359
R-THYR01000121//EST//0.24:78:74//Hs.156632:AI345108
30 R-THYR01000124//ESTs//2.8e-86:428:96//Hs.141634:AI122764
R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds//6.8e-90:449:96//Hs.87619:AF087142
R-THYR01000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217
R-THYR01000156//ESTs//6.1e-36:344:75//Hs.70279:AA57426
40 R-THYR01000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-38:278:84//Hs.154103:AF061258
R-THYR01000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEINAP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946
R-THYR01000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189
R-THYR01000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:81//Hs.155464:AF088219
R-THYR01000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:85//Hs.155464:AF088219
- 50

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R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease//3.6e-110:535:97//Hs.43445:AJ005698

R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds//4.3e-115:559:97//Hs.79672:AB014552

R-THYR01000206//ESTs//3.1e-90:507:90//Hs.32456:W29063

R-THYR01000221//ESTs, Weakly similar to !!!! ALU S UBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.1e-7 10
2:357:98//Hs.140002:AA635349

R-THYR01000241//Homo sapiens mRNA for KIAA0688 protein, complete cds//7.8e-69:524:82//Hs.141874:AB014588

R-THYR01000242//ESTs//4.2e-27:222:85//Hs.77554:W87927

R-THYR01000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:318:80//Hs.80738:X52075

R-THYR01000270//ESTs//1.9e-99:531:94//Hs.17767:N62925 20

R-THYR01000279//EST//2.7e-54:266:99//Hs.149527:AI280674

R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, c complete cds//3.5e-100:566:91//Hs.25846:AB016068

R-THYR01000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:M73547

R-THYR01000327//Autocrine motility factor receptor //9.2e-54:289:93//Hs.80731:M63175

R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds//3.4e-113:559:96//Hs.12002:AB018 30
333

R-THYR01000358//Human selenium-binding protein (hS BP) mRNA, complete cds//1.5e-48:317:87//Hs.7833:U29091

R-THYR01000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064

R-nnnnnnnnnnnnnn//ESTs//1.0:253:57//Hs.128783:AA436250

R-THYR01000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds//4.6e-69:29 40
4:84//Hs.151614:AF032456

R-THYR01000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:D38081

R-THYR01000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429

R-THYR01000401//ESTs//1.3e-109:516:99//Hs.78524:AI140601

R-THYR01000438//ESTs//2.1e-48:360:83//Hs.141203:H52638

R-THYR01000452//ESTs, Weakly similar to No definit 50

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Ion line found [C.elegans]//8.5e-40:239:90//Hs.840
 09:AI309761
 R-THYR01000471//ESTs//3.3e-36:302:80//Hs.70279:AA7
 57426
 R-THYR01000484//Homo sapiens mRNA for KIAA0737 pro
 tein, complete cds//2.2e-49:479:75//Hs.17630:AB018
 280
 R-THYR01000488//Homo sapiens mRNA for HRIHFB2038,
 partial cds//4.1e-89:471:94//Hs.28719:AB015333
 R-THYR01000501//ESTs//1.5e-46:287:89//Hs.125300:R6
 2360
 R-THYR01000502//ESTs//1.7e-08:63:96//Hs.116319:AI2
 08005
 R-THYR01000505//ESTs, Weakly similar to KIAA0281
 [H.sapiens]//3.9e-57:286:96//Hs.105861:AI206965
 R-THYR01000558//ESTs//1.7e-95:454:99//Hs.125063:AA
 648511
 R-THYR01000569//ESTs//3.2e-89:463:94//Hs.20555:W22
 193
 R-THYR01000570//ESTs//2.8e-97:471:97//Hs.8245:AA11
 5485
 R-nnnnnnnnnnnnn//Homo sapiens protein associated wi
 th Myc mRNA, completecds//2.6e-108:533:97//Hs.1514
 11:AF075587
 R-THYR01000596//ESTs//3.1e-99:527:94//Hs.6084:AA04
 5247
 R-THYR01000602//EST//6.9e-50:381:83//Hs.161917:AA4
 83223
 R-THYR01000605//ESTs, Weakly similar to monocytic
 leukaemia zinc fingerprotein [H.sapiens]//1.2e-96:
 483:96//Hs.21907:N24415
 R-THYR01000625//ESTs//5.6e-36:257:84//Hs.139657:AA
 191742
 R-THYR01000637
 R-THYR01000641//ESTs, Weakly similar to ERYTHROCYT
 E BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens]//4.
 9e-46:245:95//Hs.97398:AA398634
 R-THYR01000658//ESTs//5.8e-48:281:90//Hs.142259:AA
 828840
 R-nnnnnnnnnnnnn//ESTs//1.5e-82:389:99//Hs.155573:AA
 487384
 R-THYR01000666//ESTs//1.4e-26:179:88//Hs.98382:AA7
 79866
 R-THYR01000676//EST//6.4e-05:88:77//Hs.133424:AI06
 1063
 R-THYR01000684//ESTs//1.9e-69:374:94//Hs.144617:R7
 7109
 R-THYR01000699//ESTs//1.7e-58:394:86//Hs.26373:AA7
 00713
 R-THYR01000712

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R-THYR01000734//EST//2.0e-06:95:73//Hs.156201:AA724287
 R-THYR01000748//EST//4.1e-12:155:74//Hs.118694:AA148713
 R-THYR01000756//ESTs, Weakly similar to CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624
 R-THYR01000777
 R-THYR01000783//EST//5.6e-100:470:99//Hs.123515:AA812932
 R-THYR01000787//EST//8.0e-34:175:99//Hs.99607:AA463897
 R-THYR01000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144
 R-THYR01000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381
 R-THYR01000805//EST//2.6e-32:407:67//Hs.123424:AA813594
 R-THYR01000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067
 R-THYR01000829
 R-THYR01000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
 R-THYR01000852//EST//2.3e-20:157:85//Hs.149580:AI281881
 R-THYR01000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
 R-THYR01000865//Protein kinase, interferon-inducible double stranded RNA dependent//2.8e-44:374:79//Hs.73821:M35663
 R-THYR01000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
 R-THYR01000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
 R-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
 R-THYR01000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
 R-THYR01000951//ESTs//4.2e-11:91:89//Hs.6278:T15859
 R-THYR01000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
 R-THYR01000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
 R-THYR01000975//EST//9.8e-49:303:89//Hs.149580:AI281881
 R-THYR01000983//ESTs, Highly similar to UBIQUITIN 50

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-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:AI027524
 R-THYR01000984//ESTs//5.9e-97:481:96//Hs.142457:AI202777
 R-THYR01000988//EST//3.5e-42:241:83//Hs.162404:AA573131
 R-THYR01001003//ESTs, Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489
 R-THYR01001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
 R-THYR01001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
 R-THYR01001062//EST//1.5e-46:291:89//Hs.161917:AA483223
 R-THYR01001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
 R-THYR01001100
 R-THYR01001120//ESTs, Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:AI138834
 R-THYR01001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
 R-THYR01001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
 R-THYR01001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
 R-THYR01001142//ESTs//0.26:84:69//Hs.153434:AI287853
 R-THYR01001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
 R-THYR01001177
 R-THYR01001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
 R-THYR01001204//ESTs, Weakly similar to TH1 protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151
 R-THYR01001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
 R-THYR01001262//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end//1.3e-48:349:83//Hs.139107:K00629
 R-THYR01001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640
 R-THYR01001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
 R-THYR01001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
 R-THYR01001320//ESTs//1.4e-61:403:79//Hs.139555:N4

- 8230
R-THYR01001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//8.5e-05:326:60//Hs.82314:M31642
R-nnnnnnnnnnnn//ESTs//0.16:422:59//Hs.23876:AA082935
R-THYR01001347//ESTs, Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
R-THYR01001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
R-THYR01001365
R-THYR01001374
R-THYR01001401//Human HsLIM15 mRNA for HsLim15, complete cds//2.5e-48:467:75//Hs.37181:D64108
R-THYR01001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
R-THYR01001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
R-THYR01001406//EST//0.0023:117:66//Hs.162931:AA633197
R-THYR01001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
R-THYR01001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977
R-THYR01001434//ESTs//0.40:161:61//Hs.161993:AA503172
R-THYR01001458//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082
R-THYR01001480//Small inducible cytokine A5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219
R-THYR01001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135
R-THYR01001534//ESTs//4.6e-96:447:100//Hs.135204:AI093110
R-THYR01001537//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094
R-THYR01001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936
R-THYR01001559//ESTs//0.99:210:62//Hs.33619:AA021594
R-THYR01001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413
R-THYR01001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958
R-THYR01001584//ESTs//1.5e-64:354:95//Hs.146222:AA 50
- 397741
R-THYR01001595//ESTs//5.7e-39:366:78//Hs.22562:R54247
R-THYR01001602//Insulin-like growth factor 1 (somatomedin C)//7.4e-12:288:67//Hs.85112:X57025
R-THYR01001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886
R-THYR01001617//Homo sapiens peroxisomal acyl-CoA: dihydroxyacetonephosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190
R-THYR01001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874
R-THYR01001656//ESTs//3.8e-19:209:75//Hs.92186:AI080282
R-THYR01001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446
R-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59kDa isoform//1.6e-111:562:95//Hs.118633:AJ225089
R-THYR01001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
R-THYR01001703//ESTs//1.1e-39:142:97//Hs.110748:AI341726
R-THYR01001706//ESTs//2.2e-42:214:99//Hs.112536:AI147691
R-THYR01001721
R-nnnnnnnnnnnn//ESTs, Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184
R-THYR01001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172
R-THYR01001746//EST//0.0073:226:61//Hs.146544:AI125323
R-THYR01001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474
R-THYR01001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224
R-THYR01001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788
R-THYR01001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956
R-THYR01001895//ESTs//1.7e-08:213:64//Hs.156056:AI352123
R-THYR01001907//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314
R-VESEN1000122
R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923

- 289
R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:AI3
59321
R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA5
57178
R-Y79AA1000059//Homo sapiens mRNA for KIAA0640 pro
tein, partial cds//2.8e-51:330:89//Hs.153026:AB014
540
R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59
629
R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50
792
R-Y79AA1000181//ESTs, Weakly similar to No definit
ion line found [C.elegans]//2.4e-110:553:95//Hs.23
159:AA113849
R-Y79AA1000202//Human mRNA for KIAA0169 gene, part
ial cds//0.094:185:62//Hs.79414:D79991
R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68
103
R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:AI 20
421812
R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:AI
246624
R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:AI09
2936
R-Y79AA1000268//Human mRNA for KIAA0365 gene, part
ial cds//1.3e-44:320:84//Hs.84123:AB002363
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA
857826
R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA1 30
21635
R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3
[H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210
R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA
483808
R-Y79AA1000349//ESTs, Moderately similar to sperma
tid perinuclear RNA-binding protein Spnr [M.muscul
us]//4.4e-66:339:97//Hs.8215:AA521150
R-Y79AA1000355//ESTs, Moderately similar to !!!! A
LU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3. 40
2e-44:279:88//Hs.139007:H74314
R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA6
41018
R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R5
1613
R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA
707758
R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI35229
2
R-Y79AA1000469//ESTs, Highly similar to ancient ub 50
iquitous 46 kDa protein AUP46 precursor [M.musculu
s]//3.1e-60:362:88//Hs.6381:AI188509
R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA7
41320
R-Y79AA1000538//EST//7.9e-48:307:87//Hs.149580:AI2
81881
R-Y79AA1000539//Human kinesin-like spindle protein
HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.4
1723:U37426
R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA1
47848
R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADA
PTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.1912
1:AI125280
R-Y79AA1000574//ESTs, Weakly similar to M04B2.4
[C.elegans]//1.3e-107:564:93//Hs.16361:AI147455
R-Y79AA1000627//Homo sapiens zinc finger protein
(ZF5128) mRNA, completecds//3.4e-99:517:94//Hs.605
80:AF060503
R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETIC
AL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGIO
N [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.
129049:H28818
R-Y79AA1000734//Homo sapiens peroxisomal biogenesi
s factor (PEX11b) mRNA, complete cds//8.7e-114:58
6:95//Hs.83023:AF093670
R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETIC
AL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III [C.el
egans]//9.8e-111:563:95//Hs.19845:AI005330
R-Y79AA1000752//Homo sapiens (huc) mRNA, complete
cds//0.97:235:59//Hs.1701:L26405
R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:N9
1463
R-Y79AA1000782//Human mRNA for KIAA0246 gene, part
ial cds//1.6e-18:107:100//Hs.84753:D87433
R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI36835
9
R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA5
80512
R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA5
32642
R-nnnnnnnnnnnnn//Carboxypeptidase E//0.018:354:59//
Hs.75360:X51405R-Y79AA1000805
R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280
227
R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI
334650
R-Y79AA1000850//Homo sapiens small optic lobes hom
olog (SOLH) mRNA, complete cds//0.016:386:59//Hs.5
5836:U85647

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R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079
 R-Y79AA1000968
 R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA
 417181
 R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M8
 6049
 R-Y79AA1000985
 R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22
 851
 R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA62 10
 9067
 R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA83
 7407
 R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:A
 1271325
 R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 pro
 tein, complete cds//4.8e-53:279:83//Hs.15731:AB011
 135
 R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA3
 09047
 R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA1
 61260
 R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08
 155
 R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA
 343015
 R-Y79AA1001167
 R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T1588
 4
 R-Y79AA1001185
 R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA7
 41051
 R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W609
 33
 R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI
 025750
 R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA9
 09674
 R-Y79AA1001236//Homo sapiens mRNA for JM23 protei
 n, complete coding sequence (clone IMAGE 34581 and 40
 IMAGE 45355 and LLNLc1101133Q7 (RZPD Berlin))//1.
 1e-110:549:95//Hs.23170:AJ005892
 R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA
 481271
 R-Y79AA1001299//Human Ini1 mRNA, complete cds//9.6
 e-25:133:100//Hs.155626:U04847
 R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI
 191149
 R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA
 887084

4194

R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:A
 A604143
 R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA
 101819
 R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA5
 79859
 R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63
 891
 R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN
 -CONJUGATING ENZYME E2
 -17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95/
 /Hs.106616:AI027524
 R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA
 523704
 R-Y79AA1001533//ESTs, Moderately similar to RNA po
 lymerase I associated
 factor [M.musculus]//6.2e-46:260:94//Hs.24884:AA17
 6812
 R-nnnnnnnnnnnnn//EST//0.62:126:67//Hs.137020:AA8685
 20 63
 R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPH
 A//3.5e-95:517:91//Hs.76987:AF012872
 R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:15
 7:64//Hs.82772:J04177
 R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA7
 04508
 R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI
 126237
 R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI
 30 336204
 R-Y79AA1001613//ESTs, Weakly similar to zinc finge
 r protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA
 897542
 R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N2
 6486
 R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSO
 MAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.2625
 2:AA643235
 R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CR
 YSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//H
 s.108896:R54040
 R-nnnnnnnnnnnnn
 R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA21
 1783
 R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:A
 A418490
 R-Y79AA1001711//Human DNA sequence from clone 1119
 D9 on chromosome 20p12. Contains part of a gene fo
 r a PAK1 LIKE Serine/Threonine-Protein Kinase and
 50 part of the PLCB4 gene for Phospholipase C, beta (1

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-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and GSSs//0.085:251:63//Hs.21864:AL031652
 R-Y79AA1001781//ESTs, Weakly similar to partial CD S [C.elegans]//9.4e-87:427:97//Hs.18645:AI023798
 R-nnnnnnnnnnnn//ESTs//1.1e-112:558:97//Hs.109755:A180809
 R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530:91//Hs.72444:W23217
 R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582
 R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355
 R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:A1278630
 R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094
 R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652
 R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404
 R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275
 R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB011135
 R-Y79AA1002089//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080
 R-Y79AA1002093//Homo sapiens CT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933
 R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785
 R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275
 R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399
 R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858
 R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725
 R-nnnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715
 R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428
 R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
 R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDINGPROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843

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R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274
 R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:AB014592
 R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME[D.melanogaster]//9.0e-102:507:96//Hs.25895:AI341537
 R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
 R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288
 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:AB014534
 R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985
 R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371
 R-Y79AA1002361
 R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908
 R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000
 R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753
 R-Y79AA1002431//EST//6.6e-23:128:98//Hs.128417:AA975026
 R-nnnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]//4.4e-62:390:88//Hs.143930:AI207821
 R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870
 R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788
 R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499
 【1127】 相同性検索結果データ 6.
 全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ。以下に示す検索結果には、比較配列の長さの単位にaaとbpが混在している。各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。
 C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/Q61712
 C-HEMBA1000030

- C-HEMBA1000046
 C-HEMBA1000050
 C-HEMBA1000076
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553
 C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3-GAMMA (HNF-3C).//5E-16//166aa//36%/P35584
 C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555
 C-HEMBA1000193
 C-HEMBA1000227
 C-HEMBA1000288
 C-HEMBA1000302
 C-HEMBA1000304
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%/O35594
 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%/AL049654
 C-HEMBA1000387
 C-HEMBA1000392
 C-HEMBA1000460
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%/Q04652
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%/P22279
 C-HEMBA1000501
 C-HEMBA1000508
 C-HEMBA1000520
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%/P02826
 C-HEMBA1000534
 C-HEMBA1000555
 C-HEMBA1000568
 C-HEMBA1000588
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%/O43295
 C-HEMBA1000636
 C-HEMBA1000682
 C-HEMBA1000686
 C-HEMBA1000719
 C-HEMBA1000727
 C-HEMBA1000752
 C-HEMBA1000817
 C-HEMBA1000851
 C-HEMBA1000867
- C-HEMBA1000869
 C-HEMBA1000872
 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//1.6E-30//127aa//40%/P43366
 C-HEMBA1000918
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%/Q19124
 C-HEMBA1000946
 C-HEMBA1000968
 C-HEMBA1000971
 C-HEMBA1000975
 C-HEMBA1001009
 C-HEMBA1001022
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//1.4E-12//131aa//38%/Q01485
 C-HEMBA1001052
 C-HEMBA1001080
 C-HEMBA1001085
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%/P48059
 C-HEMBA1001109
 C-HEMBA1001122
 C-HEMBA1001133
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%/Q06730
 C-HEMBA1001140
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.8E-79//179aa//80%/P51646
 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%/AB020678
 C-HEMBA1001235
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%/AJ130733
 C-HEMBA1001281
 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%/Q60401
 C-HEMBA1001303
 C-HEMBA1001310
 C-HEMBA1001326
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)mRNA, complete cds.//1.4E-133//614bp//99%/AF057358
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%/P17081

- C-HEMBA1001388
 C-HEMBA1001398
 C-HEMBA1001405
 C-HEMBA1001407
 C-HEMBA1001413
 C-HEMBA1001415
 C-HEMBA1001446
 C-HEMBA1001450
 C-HEMBA1001455
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%/P18850
 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%/P29166
 C-HEMBA1001533
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%/AB020657
 C-HEMBA1001581
 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%/Q14141
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA).//1.6E-10//155aa//28%/Q63679
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.6E-36//365aa//33%/P33450
 C-HEMBA1001702
 C-HEMBA1001714//Homo sapiens mRNA; cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%/AL050386
 C-HEMBA1001731
 C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%/P53009
 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%/P11675
 C-HEMBA1001815
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%/Q99676
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%/Q07230
 C-HEMBA1001864
 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%/P20659
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.99.2) (ME2GLYDH).//9.3E-36//395aa//26%/Q63342
 C-HEMBA1001987
 C-HEMBA1002018
 C-HEMBA1002049
 C-HEMBA1002084
 C-HEMBA1002125
- C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%/P79293
 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%/P43694
 C-HEMBA1002191
 C-HEMBA1002199
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%/P18161
 C-HEMBA1002237
 C-HEMBA1002265
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%/AF125537
 C-HEMBA1002349
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%/AF092563
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%/P22793
 C-HEMBA1002430
 C-HEMBA1002439
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%/Q00994
 C-HEMBA1002460
 C-HEMBA1002462
 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%/P98175
 C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%/P17437
 C-HEMBA1002477
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53//257aa//36%/P48732
 C-HEMBA1002515
 C-HEMBA1002542
 C-HEMBA1002569//Homo sapiens protein associated with Hyc mRNA, completecds.//6.8E-305//951bp//99%/AF075587
 C-HEMBA1002583
 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds.//1.4E-253//1149bp//99%/AB01116
 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//0//1539bp//99%/AB018351
 C-HEMBA1002688
 C-HEMBA1002696
 C-HEMBA1002750
 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%/AJ000414
 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1532bp//99%/AB020636

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C-HEMBA1002777
 C-HEMBA1002794
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//8.2e-314//1437bp//99%/AF071185
 C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2E-304//1383bp//99%/AJ132819
 C-HEMBA1002850
 C-HEMBA1002863
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED 10 8.8 IN CHROMOSOME II.//1.5E-44//188aa//52%/Q09297
 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//1483bp//100%/AB011148
 C-HEMBA1002937
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//2E-34//300aa//34%/P16157
 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds.//0//1752bp//99%/AB020710
 C-HEMBA1002954
 C-HEMBA1002971
 C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4).//1.2E-27//63aa//100%/P14646
 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25//534aa//24%/Q02224
 C-HEMBA1003033
 C-HEMBA1003035
 C-HEMBA1003041
 C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P 30 -52).//2.5E-263//489aa//99%/075439
 C-HEMBA1003067
 C-HEMBA1003096
 C-HEMBA1003117
 C-HEMBA1003129
 C-HEMBA1003136//MANNOSYL-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSYL-1-PHOSPHATE GUANYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//8.5E-51//221aa//33%/P41940
 C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 381801.//0//1583bp//99%/AL079278
 C-HEMBA1003175
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%/P44551
 C-HEMBA1003199
 C-HEMBA1003222
 C-HEMBA1003235//TROPOMYOSIN.//0.0000023//109aa//33%/Q02088

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C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa//42%/Q06548
 C-HEMBA1003257
 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%/P32506
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.4E-229//1043bp//99%/AB024436
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//0//791bp//99%/AB011109
 C-HEMBA1003322
 C-HEMBA1003327
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.00000002//248aa//23%/Q02224
 C-HEMBA1003370
 C-HEMBA1003380
 C-HEMBA1003395
 C-HEMBA1003402
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//1732bp//98%/AB020712
 C-HEMBA1003417//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021).//1.6E-312//1414bp//99%/AL050287
 C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%/P37709
 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139
 C-HEMBA1003447
 C-HEMBA1003461
 C-HEMBA1003463
 C-HEMBA1003528
 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISLET-2 (ISLET-2).//8.8E-189//360aa//96%/P50480
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa//52%/P53384
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-I).//1.2E-31//71aa//100%/P16874
 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%/P19474
 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445aa//74%/Q13330
 C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%/P26039
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP).//4.4E-10//118aa//35%/P19682
 C-HEMBA1003615
 C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-178//501bp//97%/AB015344
 C-HEMBA1003621

4203

4204

- C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//
1.2E-75//151aa//99%/Q13207
C-HEMBA1003690//HISTONE DEACETYLASE HDA1.//2.1E-59
//249aa//47%/P53973
C-HEMBA1003711
C-HEMBA1003807
C-HEMBA1003864
C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FI
NGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%/P
16372
C-HEMBA1003959
C-HEMBA1003989
C-HEMBA1004074
C-HEMBA1004097//Mus musculus putative transcrip
tion factor mRNA, complete cds.//8.5E-221//1188bp//78
%/AF091234
C-HEMBA1004146
C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 pr
oteins, partial cds.//0//1893bp//98%/AB023145
C-HEMBA1004207//Homo sapiens leptin receptor short
form (db) mRNA, complete cds.//0//1892bp//99%/U5
0748
C-HEMBA1004227//Rattus norvegicus protein phosphat
ase 2C mRNA, complete cds.//5.7E-217//1217bp//88%/AF
095927
C-HEMBA1004246
C-HEMBA1004276//Homo sapiens AP-4 adaptor complex
beta4 subunit mRNA, complete cds.//4.8E-257//738bp
//99%/AF092094
C-HEMBA1004289
C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA,
complete cds.//0//1512bp//96%/AF132955
C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL)
mRNA, complete cds.//1.2E-316//1445bp//99%/AF0898
41
C-HEMBA1004596
C-HEMBA1004693
C-HEMBA1004736
C-HEMBA1004753
C-HEMBA1004756//Human transporter protein (g17) mR
NA, complete cds.//9.1E-34//515bp//66%/U49082
C-HEMBA1004758//Homo sapiens transcription factor
SL1 mRNA, complete cds.//2.6E-246//1249bp//94%/L3
9060
C-HEMBA1004763
C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOL
OG.//5.4E-111//314aa//58%/P08547
C-HEMBA1004771
C-HEMBA1004776
C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8
E-69//198aa//66%/P50851
C-HEMBA1004806
C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD
PROTEIN (SRP68).//8.2E-154//317aa//94%/Q00004
C-HEMBA1004850
C-HEMBA1004863//Homo sapiens mRNA; cDNA DKFZp586W2
022 (from clone DKFZp586W2022).//0//1443bp//100%/AL
080114
C-HEMBA1004923
C-HEMBA1004929
C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA00
72) (HA1357).//3.3E-27//65aa//100%/Q16401
C-HEMBA1004933
C-HEMBA1004954
C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (2
00 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//
286aa//23%/P12036
C-HEMBA1005475
C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, c
omplete cds.//0//1721bp//100%/AF133270
C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FI
NGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%/P
16372
C-HEMBA1006310//Rattus norvegicus cytosolic sortin
g protein PACS-1a (PACS-1) mRNA, complete cds.//3.
7E-225//1189bp//88%/AF076183
C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%/P26
043
C-HEMBA1006377
C-HEMBA1006467
C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34
%/Q01552
C-HEMBA1006530
C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN
B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.00000004
3//111aa//40%/Q01485
C-HEMBA1006795
C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59/
/378aa//39%/P16258
C-HEMBA1006936
C-HEMBA1007018//Homo sapiens dynein light chain-A
mRNA, complete cds.//1.5E-267//1215bp//99%/AF0788
49
C-HEMBA1007342
C-HEMBA1000008
C-HEMBA1000018
C-HEMBA1000024
C-HEMBA1000025
C-HEMBA1000036
C-HEMBA1000037//Homo sapiens erythroblast macropha

4205

4206

ge protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%//AF084928
 C-HEM BB1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLC K) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%//P11799
 C-HEM BB1000103
 C-HEM BB1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521
 C-HEM BB1000136
 C-HEM BB1000215
 C-HEM BB1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEED8.5.//2.7E-12//112aa//47%//Q09530
 C-HEM BB1000244
 C-HEM BB1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%//Q23256
 C-HEM BB1000338
 C-HEM BB1000339
 C-HEM BB1000391
 C-HEM BB1000438
 C-HEM BB1000449
 C-HEM BB1000589
 C-HEM BB1000591
 C-HEM BB1000623
 C-HEM BB1000630
 C-HEM BB1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//232aa//28%//P78970
 C-HEM BB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%//P27671
 C-HEM BB1000671
 C-HEM BB1000673
 C-HEM BB1000705
 C-HEM BB1000706
 C-HEM BB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%//U53475
 C-HEM BB1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847
 C-HEM BB1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.2E-126//613bp//97%//AF111105
 C-HEM BB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%//P39956
 C-HEM BB1000807
 C-HEM BB1000810
 C-HEM BB1000848

C-HEM BB1000852
 C-HEM BB1000870
 C-HEM BB1000887
 C-HEM BB1000908
 C-HEM BB1000927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%//AF120102
 C-HEM BB1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910
 10 C-HEM BB1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.4E-120//580bp//67%//AF099974
 C-HEM BB1000975
 C-HEM BB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%//P28575
 C-HEM BB1000991
 C-HEM BB1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%//P51523
 C-HEM BB1001014
 20 C-HEM BB1001024
 C-HEM BB1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%//P46087
 C-HEM BB1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//80%//AF010144
 C-HEM BB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%//AF034803
 C-HEM BB1001096
 30 C-HEM BB1001105
 C-HEM BB1001117
 C-HEM BB1001126
 C-HEM BB1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435
 C-HEM BB1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%//AF110267
 C-HEM BB1001153
 40 C-HEM BB1001169
 C-HEM BB1001175//ANKYRIN.//6.9E-11//169aa//31%//Q02357
 C-HEM BB1001182
 C-HEM BB1001199
 C-HEM BB1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%//AB023187
 C-HEM BB1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%//AF089897
 50 C-HEM BB1001288//Homo sapiens CGI-32 protein mRNA,

4207

4208

complete cds.//1.8E-274//642bp//99%/AF132966
 C-HEMBB1001289
 C-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.2E-79
 //196aa//80%/P17081
 C-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 tran
 scription factor (O/E-3) mRNA, complete cds.//1.3E
 -129//724bp//86%/U92703
 C-HEMBB1001331
 C-HEMBB1001339//DXS8237E PROTEIN (FRAGMENT).//0.00
 00046//124aa//37%/P98175
 C-HEMBB1001346//Homo sapiens phenylalanine-tRNA sy
 nthesase (FARS1) mRNA, nuclear gene encoding mitoch
 ondrial protein, complete cds.//1.1E-58//292bp//99
 %//AF097441
 C-HEMBB1001369
 C-HEMBB1001384//Homo sapiens COP9 complex subunit
 4 mRNA, complete cds.//0//1586bp//99%/AF100757
 C-HEMBB1001387
 C-MAMMA1002317
 C-MAMMA1002319
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.000000
 15//206aa//29%/Q02926
 C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31
 %//Q21190
 C-NT2RM1000242
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143a
 a//91%/P49028
 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (E
 C 3.6.1.34) (V-ATPASE SUBUNIT) (V-ATPASE 28 KD A
 CCESSORY PROTEIN).//1.5E-106//118aa//97%/P39942
 C-NT2RM1000669
 C-NT2RM1000781
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complet
 e cds.//6.3E-172//798bp//99%/AF092138
 C-NT2RM1001008
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complet
 e cds.//0.000000002//980bp//95%/AF085360
 C-NT2RM1001074
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.
 1.14).//0.0000056//239aa//27%/
 C-NT2RM2000006//Human DNA sequence from clone 796F
 18 on chromosome 1p36.11-36.33 Contains a pseudoge
 ne similar to MMS2, ESTs and GSSs, complete sequenc
 e.//0//1740bp//99%/AL031291
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 12
 8 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III
 SUBUNIT 2).//2.2E-144//362aa//71%/P25167
 C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOL
 IC (DH IC) (CYTOPLASMI
 C DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//

31%/P54703
 C-NT2RM2000032
 C-NT2RM2000042
 C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROL
 ASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (U
 BIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUI
 TINATING ENZYME 8).//1.3E-36//160aa//40%/P50102
 C-NT2RM2000093
 C-NT2RM2000101
 10 C-NT2RM2000191//Homo sapiens cGMP phosphodiesteras
 e A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%/
 AF067223
 C-NT2RM2000192
 C-NT2RM2000239
 C-NT2RM2000250//Homo sapiens mRNA; cDNA DKFZp564L2
 32 (from clone DKFZp564L232).//4.2E-314//1416bp//1
 00%/AL080069
 C-NT2RM2000259
 C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH G
 LYCOPROTEIN).//3.6E-19//181aa//34%/P14918
 20 C-NT2RM2000287
 C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 pro
 tein, complete cds.//3.4E-294//863bp//99%/AB02066
 6
 C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 pro
 tein, complete cds.//0//1637bp//99%/AB011132
 C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.
 //1.8E-14//245aa//29%/P11274
 C-NT2RM2000368//Homo sapiens protein kinase C-bind
 ing protein RACK7 mRNA, partial cds.//0//1506bp//9
 9%/U48251
 C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRAN
 SFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.7E-68//419
 aa//36%/P50849
 C-NT2RM2000374
 C-NT2RM2000395
 C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR
 (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACT
 OR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTICINTERM
 40 EDIATE COMPONENT).//1.6E-54//344aa//33%/P32802
 C-NT2RM2000407
 C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRA
 NSPORTER NTT73.//1E-222//237aa//89%/Q08469
 C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YP
 T52-GCN3 INTERGENIC REGION.//0.0000001//157aa//28%
 //P36113
 C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROT
 EIN (EC 2.7.1.-).//0.0000089//377aa//24%/P22211
 C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.8E-13//166
 aa//34%/P41823C-NT2RM2000502

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C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//1673bp//99%/AF061243
 C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.3E-12//282aa//32%/P17437
 C-NT2RM2000540
 C-NT2RM2000567
 C-NT2RM2000569
 C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNALIGASE) (ILERS).//1.7E-187//741aa//46%/P73505
 C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//0//3001bp//99%/D86987
 C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.8E-60//384aa//40%/P53973
 C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds.//0//2712bp//99%/AF156487
 C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//4.9E-70//838bp//69%/AF179221
 C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.4E-32//319aa//35%/Q08170
 C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//0//3791bp//99%/AB018272
 C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//0//2530bp//99%/AB014558
 C-NT2RM2000639
 C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1543bp//99%/AB014576
 C-NT2RM2000669
 C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//3.7E-142//285aa//90%/P32391
 C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//3.8E-23//184aa//36%/Q15404
 C-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//4.4E-231//1065bp//99%/AB015342
 C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//5.7E-53//266aa//43%/P41877
 C-NT2RM2000795
 C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP).//9.5E-279//545aa//98%/P23514
 C-NT2RM2000837
 C-NT2RM2000951//Homo sapiens XYL B mRNA for xylulokinase, complete cds.//1.7E-200//927bp//99%/AB015046
 C-NT2RM2000952
 C-NT2RM2000984
 C-NT2RM2001004

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C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//8.2E-154//285aa//99%/Q60809
 C-NT2RM2001065
 C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E1 0.2 IN CHROMOSOME III.//2.4E-15//266aa//26%/P46577
 C-NT2RM2001131
 C-NT2RM2001141
 C-NT2RM2001152
 10 C-NT2RM2001177//Homo sapiens mRNA; cDNA DKFZp586G1822 (from clone DKFZp586G1822).//2.1E-293//1335bp//99%/AL080109
 C-NT2RM2001194
 C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.3E-20//267aa//35%/P05143
 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5).//0.00000015//95aa//35%/P48724
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10).//3.6E-10//177aa//32%/P97924
 20 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE).//1.3E-180//328aa//99%/P13264
 C-NT2RM2001243
 C-NT2RM2001247
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.6E-166//312aa//98%/P53995
 C-NT2RM2001291
 C-NT2RM2001306//Homo sapiens mRNA; cDNA DKFZp564I052 (from clone DKFZp564I052).//0//1694bp//99%/AL080063
 30 C-NT2RM2001312
 C-NT2RM2001319
 C-NT2RM2001324//ZYGXIN.//6.8E-55//200aa//41%/Q04584
 C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.000000029//334aa//22%/Q00808
 C-NT2RM2001370
 C-NT2RM2001393
 40 C-NT2RM2001420
 C-NT2RM2001424//Homo sapiens mRNA; cDNA DKFZp586D0920 (from clone DKFZp586D0920).//0//1621bp//100%/AL050146
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2).//7.4E-121//437aa//57%/P52569
 C-NT2RM2001504
 C-NT2RM2001524
 C-NT2RM2001544
 50 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE

4211

4212

SE P5 PRECURSOR (EC 5.3.4.1).//6.9E-27//90aa//42%/P38660
 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.3E-61//312aa//44%/P19474
 C-NT2RM2001582
 C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds.//0//1000bp//100%/AB014610
 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ.//5.1E-26//204aa//34%/P28692
 C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2390bp//99%/AB007931
 C-NT2RM2001930
 C-NT2RM2001935
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//2.7E-27//216aa//34%/P28320
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN A AC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23%/P38250
 C-NT2RM2001982
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//1.9E-39//253aa//35%/P37838
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//1.3E-10//232aa//28%/Q12730
 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G 6.03 IN CHROMOSOME I.//3.1E-12//206aa//30%/Q09782
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//0.00000029//83aa//44%/P40796
 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION.//1.1E-89//425aa//41%/P46837
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds.//0//1959bp//99%/AB016789
 C-NT2RM2002049
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.00000099//338aa//24%/Q07878
 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%/Q61990
 C-NT2RM2002091
 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840
 C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%/P4

9695

C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805
 C-NT2RM2002178//Homo sapiens mRNA; cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%/AL117402
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%/P25167
 10 C-NT2RM4000061
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%/P52742
 C-NT2RM4000139//R. norvegicus trg mRNA.//2.3E-114//1161bp//72%/X68101
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//4.8E-13//686aa//23%/P25386
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%/P16381
 C-NT2RM4000197
 20 C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%/AB018255
 C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%/L20303
 C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%/M99438
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637
 30 C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%/AF083246
 C-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL 83 PROTEIN).//1.5E-21//208aa//35%/Q24371
 C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%/AB025412
 C-NT2RM4000395
 C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H 10.03C IN CHROMOSOME I.//8E-20//393aa//24%/Q10297
 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nfS) mRNA, complete cds.//0//2092bp//99%/AF097025
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6; PEPTIDE P-H].//4.8E-11//242aa//31%/PO4280
 C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955
 50 C-NT2RM4000511

4213

4214

C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884
 C-NT2RM4000520
 C-NT2RM4000585
 C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%/AF186273
 C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%/AB014587
 C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%/AB020657
 C-NT2RP1000040
 C-NT2RP1000063
 C-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%/X98834
 C-NT2RP1000101
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%/P93471
 C-NT2RP1000112
 C-NT2RP1000124
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDF).//4.5E-50//181aa//60%/P51859
 C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%/AB023165
 C-NT2RP1000170
 C-NT2RP1000191
 C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%/Q02357
 C-NT2RP1000243
 C-NT2RP1000259
 C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%/AF067730
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%/AF053551
 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%/P32447
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%/P25343
 C-NT2RP1000357
 C-NT2RP1000376//Homo sapiens mRNA; cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%/AL080187
 C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%/AB011159
 C-NT2RP1000416
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.8E-94//

1019bp//63%/AF111423
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%/Q08257
 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26C10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%/P34580
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%/P09653
 C-NT2RP1000481
 C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%/D87686
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%/P49020
 C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%/P97367
 C-NT2RP1000581
 C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%/P25233
 C-NT2RP1000688
 C-NT2RP1000695
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%/E14379
 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%/AF101434
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%/Q07960
 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%/AF067223
 C-NT2RP1000846
 C-NT2RP1000851
 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%/Q13823
 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbCH5B (UBCH5B) mRNA, complete cds.//4.6E-105//504bp//99%/U39317
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%/Q04652
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa

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//25%/Q13823
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%/M17885
 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%/P19338
 C-NT2RP1000980
 C-NT2RP1000988
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78// 10 1529bp//61%/L01790
 C-NT2RP1001014
 C-NT2RP1001395
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%/P91917
 C-NT2RP1001424
 C-NT2RP1001449
 C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%/AJ005257
 C-NT2RP1001466
 C-NT2RP1001475
 C-NT2RP1001482
 C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%/Q08891
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%/P42803
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%/035566 30
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%/P47758
 C-NT2RP1001616
 C-NT2RP1001665//CALMODULIN.//0.00000051//83aa//30%/P02594
 C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%/034136
 C-NT2RP2000007
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%/P51523
 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//1.8E-22//184aa//34%/Q01730
 C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tld56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%/AF061749
 C-NT2RP2000054
 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSIL 50

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ON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%/P49446
 C-NT2RP2000067
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//3.4E-51//383aa//32%/P33450
 C-NT2RP2000079
 C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%/AB018338
 C-NT2RP2000091
 C-NT2RP2000097
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%/AB018356
 C-NT2RP2000120
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L.//2.5E-117//541aa//42%/P41877
 C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%/AB023206
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%/P35585
 C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%/P41891
 C-NT2RP2000157//ML02 PROTEIN.//2.6E-11//62aa//40%/Q09329
 C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4E-315//1430bp//99%/AB023225
 C-NT2RP2000173
 C-NT2RP2000175
 C-NT2RP2000195
 C-NT2RP2000205
 C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%/AB020699
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%/P35568
 C-NT2RP2000232
 C-NT2RP2000233
 C-NT2RP2000239
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//3.4E-21//210aa//33%/P56558
 C-NT2RP2000270
 C-NT2RP2000274
 C-NT2RP2000283
 C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//1.6E-27//576aa//25%/Q102

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C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT). //3.3E-186//256aa//60%/Q99676
C-NT2RP2000298
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds. //4.3E-279//193bp//99%/U82381
C-NT2RP2000328
C-NT2RP2000329//GTP: AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3). //2E-111//226aa//92%/P08760
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116. //6.3E-115//674aa//46%/P17564
C-NT2RP2000369
C-NT2RP2000412
C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F). //4.3E-228//415aa//100%/P52597
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-6-phosphate mutase mRNA, complete cds. //0//1757bp//99%/AF102265
C-NT2RP2000438
C-NT2RP2000448//KES1 PROTEIN. //8.7E-54//392aa//38%/P35844
C-NT2RP2000503
C-NT2RP2000510
C-NT2RP2000516
C-NT2RP2000603
C-NT2RP2000617
C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds. //0//2482bp//99%/AB014514
C-NT2RP2000656
C-NT2RP2000658
C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-). //1.3E-27//349aa//32%/Q01577
C-NT2RP2000704
C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNALIGASE) //2.7E-100//488aa//44%/O32038
C-NT2RP2000764//NIFS PROTEIN. //6.6E-36//252aa//42%/P12623
C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds. //0//3347bp//99%/AB020680
C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A). //0.000000056//179aa//29%/Q99104
C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120). //0.00000011//96aa//29%/P13466
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT. //0.000000079//172aa//28%/P26174
- C-NT2RP2000819
C-NT2RP2000841
C-NT2RP2000845
C-NT2RP2000863
C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2. //0//694aa//99%/O60841
C-NT2RP2000892
C-NT2RP2000931//MATRIN 3. //2.4E-289//467aa//95%/P43244
C-NT2RP2000932//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043). //0//2487bp//99%/AL050390
C-NT2RP2000938
C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds. //0//3458bp//99%/AB018298
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds. //0//1989bp//96%/AB024704
C-NT2RP2000985
C-NT2RP2001036
C-NT2RP2001044
C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488. //0//2749bp//99%/AB007957
C-NT2RP2001065
C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMO OXIDASE). //5.8E-46//222aa//45%/Q20939
C-NT2RP2001081//SYNAPTOTAGMIN IV. //4.2E-118//430aa//54%/P50232
C-NT2RP2001094
C-NT2RP2001119
C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein. //0//2514bp//99%/AJ132440
C-NT2RP2001218
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMHC). //2.2E-10//366aa//28%/P14105
C-NT2RP2001381
C-NT2RP2001397//Homo sapiens mRNA; cDNA DKFZp434B174 (from clone DKFZp434B174). //0//1495bp//100%/AL080146
C-NT2RP2001427
C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds. //0//1748bp//99%/AB018340
C-NT2RP2001675
C-NT2RP2001721
C-NT2RP2001907
C-NT2RP2001969
C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds. //4.7E-177//1

- 538bp//74%//AF062378
 C-NT2RP2002046
 C-NT2RP2002154
 C-NT2RP2002208
 C-NT2RP2002270//AF-9 PROTEIN.//0.00000012//74aa//36%//P42568
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%//Y16521
 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds.//8.4E-254//1158bp//99%//AB015594
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%//AF038958
 C-NT2RP2002426
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%//AB005289
 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B041 6.5 IN CHROMOSOME X.//6.2E-19//288aa//26%//Q11073
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN A LG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%//P12815
 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%//P55345
 C-NT2RP2002621
 C-NT2RP2002672
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F1 2.15C IN CHROMOSOME II.//1.9E-14//210aa//30%//O14345
 C-NT2RP2002769
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%//P29764
 C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%//AF038392
 C-NT2RP2002954
 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%//P51669
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.0000001//98aa//36%//P10129
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%//AB026190
 C-NT2RP2003108
 C-NT2RP2003117
 C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%//AF 079765
 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%//Q04652
 C-NT2RP2003177
 C-NT2RP2003194
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%//AF151811
 C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 methylating protein, complete cds.//0//1526bp//99%//AB006572
 C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%//P26337
 C-NT2RP2003367
 C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%//P38378
 C-NT2RP2003446
 C-NT2RP2003533
 C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%//P74261
 C-NT2RP2003596
 C-NT2RP2003629
 C-NT2RP2003687
 C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%//Q05481
 C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%//P51669
 C-NT2RP2003793
 C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%//O09175
 C-NT2RP2003986
 C-NT2RP2004042
 C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered piece s.//8.2E-202//926bp//100%//AL096820
 C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%//P38120
 C-NT2RP2004392//MNN4 PROTEIN.//1.4E-11//143aa//27%//P36044
 C-NT2RP2004463
 C-NT2RP2004602
 C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%//AB023139
 C-NT2RP2004655//Homo sapiens mRNA for leucine rich

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protein. //8.5E-233//1061bp//99%/AJ006291
 C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G
 9.10C IN CHROMOSOME 1. //5.6E-64//616aa//33%/Q9235
 5
 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (LEUCRS). //9.5E-73//153aa//59%/Q10490
 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA). //3.7E-135//414aa//62%/P53588
 C-NT2RP2004802
 C-NT2RP2004841
 C-NT2RP2004936
 C-NT2RP2004959//P54 PROTEIN PRECURSOR. //0.00000095//297aa//20%/P13692
 C-NT2RP2004999
 C-NT2RP2005000
 C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds. //0//1694bp//99%/AB014515
 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein. //0//1693bp//99%/AJ011779
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1. //3.3E-47//155aa//59%/P32447
 C-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myo-regulated dead boxprotein). //0//2388bp//98%/X98743
 C-NT2RP2005140
 C-NT2RP2005147
 C-NT2RP2005159
 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds. //0//2087bp//99%/AF097025
 C-NT2RP2005270
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds. //0//2122bp//99%/D89053
 C-NT2RP2005293
 C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds. //0//1515bp//99%/AB014576
 C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds. //0//2199bp//99%/AF072247
 C-NT2RP2005393//AUTOANTIGEN NCP-1. //7.2E-39//224aa//35%/Q13823
 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //1.2E-13//185aa//38%/Q08170
 C-NT2RP2005441
 C-NT2RP2005453
 C-NT2RP2005464

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C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM 2. //3E-44//252aa//41%/P38127
 C-NT2RP2005472
 C-NT2RP2005495
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55). //5.2E-81//166aa//88%/P36876
 C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds. //0//1825bp//99%/AF151803
 C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds. //0//3994bp//99%/AF092563
 C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds. //2.4E-304//1687bp//85%/AF035526
 C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds. //0//2856bp//99%/AB007963
 C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE). //2E-20//181aa//36%/Q39366
 C-NT2RP2005555
 C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds. //1E-46//576bp//70%/AF062529
 C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds. //8.9e-313//1455bp//98%/AF062085
 C-NT2RP2005622
 C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1). //1E-11//128aa//36%/P47623
 C-NT2RP2005637
 C-NT2RP2005640
 C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1). //1.2E-13//74aa//45%/P56101
 C-NT2RP2005669//Homo sapiens mRNA for DEDD protein. //3.9E-209//957bp//99%/AJ010973
 C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds. //4.4E-200//908bp//99%/AF089814
 C-NT2RP2005683
 C-NT2RP2005690
 C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds. //0//1684bp//99%/AB018342
 C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODPI PROTEIN). //0.00000003//169aa//28%/P38074
 C-NT2RP2005748
 C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds. //0//1968bp//99%

- //AF068868
C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%//AF082516
C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%//P47943
C-NT2RP2005767//G.gallus PB1 gene.//5E-163//1158bp//81%//X90849
C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds.// 10 2.7E-180//656bp//99%//AF151351
C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%//Q02038
C-NT2RP2005781
C-NT2RP2005804
C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%//P34223
C-NT2RP2005853
C-NT2RP2005868
C-NT2RP2005886
C-NT2RP2005890
C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%//AB023188
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%//P48837
C-NT2RP2006038
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%//Q08170
C-NT2RP2006052
C-NT2RP2006069
C-NT2RP2006071
C-NT2RP2006100//Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102).//0//1759bp//99%//AL049970
C-NT2RP2006106
C-NT2RP2006141
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%//AB014554
C-NT2RP2006196
C-NT2RP2006200
C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%//X96484
C-NT2RP2006237
C-NT2RP2006238
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAINLC1].//2E-59//388aa//32%//P4 50
- 6821
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%//AF035262
C-NT2RP2006333
C-NT2RP2006365
C-NT2RP2006393
C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//0.00000034//50aa//50%//Q61658
C-NT2RP2006456
C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%//AJ006266
C-NT2RP2006467
C-NT2RP2006472
C-NT2RP2006565//Sus scrofa mRNA for SCAMP1 protein.//0//1276bp//84%//Y15710
C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%//P24461
20 C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%//P09543
C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%//AB020708
C-NT2RP3000072
C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%//AB011164
C-NT2RP3000220
C-NT2RP3000251
30 C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%//AF120334
C-NT2RP3000312
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%//AJ242978
C-NT2RP3000333
C-NT2RP3000348
C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.00000028//185aa//31%//025074
40 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%//AB019219
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%//P35293
C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOXPROTEIN 13)//1.7E-139//679aa//41%//043143

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C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%/AF071185
 C-NT2RP3000484
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%/P28160
 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%/P15151
 C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%/Q07283
 C-NT2RP3000599
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%/P51523
 C-NT2RP3000644
 C-NT2RP3000661
 C-NT2RP3000665
 C-NT2RP3000690
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%/Q94650
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%/Q61982
 C-NT2RP3000836
 C-NT2RP3000841
 C-NT2RP3000850
 C-NT2RP3000852
 C-NT2RP3000859
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%/U53445
 C-NT2RP3000869
 C-NT2RP3000901
 C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA A, complete cds.//0//3199bp//99%/AF064257
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%/AF015264
 C-NT2RP3000980
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159
 C-NT2RP3001004
 C-NT2RP3001081
 C-NT2RP3001084
 C-NT2RP3001096//Rattus norvegicus leprecan (leprel) mRNA, complete cds.//1.7E-94//787bp//66%/AF087433
 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%/P55201
 C-NT2RP3001109
 C-NT2RP3001116
 C-NT2RP3001119
 C-NT2RP3001133

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C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%/AB018305
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MADD1-SCY1 INTERGENIC REGION.//1.7E-10//196aa//27%/P53154
 C-NT2RP3001214
 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%/P35663
 C-NT2RP3001221//GAMMA-BUTYROBETAINE, 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.9E-31//353aa//30%/P80193C-NT2RP3001236
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%/P14873
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%/AB020718
 C-NT2RP3001307
 C-NT2RP3001325
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%/AB025905
 C-NT2RP3001392
 C-NT2RP3001396
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%/P49711
 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//25%/P53009
 C-NT2RP3001420
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%/O33529
 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%/O09053
 C-NT2RP3001457
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%/P11632
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA A, complete cds.//0//1475bp//99%/U13395
 C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//0//2295bp//99%/AF064801
 C-NT2RP3001529//SP00B-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%/P20964
 C-NT2RP3001621
 C-NT2RP3001629
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%/Q92609
 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.8E-0

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- 9//132aa//31%/022468
 C-NT2RP3001676
 C-NT2RP3001679
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.
 E.//1.6E-11//348aa//27%/P24733
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).
 N.//7.4E-18//249aa//30%/Q04652
 C-NT2RP3001896
 C-NT2RP3001915
 C-NT2RP3001929
 C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98/
 /269aa//62%/P52742C-NT2RP3004466
 C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED
 D PROTEIN VPS35.//3.3E-113//466aa//42%/P34110
 C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 pro
 tein, partial cds.//0//1520bp//99%/AB014532
 C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 pro
 tein, partial cds.//0//974bp//95%/AB011126
 C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN
 B) (ANKYRIN, NONERYTHROID).//0.00000038//150aa//2
 88%/Q01484
 C-NT2RP3004572//Homo sapiens cofactor of initiator
 function (CIF150) mRNA, complete cds.//0//1770bp/
 /99%/AF026445
 C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 pro
 tein, complete cds.//0//1639bp//99%/AB007946
 C-NT2RP3004594//Homo sapiens mRNA for AND-1 protei
 n.//0//1807bp//99%/AJ006266
 C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75
 //464aa//35%/Q02084
 C-NT2RP3004618//Homo sapiens putative RNA-binding
 protein Q99 mRNA, complete cds.//0//3972bp//98%/A
 F093097
 C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82)
 (EASILY SHOCKED PROTEIN).//1.7E-72//254aa//45%/P5
 4352
 C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.6
 E-98//239aa//64%/P35526
 C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.
 //4.9E-51//335aa//37%/Q64375
 C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 pro
 tein, complete cds.//0//3013bp//99%/AB020657
 C-NT2RP4000109//Homo sapiens mRNA for MEGF5, parti
 al cds.//0//2161bp//99%/AB011538
 C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECI
 FICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNI
 T).//0//728aa//99%/Q10568
 C-NT2RP4000129
 C-NT2RP4000147//Drosophila melanogaster putative A
 RF1 GTPase activatingprotein (ARF1-GAP) mRNA, comp 50
- lete cds.//3.8E-28//528bp//67%/AF011427
 C-NT2RP4000150
 C-NT2RP4000151
 C-NT2RP4000159
 C-NT2RP4000185
 C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 pro
 tein, partial cds.//0//4149bp//99%/AB014600
 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PREC
 URSOR (AGSA).//5.9E-15//104aa//40%/P15287
 10 C-NT2RP4000243//Homo sapiens mRNA for cartilage-as
 sociated protein (CASP).//0//1932bp//99%/AJ006470
 C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1
 (NDPP-1).//2.7E-84//208aa//76%/Q03173
 C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.
 1.9).//5.5E-29//153aa//43%/023968
 C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G
 8.09C IN CHROMOSOME I.//3.5E-297//1024aa//55%/P87
 115
 C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (AT
 P PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.5E-26
 //237aa//28%/Q01631
 C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX
 PROTEIN (UHS KERATIN).//0.0000003//101aa//32%/P26
 372
 C-NT2RP4000355
 C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 pro
 tein, complete cds.//0//4074bp//99%/AB018281
 C-NT2RP4000367//Homo sapiens IkappaB kinase comple
 x associated protein (IKAP) mRNA, complete cds.//
 30 0//4782bp//99%/AF044195
 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEAS
 E FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%
 //075570
 C-NT2RP4000376//Homo sapiens mRNA for phospholipas
 e A2 activating protein.//0//2412bp//99%/AJ238243
 C-NT2RP4000381
 C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110
 //435aa//50%/P52738C-NT2RP4000415
 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2
 40 -MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDA
 SE) (FRAGMENT).//2.6E-51//438aa//33%/P45701
 C-NT2RP4000448//Homo sapiens mRNA; cDNA DKFZp566G0
 746 (from clone DKFZp566G0746).//0//3991bp//99%/A
 L050078
 C-NT2RP4000449
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTE
 IN ICPO.//0.0000003//175aa//27%/P09309
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROL
 ASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15)
 (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQ

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UITINATING ENZYME 15). //2.5E-37//291aa//38%/P5010
 1
 C-NT2RP4000480
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (M
 RNA TRANSPORT REGULATOR MTR4). //1.9E-67//721aa//29
 %//Q09475
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1). //8.8
 E-50//214aa//50%/P40484
 C-NT2RP4000500
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1. // 10
 1.5E-106//495aa//45%/P45818
 C-NT2RP4000524
 C-NT2RP4000541
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN). //7.4E
 -14//233aa//31%/P40319
 C-NT2RP4000560
 C-NT2RP4000588
 C-NT2RP4000614//Homo sapiens TLS-associated protei
 n TASR-2 mRNA, complete cds. //2.9E-188//863bp//99%
 //AF067730
 C-NT2RP4000638
 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTE
 IN ICPO. //0.00000037//175aa//27%/P09309
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTH
 ESIS PROTEIN SPSE. //1.1E-32//350aa//30%/P39625
 C-NT2RP4000704
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B041
 6.5 IN CHROMOSOME X. //1.1E-13//295aa//27%/Q11073
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEI
 N. //3.2E-191//199aa//78%/P10267
 C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 pro
 tein, partial cds. //0//3392bp//95%/AB023148
 C-NT2RP4000737
 C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 pro
 tein, complete cds. //0//3574bp//99%/AB023229
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CP
 T1-SPC98 INTERGENIC REGION. //0.000000032//67aa//31
 %//P53915
 C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 pro
 tein, complete cds. //0//1927bp//99%/AB007939
 C-NT2RP4000833
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger
 protein SALL1. //4.3E-94//810bp//65%/Y18265
 C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEI
 N HET-E-1. //8.5E-21//271aa//28%/Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (AR
 GINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CY
 TOSOL AMINOPEPTIDASE IV) (AP-B). //5.7E-82//324aa//
 48%/O09175
 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGME 50

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NT). //4.1E-85//174aa//55%/P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN. //6.2E
 -91//173aa//87%/O35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1
 S9 PROTEIN). //9.6E-96//513aa//42%/P22314
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLA
 GEN-BINDING 59 KD PROTEIN). //2.6E-26//227aa//36%/Q06828
 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROL
 ASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE D
 UB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-
 1) (DEUBIQUITINATING ENZYME 1). //1.5E-76//346aa//4
 3%/Q61068
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protei
 n. //0//2487bp//99%/Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICAS
 E MJ1505. //0.00000014//185aa//25%/Q58900
 C-NT2RP4000955
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERA
 SE P5 PRECURSOR (EC 5.3.4.1). //1.4E-26//90aa//42%/P38660
 C-NT2RP4000975
 C-NT2RP4000979
 C-NT2RP4000984
 C-NT2RP4000989//UNC-47 PROTEIN. //0.0000082//173aa//
 25%/P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135
 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBU
 NIT 2) (RPA135). //0//838aa//87%/P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8. //3.7E-16//401a
 a//26%/P39968
 C-NT2RP4001006
 C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 pro
 tein, complete cds. //0//2482bp//99%/AB023181
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (E
 C 6.1.1.4) (LEUCINE--TRNA LIGASE) //1.5E-92//443aa//
 44%/Q09996
 C-NT2RP4001057
 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.
 //6.7E-51//335aa//37%/Q64375
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC
 3.6.1.38) (GOLGI CA2+-ATPASE). //1.3E-123//563aa//4
 6%/P13586
 C-NT2RP4001080//Homo sapiens mRNA for Rod1, comple
 te cds. //0//1439bp//99%/AB023967
 C-NT2RP4001086
 C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITA
 SE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA
 EDITING ENZYME 1). //2.6E-17//121aa//36%/P51400
 C-NT2RP4001100

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C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT. //1.9E-115//224aa//100%/P38378
 C-NT2RP4001122//TIPD PROTEIN. //1.4E-65//253aa//41%
 //015736
 C-NT2RP4001126//TRICHOHYALIN. //2.9E-18//380aa//26%
 //Q07283
 C-NT2RP4001138
 C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLA
 LASE (EC 3.5.1.18) (SDAP). //0.00000021//93aa//33%
 /P44514
 C-NT2RP4001148//SOF1 PROTEIN. //1.3E-104//236aa//52%
 %/P33750
 C-NT2RP4001149
 C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLEC
 ULE PRECURSOR (NR-CAM) (BRAVO). //3.4E-29//385aa//29%
 %/P35331
 C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE
 TRANSLOCATOR PRECURSOR (CTPT). //4.7E-29//227aa//35%
 %/P52178
 C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds. //4.4E-104//1460bp
 //65%/U95760
 C-NT2RP4001207
 C-NT2RP4001210
 C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5
 PRECURSOR (EC 5.3.4.1). //6.2E-27//90aa//42%
 /P38660
 C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN)
 N). //1.8E-103//508aa//43%/Q04652
 C-NT2RP4001235
 C-NT2RP4001256
 C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cds. //0//2876bp//99%/AB020682
 C-NT2RP4001274//Human transporter protein (gl7) mRNA, complete cds. //4.4E-58//1196bp//61%/U49082
 C-NT2RP4001276//TRICHOHYALIN. //7.9E-09//126aa//32%
 //Q07283
 C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT). //5.9E-17//296aa//29%/P24391
 C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5. //8.5E-213//1129bp//92%/AJ001119
 C-NT2RP4001339//Homo sapiens mRNA for AMMER1 protein. //9.2E-160//736bp//99%/AJ007014
 C-NT2RP4001343
 C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds. //2.7E-310//1400bp//100%/AB017494

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C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds. //1.4E-58//2425bp//59%/U53445
 C-NT2RP4001353
 C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN). //1.6E-19//222aa//30%
 /Q08180
 C-NT2RP4001373
 C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1). //9.2E-17//146aa//35%/P18160
 C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D 3.06 IN CHROMOSOME I. //2E-53//436aa//30%/Q10085
 C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete cds. //0//2716bp//99%/AB023140
 C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT). //7.7E-190//422aa//82%/Q14141
 C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT). //1.2E-138//419aa//54%/Q99676
 C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds. //2.7E-66//738bp//71%
 %/AF129131
 C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE). //0//962aa//78%/Q02218
 C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1. //1E-27//374aa//29%/P39010
 C-NT2RP4001502
 C-NT2RP4001507
 C-NT2RP4001524
 C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NO T1/CDC39-HMR INTERGENIC REGION. //5.7E-54//242aa//38%
 %/P25656
 C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds. //0//3202bp//99%/AF152961
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-). //4.7E-09//216aa//24%/P96902
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN. //0.00000054//213aa//26%/Q02453
 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1. //1.8E-10//109aa//36%/P35197
 C-NT2RP4001571
 C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds. //0//3046bp//99%/AF100756
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein. //0//1087bp//87%/AJ223830
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNALIGASE) (ILERS). //1.7E-141//373aa//47%/P73505

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C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cds.//0//1897bp//99%/AB020676

C-NT2RP4001614

C-NT2RP4001634

C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN M ET18/MMS19.//5.1E-46//234aa//32%/P40469

C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%/P25323

C-NT2RP4001677

C-NT2RP4001679

C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568

C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%/Q10282

C-NT2RP4001730//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUCT).//6.4E-170//1168aa//33%/Q09332

C-NT2RP4001739

C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%/P51523

C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete cds.//0//3144bp//99%/AB023232

C-NT2RP4001803

C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFAL1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/035566

C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%/P55083

C-NT2RP4001828

C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds.//6.3E-99//555bp//73%/AF155595

C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%/P37709

C-NT2RP4001893//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043).//0//1306bp//98%/AL050390

C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000014//345aa//25%/Q00808

C-NT2RP4001901

C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258aa//32%/Q12024

C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//38%/P49711

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE MET

HYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE).//1.5E-13//211aa//28%/Q43209

C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%/P13816

C-NT2RP4001953

C-NT2RP4001966

C-NT2RP4001975

C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370aa//27%/Q04652

C-NT2RP4002052

C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOXPROTEIN 13)//1E-137//679aa//40%/043143

C-NT2RP4002071

C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3E-150//722aa//39%/Q05481

C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNIT S) (TFIIA-42) (TFIIAL).//0.0000067//250aa//31%/P52655

C-NT2RP4002298

C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//53%/P38938

C-NT2RP4002791

C-NT2RP4002888//Homo sapiens mRNA; cDNA DKFZp434F172 (from clone DKFZp434F172).//0//2557bp//99%/AL080202

C-NT2RP4002905

C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552

C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5E-15//280aa//27%/Q00808

C-NT2RP5003492

C-NT2RP5003500

C-NT2RP5003506

C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR).//3.3E-23//219aa//40%/P37116

C-NT2RP5003524

C-NT2RP5003534

C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262

C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//0.0000042//102aa//32%/014727

C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%/AF058922

C-OVARC1000035

C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//0.00000032//60aa//

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/45%/P80022
 C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174
 aa//26%/Q02874
 C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 AC
 CESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.4E-14//25
 9aa//30%/P51610
 C-OVARC1000113
 C-OVARC1000139//Homo sapiens CGI-21 protein mRNA,
 complete cds.//0//1562bp//99%/AF132955
 C-OVARC1000148
 C-OVARC1000151//Homo sapiens partial mRNA for puta
 tive protein p38 interacting with transcription fa
 ctor Spl.//2.5E-95//461bp//98%/AJ242975
 C-OVARC1000168
 C-OVARC1000209//Oryza sativa submergence induced p
 rotein 2A mRNA, complete cds.//1.8E-32//511bp//65%
 //AF068332
 C-OVARC1000212
 C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA
 (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER 0
 F PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.2E-120//3
 51aa//54%/Q16665
 C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSO
 R (EC 3.4.11.22) (POLYPEPTIDASE) (LEUCINE AMINOPEPT
 IDASE IV) (LAPIV) (AMINOPEPTIDASE III) (AMINOPEPTID
 ASE YSCI).//5.4E-53//384aa//30%/P14904
 C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//
 87%/P23249
 C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2)./
 /2.7E-40//154aa//38%/P29363
 C-OVARC1000321
 C-OVARC1000326
 C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GC
 N4-WBP1 INTERGENIC REGION.//5.9E-14//200aa//27%/P
 40004.
 C-OVARC1000347
 C-OVARC1000384
 C-OVARC1000411
 C-OVARC1000420
 C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%/Q04
 205
 C-OVARC1000443//Homo sapiens mRNA; cDNA DKFZp434A0
 73 (from clone DKFZp434A073).//0//1216bp//99%/ALO
 80126
 C-OVARC1000461
 C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//
 1.2E-25//227aa//25%/P11075
 C-OVARC1000466
 C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATA
 SE 3 (EC 3.1.3.48) (EC3.1.3.16) (DUAL SPECIFICITY

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PROTEIN PHOSPHATASE VHR).//3.1E-10//125aa//35%/P5
 1452
 C-OVARC1000479//Homo sapiens mRNA for KIAA0829 pro
 tein, partial cds.//0//1919bp//99%/AB020636
 C-OVARC1000520//Homo sapiens supervillin mRNA, com
 plete cds.//2.2E-157//892bp//91%/AF051850
 C-OVARC1000564
 C-OVARC1000576
 C-OVARC1000588
 10 C-OVARC1000605
 C-OVARC1000640
 C-OVARC1000649//Human squamous cell carcinoma of e
 sophagus mRNA for GRB-7 SH2 domain protein, comple
 te cds.//0//1812bp//98%/D43772
 C-OVARC1000661
 C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-4
 6//121aa//79%/P08886
 C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E
 -17//127aa//33%/Q58343
 20 C-OVARC1001034//Mus musculus Fn54 mRNA, partial cd
 s.//1.5E-178//1113bp//86%/AF001533
 C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 pr
 otein.//0//1172bp//97%/AJ130978
 C-OVARC1001065//Homo sapiens CGI-12 protein mRNA,
 complete cds.//1E-215//1027bp//98%/AF132946
 C-OVARC1001162
 C-OVARC1001243
 C-OVARC1001296
 C-OVARC1001360
 30 C-OVARC1001381//Homo sapiens mRNA for candidate tu
 mor suppressor involved in B-CLL.//6E-148//683bp//
 99%/AJ224819
 C-OVARC1001425
 C-PLACE1000005
 C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43
 %//P53538
 C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE
 (EC 4.2.1.55) (CROTONASE).//2.8E-29//134aa//43%/P
 52046
 C-PLACE1000184//Homo sapiens mRNA for KIAA0832 pro
 tein, complete cds.//5.5E-312//1411bp//99%/AB0206
 39
 C-PLACE1000185
 C-PLACE1000213//Homo sapiens mRNA for KIAA0977 pro
 tein, complete cds.//0//1904bp//99%/AB023194
 C-PLACE1000347
 C-PLACE1000374
 C-PLACE1000380//Homo sapiens mRNA for KIAA0853 pro
 tein, partial cds.//0//2208bp//99%/AB020660
 50 C-PLACE1000383//Homo sapiens mRNA for MTMR1 protei

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n. //0//753bp//99%/AJ224979
 C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN). //2.7E-30//352aa//31%/P15151
 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF). //1.2E-132//334aa//72%/P23246
 C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE). //0.0000028//134aa//29%/P53368
 C-PLACE1000435
 C-PLACE1000444
 C-PLACE1000562
 C-PLACE1000564
 C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINENUCLEOTIDE-BINDING PROTEIN 1). //1.6E-270//437aa//86%/P32455
 C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds. //0//2393bp//99%/AB020657
 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds. //2E-55//779bp//67%/AF044201
 C-PLACE1000636//MALE STERILITY PROTEIN 2. //1.2E-39//261aa//27%/Q08891
 C-PLACE1000716
 C-PLACE1000748
 C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds. //4.6E-250//1189bp//97%/AB028449
 C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds. //0//2002bp//99%/AB014548
 C-PLACE1000798
 C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148W. //2.5E-49//181aa//54%/P32899
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1. //2.6E-19//404aa//26%/P39010
 C-PLACE1000948
 C-PLACE1000972
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN). //4.4E-22//129aa//35%/Q03070
 C-PLACE1001000
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds. //0//1500bp//99%/AF065485
 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN). //4.3E-54//257aa//46%/Q04652
 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM). //3E-33//138aa//42%/Q61103
 C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8. //2.3E-61//132aa//46%/Q12929
 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence. //0//2118bp//99%/AC005412

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C-PLACE1001412
 C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered pieces. //0//1440bp//99%/AL031660
 C-PLACE1001503
 C-PLACE1001570
 C-PLACE1001610
 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE I). //4E-81//263aa//56%/P08635
 C-PLACE1001729
 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10. //3.5E-75//439aa//41%/P16381
 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMN). //5.4E-63//427aa//35%/Q57290
 C-PLACE1001810
 C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds. //0//1995bp//99%/AF058953
 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16). //2E-27//270aa//31%/P94524
 C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds. //0//1196bp//99%/AF131737
 C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds. //0//1729bp//99%/AF099935
 C-PLACE1001928
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4). //1.4E-78//496aa//37%/Q49091
 C-PLACE1002046//LICATIN (FRAGMENT). //1.7E-240//560aa//80%/Q61211
 C-PLACE1002072
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE). //0.0000053//188aa//29%/P49606
 C-PLACE1002140
 C-PLACE1002163
 C-PLACE1002170
 C-PLACE1002433
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN). //0.0000042//133aa//29%/Q13105
 C-PLACE1002465
 C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds. //6.7E-214//956bp//94%/AB018256
 C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds. //0//1750bp//99%/AF068180
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001. //9E-45//305aa//33%/Q15391
 C-PLACE1002794
 C-PLACE1002815

- C-PLACE1002839
 C-PLACE1002851
 C-PLACE1002941
 C-PLACE1002996
 C-PLACE1003045
 C-PLACE1003092
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-7
 9//253aa//60%/Q13268C-PLACE1003108
 C-PLACE1003145
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 10
 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBI
 QUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//5
 1%/P42743
 C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48
 %//P33750
 C-PLACE1003200
 C-PLACE1003296//Homo sapiens mRNA; cDNA DKFZp434G1
 73 (from clone DKFZp434G173).//0//1706bp//99%/AL0
 80133
 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGE 20
 R PROTEIN HPF1).//6.9E-206//396aa//86%/P51522
 C-PLACE1003334
 C-PLACE1003342
 C-PLACE1003353//Homo sapiens breast cancer antiest
 rogen resistance 3 protein (BCAR3) mRNA, complete
 cds.//0//2435bp//99%/U92715
 C-PLACE1003369
 C-PLACE1003602//Homo sapiens mRNA expressed in pla
 centa.//5.9E-278//1275bp//99%/D83200
 C-PLACE1003611
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEI
 N.//3.2E-10//380aa//25%/P18824
 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-R
 ICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//20
 9aa//34%/Q08170
 C-PLACE1003711
 C-PLACE1003723
 C-PLACE1003762
 C-PLACE1003771
 C-PLACE1003784
 C-PLACE1003923
 C-PLACE1003936
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, G
 AMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.4E-124//32
 6aa//73%/P80385
 C-PLACE1004104
 C-PLACE1004114
 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN
 BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.1E-1
 81//340aa//96%/P29387
- C-PLACE1004149
 C-PLACE1004156
 C-PLACE1004161
 C-PLACE1004183//Homo sapiens for TOM1-like protei
 n.//0//1279bp//97%/AJ010071
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//4.5E
 -10//208aa//27%/Q62556
 C-PLACE1004203//Homo sapiens GPI-anchored membrane
 protein CDw108 precursor, mRNA, complete cds.//0/
 /1882bp//99%/AF069493
 C-PLACE1004258
 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2
 (EC 3.4.21.-).//9.7E-36//389aa//31%/O15393
 C-PLACE1004277//Homo sapiens two pore domain K+ ch
 annel (TASK-2) mRNA, complete cds.//0//1498bp//99%
 //AF084830
 C-PLACE1004289
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48
 %//P33750
 C-PLACE1004316//H.sapiens mRNA for apoptosis speci
 fic protein.//0//1767bp//99%/Y11588
 C-PLACE1004358//Homo sapiens connector enhancer of
 KSR-like protein CNK1mRNA, complete cds.//0//2512
 bp//99%/AF100153
 C-PLACE1004376
 C-PLACE1004388
 C-PLACE1004405
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.
 -).//1.2E-39//385aa//33%/Q63448
 30 C-PLACE1004437//Human NAD+-specific isocitrate deh
 ydrogenase beta subunit precursor, mRNA, nuclear g
 ene encoding mitochondrial protein, completecds.//
 0//985bp//99%/U49283
 C-PLACE1004451
 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002
 //218aa//23%/P25823
 C-PLACE1004473
 C-PLACE1004510//Homo sapiens cofactor of initiator
 function (CIF150) mRNA, complete//1.3E-209//954bp
 40 //99%/AF026445
 C-PLACE1004516
 C-PLACE1004548
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECI
 FICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNI
 T).//0//525aa//99%/Q10568
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//
 264aa//32%/Q13438
 C-PLACE1004645
 C-PLACE1004646//B.taurus mRNA for retinal pigment
 50 epithelial membrane receptor p63.//4.4E-42//985bp/

- /59%/X66277
 C-PLACE1004664
 C-PLACE1004672
 C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN A LG-2 (PMP41) (ALG-257).//1.6E-95//191aa//96%/P12815
 C-PLACE1004691
 C-PLACE1004722
 C-PLACE1004736
 C-PLACE1004740
 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-RECOGNIN).//4.4E-35//578aa//27%/O60152
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3GalVI, complete cds.//7.1E-224//790bp//98%/AB022918
 C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%/P30337
 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//4.7E-65//695aa//29%/Q01631
 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%/Q08170
 C-PLACE1004824
 C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q08891
 C-PLACE1004885
 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%/O42643
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.9E-48//198aa//44%/P06151
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%/AF099936
 C-PLACE1004934
 C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794
 C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B041 6.5 IN CHROMOSOME X.//2E-14//205aa//26%/Q11073
 C-PLACE1004982
 C-PLACE1005026
 C-PLACE1005027
 C-PLACE1005046
 C-PLACE1005077
 C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%/L40401
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%/Q04652
- C-PLACE1005111
 C-PLACE1005181
 C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%/P05636
 C-PLACE1005206
 C-PLACE1005232
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PK PA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577
 C-PLACE1005261
 10 C-PLACE1005266
 C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%/AB011182
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%/P53352
 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760
 C-PLACE1005308
 20 C-PLACE1005313
 C-PLACE1005327
 C-PLACE1005335
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACILHYDROLYASE).//8.6E-09//194aa//27%/O33335
 C-PLACE1005374
 C-PLACE1005480
 C-PLACE1005481
 30 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%/AJ006276
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C1 0.5 IN CHROMOSOME III.//5.6E-52//173aa//57%/Q09251
 C-PLACE1005550
 C-PLACE1005554
 C-PLACE1005623
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, completecds.//0//2130bp//99%/AF083255
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%/P31350
 C-PLACE1005730
 C-PLACE1005755
 C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE I).//2.5E-79//209aa//53%/P08635
 50 C-PLACE1005803

- C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase
1B mRNA, complete cds.//1.1E-217//994bp//99%//AF0
27156
- C-PLACE1005851
- C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%//
P54120
- C-PLACE1005923
- C-PLACE1005925
- C-PLACE1005934
- C-PLACE1005936
- C-PLACE1005951
- C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.
1.-).//6.7E-30//198aa//37%//P43636
- C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSO
R (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-54//455aa//
32%//P14904
- C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TF
IID 90 KD SUBUNIT (TAFII-90).//0.00000014//254aa//
25%//P38129
- C-PLACE1005990
- C-PLACE1006011//Homo sapiens mRNA for poly(ADP-rib
ose) polymerase-2.//0//1564bp//99%//AJ236876
- C-PLACE1006040//Homo sapiens mRNA for alpha endosu
lfin.//4.7E-161//744bp//99%//X99906
- C-PLACE1006119//Homo sapiens Ran-GTP binding prote
in mRNA, partial cds.//1.5E-148//681bp//99%//AF039
023
- C-PLACE1006139
- C-PLACE1006159
- C-PLACE1006167
- C-PLACE1006170//Homo sapiens mRNA for KIAA0899 pro
tein, partial cds.//4.5E-293//953bp//99%//AB020706
- C-PLACE1006195
- C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICAS
E C12C2.06.//2.7E-116//496aa//48%//Q09747
- C-PLACE1006225
- C-PLACE1006236
- C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG
-S2) (DECORIN).//2E-16//244aa//31%//P28675
- C-PLACE1006246
- C-PLACE1006325//Homo sapiens mRNA; cDNA DKFp564J1
42 (from clone DKFp564J142).//3.8E-278//1271bp//9
9%//AL080066
- C-PLACE1006335
- C-PLACE1006357
- C-PLACE1006385//Homo sapiens epsin 2a mRNA, comple
te cds.//0//1168bp//99%//AF062085
- C-PLACE1006412
- C-PLACE1006414
- C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45/ 50
- /122aa//43%//P49910
- C-PLACE1006445
- C-PLACE1006470
- C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-5
5//142aa//85%//Q90595
- C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD
PROTEIN (SRP68).//1.1E-229//367aa//96%//Q00004
- C-PLACE1006492
- C-PLACE1006531
- 10 C-PLACE1006552
- C-PLACE1006598//Homo sapiens clone NH0310K15, WORK
ING DRAFT SEQUENCE, 4unordered pieces.//0//2182bp/
/99%//AC007383
- C-PLACE1006615
- C-PLACE1006626//Homo sapiens mRNA for KIAA0928 pro
tein, partial cds.//0//1760bp//99%//AB023145
- C-PLACE1006673
- C-PLACE1006678//Homo sapiens mRNA for type II memb
rane protein, completecds, clone:HP10328.//5.8E-24
//734bp//62%//AB015630
- 20 C-PLACE1006704
- C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (F
LAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
(FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-1
3//177aa//33%//Q59263
- C-PLACE1006782
- C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOL
OG.//9.8E-213//232aa//80%//P08547
- C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROL
ASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (U
BIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUI
TINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//
2E-15//188aa//29%//P35123
- C-PLACE1006883
- C-PLACE1006901
- C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%
//Q99181
- C-PLACE1006932
- C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.
6 IN CHROMOSOME III.//6.7E-48//278aa//41%//Q10000
- C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E
-86//522aa//36%//P97998
- C-PLACE1006958//Homo sapiens mRNA for heat shock p
rotein apg-1, completecds.//0//1770bp//99%//AB0234
21
- C-PLACE1006961
- C-PLACE1006962
- C-PLACE1006966
- C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DEL
AYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35/

4245

/180aa//33%/Q14542
 C-PLACE1007021
 C-PLACE1007105
 C-PLACE1007178
 C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPHORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%/P54304
 C-PLACE1007238
 C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-T1, complete cds.//6.5E-216//1068bp//96%/D50495
 C-PLACE1007242
 C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%/P34579
 C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%/Y15908
 C-PLACE1007274
 C-PLACE1007282
 C-PLACE1007301
 C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%/AF117649
 C-PLACE1007342
 C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%/AF096870
 C-PLACE1007367
 C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%/P27715
 C-PLACE1007386
 C-PLACE1007402
 C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%/Q17320
 C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%/P27487
 C-PLACE1007450
 C-PLACE1007452
 C-PLACE1007460
 C-PLACE1007484
 C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%/P52734
 C-PLACE1007507
 C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%/P08728

4246

C-PLACE1007524
 C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9e-316//1485bp//98%/AF159164
 C-PLACE1007544
 C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME III.//1E-49//361aa//36%/P34537
 C-PLACE1007583
 C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%/Q99676
 C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%/AB023194
 C-PLACE1007621
 C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%/P32506
 C-PLACE1007645
 C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952bp//99%/AB023194
 C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.7E-09//279aa//28%/Q26457
 C-PLACE1007690
 C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%/P43535
 C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%/AF061243
 C-PLACE1007725
 C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%/P10265
 C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%/AB014585
 C-PLACE1007746
 C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%/AB019602
 C-PLACE1007810
 C-PLACE1007843
 C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//99%/AP000010
 C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%/AB018309
 C-PLACE1007897
 C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSINII).//2.6E-14//370aa//25%/Q99323
 C-PLACE1007954
 C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%/AF084530

4247

4248

C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//0//2300bp//99%/AF079529

C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//48%/P52272

C-PLACE1007990

C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%/Q63622

C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4unordered pieces.//0//1833bp//99%/AC005628

C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6e-318//613aa//94%/P52590

C-PLACE1008095

C-PLACE1008122

C-PLACE1008129

C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.3E-24//395aa//31%/Q09531

C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%/P37709

C-PLACE1008209

C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.3E-283//671aa//77%/P53620

C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%/P12689

C-PLACE1008280

C-PLACE1008309

C-PLACE1008329

C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%/AB014579

C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%/P05432

C-PLACE1008401

C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%/P41541

C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%/Q06527

C-PLACE1008457

C-PLACE1008465

C-PLACE1008488

C-PLACE1008524//Human DNA sequence from clone 34B21 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZU5 domain similar to part of Tight Junction Protein Z01 (TJP1) and UNC5 Homologs, the gene for a novel BZRP (peripheral b

enzodiazapine recepto//0//1980bp//99%/AL031778

C-PLACE1008531

C-PLACE1008532

C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%/P22620

C-PLACE1008568

C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%/P37199

C-PLACE1008621

C-PLACE1008626

C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%/AJ006591

C-PLACE1008629

C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%/AF044333

C-PLACE1008693

C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%/AF038406

C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%/035345

C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.3E-269//1225bp//99%/AJ004974

C-PLACE1008813

C-PLACE1008854

C-PLACE1008867

C-PLACE1008887

C-PLACE1008902

C-PLACE1008925

C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%/P12623

C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%/AJ003112

C-PLACE1009045

C-PLACE1009060//BR01 PROTEIN.//6.7E-19//567aa//24%/P48582

C-PLACE1009090

C-PLACE1009091

C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%/P30432

C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452aa//67%/P51814

C-PLACE1009110

C-PLACE1009111
 C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP). //2E-68//181aa//43%/Q05086
 C-PLACE1009158
 C-PLACE1009166
 C-PLACE1009174
 C-PLACE1009186
 C-PLACE1009190
 C-PLACE1009230
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product. //2.1E-132//1229bp//75%/AF107295
 C-PLACE1009328
 C-PLACE1009335
 C-PLACE1009338
 C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2. //2.5E-10//151aa//29%/Q12067
 C-PLACE1009375
 C-PLACE1009388
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I. //0.00000047//165aa//33%/Q09820
 C-PLACE1009434
 C-PLACE1009443
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA). //7.8E-71//82aa//89%/P42356
 C-PLACE1009459
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP). //3.1E-289//550aa//93%/P54319
 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III. //3.9E-40//179aa//37%/P34580
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR). //8.1E-99//28aa//75%/Q99418
 C-PLACE1009542
 C-PLACE1009571
 C-PLACE1009581
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //5.1E-54//291aa//40%/Q00808
 C-PLACE1009607
 C-PLACE1009621
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN. //1.3E-60//209aa//41%/P25159
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN). //1.5E-285//538aa//99%/P55161
 C-PLACE1009665

C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds. //0//1854bp//100%/AF062534
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I. //7E-33//166aa//43%/Q09876
 C-PLACE1009721//MSF1 PROTEIN. //1.7E-22//176aa//33%/P35200
 C-PLACE1009731//AIG1 PROTEIN. //1.6E-22//274aa//28%/P54120
 10 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds. //4.3E-294//1329bp//100%/AB012190
 C-PLACE1009794
 C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds. //0//2685bp//99%/AB020712
 C-PLACE1009886
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION. //1.9E-108//277aa//43%/P53145
 20 C-PLACE1009971
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84). //4.6E-59//450aa//34%/P28175
 C-PLACE1009995//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123). //0//1962bp//99%/AL080122
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds. //5.2E-70//736bp//73%/U48288
 C-PLACE1010023
 30 C-PLACE1010031
 C-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein. //6E-279//1402bp//94%/X84692
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //0//2019bp//99%/AF065482
 C-PLACE1010076
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-). //1.4E-268//506aa//98%/Q62671
 C-PLACE1010102
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN). //7.3E-114//537aa//44%/Q04652
 40 C-PLACE1010106//Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418). //0//1974bp//99%/AL049385
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TFE3). //1.7E-20//156aa//42%/P22082
 C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I). //0.00000046//431aa//23%/P35662
 50 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-R

ICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN). //9.8E-11//95aa//49% //Q01130

C-PLACE1010202

C-PLACE1010261//SEGREGATION DISTORTER PROTEIN. //1.6E-77//214aa//62%//P25722

C-PLACE1010274//Homo sapiens mRNA; cDNA DKFZp5640123 (from clone DKFZp5640123). //0//1964bp//99%//AL080122

C-PLACE1010293

C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT). //1.1E-09//350aa//22%//P52178

C-PLACE1010324

C-PLACE1010329

C-PLACE1010362//1-PHOSPHATIDYLYNOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLYNOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC). //0.000000002//126aa//29%//P34024

C-PLACE1010364

C-PLACE1010383

C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds. //0//2121bp//99%//AB020643

C-PLACE1010491

C-PLACE1010492

C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds. //0//1981bp//99%//AB022718

C-PLACE1010529

C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01. //0.00000012//616aa//24%//P25386

C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds. //0//1904bp//99%//AB017546

C-PLACE1010616

C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNTC). //0.00000016//120aa//28%//P02642

C-PLACE1010629

C-PLACE1010630

C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13. //5.7E-75//423aa//39%//Q01755

C-PLACE1010714

C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds. //4E-299//1091bp//99%//AB019987

C-PLACE1010743//Homo sapiens myosin-Ixb splice variant (Myo9b) mRNA, partial cds. //8.9E-91//668bp//82%//AF020267

C-PLACE1010771//M. musculus HCNGP mRNA. //7.4E-168//966bp//89%//X68061

C-PLACE1010786

C-PLACE1010800

C-PLACE1010811

C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //1.3E-143//407aa//58%//Q05481

C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds. //0//1885bp//99%//AB011182

C-PLACE1010900

10 C-PLACE2000050

C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCHPROTEIN). //2.4E-191//828aa//48%//P21783

C-PLACE4000590

C-PLACE4000638

C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN). //7.9E-17//201aa//34%//P49816

C-Y79AA1001647

【1128】 相同性検索結果データ 7.

20 実施例 16 で選抜した 54 クロノンの 5' 末端クロノン配列に対する SwissProt 相同性検索結果データ

各データは、クロノン配列名、トップヒットデータの Definition、P 値: 比較配列の長さ (base): 相同性 (%), トップヒットデータの Organism、トップヒットデータの Accession No. の順に // で区切って記載した。なお、相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

F-HEMBA1000497//METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G). //0.13//52//38//P25860

30 F-HEMBA1001750//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E). //2.2e-28//104//59//Q24574

F-HEMBA1003854//VERPROLIN. //0.012//138//31//P37370

F-HEMBA1004193//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) (FRAGMENT). //0.93//39//33//Q37131

F-HEMBA1004860//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIPIP 2). //0.90//20//50//P38524

F-HEMBA1005572//ZINC FINGER PROTEIN 124 (HZF-16). //7.6e-46//141//58//Q15973

F-HEMBA1006038//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENT). //0.0033//32//46//P70560

F-HEMBA1006092//VERPROLIN. //1.0//62//35//P37370

F-HEMBA1006406//MATING PHEROMONE ER-10 PRECURSOR (EUPHOMONE R10). //0.30//41//36//P12350

F-HEMBA1006650//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR. //0.089//21//52//Q02593

50 F-HEMBA1006812//HEAT SHOCK PROTEIN HTGA (HEAT SHOC

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K PROTEIN HTPY). //0.38//156//30//P28697
 F-HEMBB1000672
 F-HEMBB1001197//DNA-BINDING PROTEIN 65 (PROTEIN GP 65). //1.0//30//36//P16012
 F-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1). //3.7e-54//241//47//P47853
 F-MAMMA1001252//HYPOTHETICAL 9.1 KD PROTEIN IN NIR Q 3' REGION (ORF3). //0.59//48//39//Q51483
 F-MAMMA1002094
 F-NT2RM4000634//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11). //0.26//58//27//P06333
 F-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT). //8.9e-20//83//48//P10895
 F-NT2RM4000783//ZINC FINGER PROTEIN (FRAGMENT). //1.0//42//40//P19326
 F-NT2RM4000857//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACIDLABILE CHAIN PRECURSOR (ALS). //6.0e-23//207//32//002833
 F-NT2RM4001178//HOMEODOMAIN PROTEIN OTX3 (ZOTX3). //0.012//156//28//Q90267
 F-NT2RM4002420//GLUTAMIC ACID-RICH PROTEIN PRECURSOR. //0.0012//81//37//P13816
 F-NT2RP2000198//CREB-BINDING PROTEIN. //0.29//98//37//Q92793
 F-NT2RP2000551//PROTEIN Q300. //0.00017//23//60//Q02722
 F-NT2RP2000660//HYPOTHETICAL PROTEIN MJ0401. //1.0//41//29//Q57844
 F-NT2RP2001214//MALE SPECIFIC SPERM PROTEIN MST84D C. //0.27//13//61//Q01644
 F-NT2RP2001460//PROTEIN KINASE C-LIKE (EC 2.7.1.-). //0.089//99//29//Q99014
 F-NT2RP2001756//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT). //4.0e-13//177//28//P16372
 F-NT2RP2002056//HYPOTHETICAL 6.0 KD PROTEIN IN THI 12 5' REGION. //0.37//12//75//P53820
 F-NT2RP2002677//NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3). //0.99//61//32//Q42616
 F-NT2RP2002755//OCTAPEPTIDE-REPEAT PROTEIN T2. //3.3e-10//90//35//Q06666F-NT2RP2002843//CYTOCHROME B. //0.78//103//26//P48884
 F-NT2RP2003101//ATPASE INHIBITOR, MITOCHONDRIAL HOMOLOG. //0.40//28//46//P37209
 F-NT2RP2003799//HYPOTHETICAL PROTEIN MJ0116.1. //0.80//55//32//P81303
 F-NT2RP2004095

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F-NT2RP2004732
 F-NT2RP2004920//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE. //0.18//18//55//Q48251
 F-NT2RP2005454
 F-NT2RP2005776//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE) (FRAGMENT). //7.4e-38//136//41//P51003
 F-NT2RP2005806//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR. //4.0e-08//180//28//P32323
 10 F-NT2RP2005882
 F-NT2RP3001282//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB. //0.0022//69//39//P39217
 F-NT2RP3001723//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3). //0.00035//127//31//P15276
 F-NT2RP3002099//NONHISTONE CHROMOSOMAL PROTEIN HMG-17. //0.97//71//28//P05204
 F-NT2RP3003155//CCAAT DISPLACEMENT PROTEIN (HOMEODOMAIN PROTEIN CLOX) (CLOX-1) (FRAGMENT). //0.064//110//34//P39881
 20 F-NT2RP3004028//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT). //0.020//95//29//P15583
 F-OVARC1000008//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN). //2.8e-05//165//29//P17437
 F-OVARC1000724//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.035//152//30//P10162
 F-OVARC1000751//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (VIMW118 PROTEIN). //0.38//124//31//P28284
 30 F-OVARC1001029
 F-PLACE1000814//EC PROTEIN HOMOLOG 2 (FRAGMENT). //0.45//61//24//Q42377
 F-PLACE1003030//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29). //0.70//121//32//P47845
 F-PLACE1005549//RHO1 GDP-GTP EXCHANGE PROTEIN 1 (PROTEIN KINASE C SUPPRESSOR SKC1). //3.2e-08//205//24//P53046
 F-PLACE1007218//IG KAPPA CHAIN V-III REGION (PC 7210). //0.99//52//38//P01668
 【1129】 相同性検索結果データ 8. 実施例 16 で選抜した 54 クロンの 5' 末端 クロンの配列に対する EST と S TS を除いた GenBank 相同性検索結果データ
 各データは、クロン配列名、トップヒットデータの Definition、P 値: 比較配列の長さ (base): 相同性 (%), トップヒットデータの Accession No. の順に // で区切って記載した。なお、相同性のスコアの P 値が 1 より大であつ

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た場合はデータは示さない。

F-HEMBA1000497

F-HEMBA1001750//Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs.//6.6e-101//473//99//V00710

F-HEMBA1003854//Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS***, 18 unordered pieces.//1.7e-05//412//61//AC005081

F-HEMBA1004193//Human BAC clone RG343H22 from 7q31, complete sequence.//0.77//466//59//AC002386

F-HEMBA1004860//Human pigment epithelium-derived factor gene, complete cds.//6.7e-07//492//57//U29953

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt].//2.9e-47//341//77//S54641

F-HEMBA1006038//Human DNA sequence from clone 989H11 on chromosome 22q13.1-13.2, complete sequence.//0.28//436//59//Z83851

F-HEMBA1006092//Human chromosome 16p13.11 BAC clone CIT987SK-29B12 complete sequence.//0.28//309//60//U95738

F-HEMBA1006406//HS_2268_B2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=14 Row=F, genomic survey sequence.//3.7e-69//340//99//AQ070566

F-HEMBA1006650//H.sapiens CpG island DNA genomic Msel fragment, clone 5h5, forward read cpg5h5.fla.//9.4e-24//143//96//Z55730

F-HEMBA1006812//X.laevis xUBFalpha mRNA for upstream binding factor 2.//0.96//234//64//X59863

F-HEMBA100672//CIT-HSP-2350H6.TF CIT-HSP Homo sapiens genomic clone 2350H6, genomic survey sequence.//1.1e-68//375//94//AQ059158

F-HEMBA1001197//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//2.8e-10//229//66//U95760

F-HEMBA1001871//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//1.2e-27//619//62//AF038127

F-MAMMA1001252

F-MAMMA1002094//H.sapiens CpG island DNA genomic Msel fragment, clone 184g7, forward read cpg184g7.fla.//3.4e-29//167//97//Z59993

F-NT2RM4000634//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//1.4e-21//230//73//L49136

F-NT2RM4000657//Human mRNA for phospholipase C, complete cds.//0.029//245//61//D42108

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F-NT2RM4000783//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//3.7e-36//324//70//AC005199

F-NT2RM4000857//RPCI11-49P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-49P19, genomic survey sequence.//1.5e-62//322//97//AQ051961

F-NT2RM4001178//Streptomyces coelicolor cosmid 7H1.//0.0025//296//62//AL021411

10 F-NT2RM4002420//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//0.00013//121//76//AC005670

F-NT2RP2000198//Human platelet glycoprotein IX mRNA, 3' end.//0.016//246//62//M25827

F-NT2RP2000551//Rattus norvegicus microsatellite sequence clone 82G9.//2.0e-08//223//69//AJ233812

F-NT2RP2000660//Homo sapiens chromosome 19, cosmid R30953, complete sequence.//0.0073//209//66//AC005622

F-NT2RP2001214

20 F-NT2RP2001460//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.0//80//76//AC005189

F-NT2RP2001756//CIT-HSP-2373P1.TR CIT-HSP Homo sapiens genomic clone 2373P1, genomic survey sequence.//3.0e-38//220//94//AQ110589

F-NT2RP2002056//Genomic sequence from Human 17, complete sequence.//1.2e-80//317//91//AC002094

30 F-NT2RP2002677//Homo sapiens chromosome 10 clone CIT987SK-1031G15 map 10q25, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.//0.032//141//70//AC006097

F-NT2RP2002755//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 9/13.//1.8e-22//377//69//AP000018

F-NT2RP2002843//Homo sapiens BAC clone RG030L05 from 7q22, complete sequence.//6.5e-16//311//63//AC005050

F-NT2RP2003101//Human FMR1 gene, 5' end.//0.32//105//67//L19476

40 F-NT2RP2003799//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//1.6e-33//119//96//X52233

F-NT2RP2004095//HS_3083_A1_A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3083 Col=3 Row=A, genomic survey sequence.//1.0e-14//154//79//AQ106698

F-NT2RP2004732//CIT-HSP-631P16.TP CIT-HSP Homo sapiens genomic clone 631P16, genomic survey sequence.//2.3e-20//120//99//B79035

50 F-NT2RP2004920//Plasmodium falciparum MAL3P4, comp

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lete sequence.//0.030//397//59//AL008970
 F-NT2RP2005454//Plasmodium falciparum chromosome
 2, section 47 of 73 of the complete sequence.//0.97
 //455//56//AE001410
 F-NT2RP2005776//H.sapiens PAP mRNA.//1.0e-33//451/
 /68//X76770
 F-NT2RP2005806//Mus musculus musculus sex determin
 ing protein (Sry) gene, complete cds.//0.029//412/
 /60//U70652
 F-NT2RP2005882//Human DNA sequence from PAC 389A20
 on chromosome X contains ESTs STS, CpG islands an
 d polymorphic CA repeat.//9.4e-25//155//90//Z93242
 F-NT2RP3001282//RPCI11-52L16.TJ RPCI-11 Homo sapie
 ns genomic clone RPCI-11-52L16, genomic survey seq
 uence.//3.2e-21//122//100//AQ052775
 F-NT2RP3001723//H.sapiens CpG island DNA genomic M
 sel fragment, clone 13g5, reverse read cpg13g5.rtl
 a.//2.2e-18//163//85//Z56771
 F-NT2RP3002099//Homo sapiens chromosome 17, clone
 hCIT.296_K_1, complete sequence.//1.3e-76//351//86/
 /AC005180
 F-NT2RP3003155
 F-NT2RP3004028//Sequence 1 from patent US 5618695.
 //3.3e-13//217//70//I40055
 F-OVARC1000008//0.0040//674//57//M82836
 F-OVARC1000724//Herpes simplex virus type I immedi
 ate early (IE) gene 3 for transcriptional activator
 IE175 (= ICP 4).//1.1e-07//519//59//X06461
 F-OVARC1000751//Homo sapiens DNA from chromosome 1
 9, cosmid R29144, complete sequence.//7.2e-11//509
 //62//AC004221
 F-OVARC1001029//Human DNA sequence from clone 1940
 8 on chromosome 6q24.1-25.3 Contains STS and GSSs,
 complete sequence.//1.1e-05//388//61//AL031769
 F-PLACE1000814//Homo sapiens BAC clone GS011E15 fr
 om 5q31, complete sequence.//1.4e-84//717//78//AC0
 02427
 F-PLACE1003030
 F-PLACE1005549//Human guanine nucleotide regulator
 y protein (NET1) mRNA, complete cds.//4.9e-56//709/
 /68//U02081
 F-PLACE1007218//Homo sapiens chromosome 20 clone R
 P3-387E22, *** SEQUENCING IN PROGRESS ***, in unor
 dered pieces.//3.1e-39//214//98//AL031660

【1130】 相同性検索結果データ 9.

実施例 16 で選抜した 54 クロノンの 3' 末端クロノン配列
 に対する EST と STS を除いた GenBank 相同性検索結果デー
 タ

各データは、クロノン配列名、トップヒットデータの De
 finition、P 値: 比較配列の長さ (base): 相同性(%): ト

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ップヒットデータの Accession No. の順に // で区切って記
 載した。なお、同一クロノンで 5' 末端配列に対応する 3'
 末端配列が決定されていないものは空欄とした。相同性
 のスコアの P 値が 1 より大であった場合はデータは示さ
 ない。

R-HEMBA1000497//***ALU WARNING: Human Alu-J subfam
 ily consensus sequence.//1.4e-38//185//84//U14567
 R-HEMBA1001750//Hansenula wingei mitochondrial DN
 A, complete sequence.//1.7e-07//399//59//D31785
 R-HEMBA1003854//Human DNA sequence from clone 224A
 6 on chromosome 1p35.1-36.23 Contains part of a ge
 ne similar to Mouse Wnt-4 protein, the gene for CDC
 42 (cell division cycle 42 (GTP-binding protein, 2
 5kd)), ESTs, STSs, GSSs and a CpG Island, complete
 sequence.//1.4e-75//309//85//AL031281
 R-HEMBA1004193//***ALU WARNING: Human Alu-J subfam
 ily consensus sequence.//1.1e-34//188//81//U14567
 R-HEMBA1004860//Homo sapiens 12q13.1 PAC RPCI3-197
 B17 (Roswell Park Cancer Institute Human PAC libra
 ry) complete sequence.//1.3e-06//239//66//AC004241
 R-HEMBA1005572//Homo sapiens chromosome 21 PAC RPC
 IP704E14135Q2, complete sequence.//3.1e-21//341//6
 7//AJ010598
 R-HEMBA1006038//Homo sapiens chromosome 19, cosmid
 R34094, complete sequence.//1.7e-24//307//71//AC0
 04678
 R-HEMBA1006092//H.Sapiens mRNA for alpha2-subunit
 of soluble guanylyl cyclase.//0.76//246//62//X6328
 2
 R-HEMBA1006406//Human DNA sequence from clone 113J
 7 on chromosome Xp11.22-11.4. Contains part of a p
 utative Homeobox (pseudo?) gene, ESTs and an STS, c
 omplete sequence.//1.3e-31//297//77//AL023574
 R-HEMBA1006650//Homo sapiens BAC clone BK085E05 fr
 om 22q12.1-qter, complete sequence.//1.8e-15//350/
 /65//AC003071
 R-HEMBA1006812//Homo sapiens chromosome X clone RP
 3-424J12, *** SEQUENCING IN PROGRESS ***, in unor
 dered pieces.//1.8e-55//430//81//Z82207
 R-HEMBA1000672//Homo sapiens clone UWCC:y54c283 fr
 om 6p21, complete sequence.//9.1e-39//437//71//AC0
 06166
 R-HEMBA1001197//Homo sapiens PAC clone DJ0964C11 f
 rom 7p14-p15, complete sequence.//1.5e-37//275//85/
 /AC004593
 R-HEMBA1001871//Plasmodium falciparum chromosome 1
 2 clone 3D7, *** SEQUENCING IN PROGRESS ***, 5 uno
 rdered pieces.//0.00097//410//59//AC004688
 R-HEMBA1001252//Homo sapiens clone 201104, *** SEQ
 UENCING IN PROGRESS ***, 4 unordered pieces.//2.9e

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-13//364//64//AC004529
 R-MAMMA1002094//HS_3163_A1_A09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=17 Row=A, genomic survey sequence.//5.9e-41//256//91//AQ141441
 R-NT2RM4000634//Homo sapiens chromosome 19, cosmid R30783, complete sequence.//1.6e-21//283//73//AC005258
 R-NT2RM4000657
 R-NT2RM4000783
 R-NT2RM4000857//RPCI11-63K2.TK RPCI-11 Homo sapiens genomic clone RPCI-11-63K2, genomic survey sequence.//4.0e-07//62//98//AQ203073
 R-NT2RM4001178
 R-NT2RM4002420
 R-NT2RP2000198//Homo sapiens Chromosome 16 BAC clone CIT987-SK37914 -complete genomic sequence, complete sequence.//0.58//108//67//AC002307
 R-NT2RP2000551//Homo sapiens DNA, pseudoautosomal boundary-like sequencePABL2.//6.2e-72//391//87//D30043
 R-NT2RP2000660//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//0.0058//166//69//AC005324
 R-NT2RP2001214//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Varlp (varl) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//0.93//117//65//U49822
 R-NT2RP2001460
 R-NT2RP2001756//CIT-HSP-2382021.TR CIT-HSP Homo sapiens genomic clone 2382021, genomic survey sequence.//3.4e-91//507//92//AQ114228
 R-NT2RP2002056//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//0.00022//225//69//Z97181
 R-NT2RP2002677//CIT-HSP-2349K20.TF CIT-HSP Homo sapiens genomic clone 2349K20, genomic survey sequence.//3.1e-29//178//94//AQ062168
 R-NT2RP2002755//Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X*.//5.3e-39//449//72//Z81014
 R-NT2RP2002843//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence.//0.0097//498//59//AC005412
 R-NT2RP2003101//CIT-HSP-238301.TR CIT-HSP Homo sapiens genomic clone 238301, genomic survey sequence.//1.2e-32//344//75//AQ196754
 R-NT2RP2003799///3.6e-05//408//60//AL010237

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R-NT2RP2004095//Plasmodium falciparum chromosome 4 strain 3D7, *** SEQUENCING IN PROGRESS ***, in un ordered pieces.//2.1e-10//455//61//AL034557
 R-NT2RP2004732//Human DNA sequence from clone 703H14 on chromosome 1q23.2-24.3 Contains 3' end of a novel gene, ESTs, CA repeat(D1S445), STS, GSSs, complete sequence.//5.1e-51//383//74//AL031287
 R-NT2RP2004920//Homo sapiens chromosome 5, P1 clone 878H11 (LBNL H45), complete sequence.//0.062//315//61//AC005219
 R-NT2RP2005454//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs. polymorphic CA repeat, CpG island, CpG island genomic fragments.//0.75//246//63//Z86062
 R-NT2RP2005776//Homo sapiens PAC clone DJ1189D06 from 7p15.3-p14, complete sequence.//0.91//232//61//AC005232
 R-NT2RP2005806//Human neurofibromatosis type 1 (NF1) gene, intron 19a, complete sequence.//1.3e-19//405//66//U37368
 R-NT2RP2005882//Plasmodium falciparum MAL3P1, complete sequence.//1.1e-09//533//60//Z97348
 R-NT2RP3001282//Plasmodium falciparum MAL3P8, complete sequence.//0.00026//499//58//AL034560
 R-NT2RP3001723//Human BAC clone RC354L07 from 7q31, complete sequence.//0.00035//337//61//AC002466
 R-NT2RP3002099//Homo sapiens chromosome 17, clone hCIT.296_K_1, complete sequence.//1.8e-44//307//86//AC005180
 R-NT2RP3003155
 R-NT2RP3004028//F14A6-Sp6 IGF Arabidopsis thaliana genomic clone F14A6, genomic survey sequence.//0.95//95//65//B21351
 R-OVARC1000008
 R-OVARC1000724//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.91//83//71//AC005161
 R-OVARC1000751//HS_2222_A2_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=18 Row=E, genomic survey sequence.//2.8e-12//176//72//AQ033143
 R-OVARC1001029//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence LivermoreX library) and PAC RPCI1-93D11 (from Roswell Park Cancer Center) complete sequence.//1.2e-09//165//75//AC002357
 R-PLACE1000814//Homo sapiens BAC clone GS465N13 from 7p15-p21, complete sequence.//6.2e-52//514//75//AC004744
 R-PLACE1003030//Homo sapiens snRNA activating prot

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ein complex 190kD subunit (SNAP190) mRNA, complete cds. //9.6e-33//225//90//AF032387

R-PLACE1005549//Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence. //0.097//323//61//AB007644

R-PLACE1007218//Homo sapiens chromosome 20 clone R P3-387E22, *** SEQUENCING IN PROGRESS *** in unordered pieces. //1.1e-88//497//91//AL031660

【1131】 相同性検索結果データ 10.

実施例 16 で選抜した 54 クローンの 5' 末端クローン配列に対する Human Unigene 相同性検索結果データ

各データは、クローン配列名、トップヒットデータの Title、P 値: 比較配列の長さ (base): 相同性 (%)、トップヒットデータの Accession No. の順に // で区切って記載した。なお、相同性のスコアの P 値が 1 より大であった場合はデータは示さない。

F-HEMBA1000497//oul5a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1626332 3', mRNA sequence. //1.0//186//65//AI018130

F-HEMBA1001750//Human mRNA for TI-227H. //2.5e-101//473//99//D50525

F-HEMBA1003854//Homo sapiens mRNA for KIAA1031 protein, partial cds. //7.2e-06//103//80//AB028954

F-HEMBA1004193//Homo sapiens mRNA for TL132. //0.75//334//59//AJ012755

F-HEMBA1004860//ny07e01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1271064 3' similar to contains Alu repetitive element; , mRNA sequence. //3.7e-06//140//70//AA749151

F-HEMBA1005572//HZF-16=Kruppel-related zinc finger gene homolog {alternatively spliced} [human, hepatoblastoma cell line, HEP-G2, mRNA, 2080 nt]. //1.1e-48//341//77//S54641

F-HEMBA1006038//Homo sapiens gene for insulin receptor substrate-2, complete cds. //0.036//297//60//AB000732

F-HEMBA1006092//ab80f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853295 3' similar to contains Alu repetitive element; , mRNA sequence. //0.65//150//63//AA663266

F-HEMBA1006406//ws26e11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498348 3' similar to TR:002710 002710 GAG POLYPROTEIN. ; , mRNA sequence. //1.4e-32//518//67//AI989639

F-HEMBA1006650//Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds. //1.3e-19//136//90//AF006087

F-HEMBA1006812//zh49f01.s1 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:415417

3', mRNA sequence. //1.3e-120//579//98//W80404F-HEM 50

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BB1000672//Homo sapiens mRNA for KIAA1040 protein, partial cds. //0.00047//706//57//AB028963

F-HEMBA1001197//tq45e03.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2211772 3' similar to TR:001940 001940 STRAWBERRY NOTCH ; , mRNA sequence. //1.2e-16//117//92//AI580023

F-HEMBA1001871//Human chondroitin/dermatan sulfate proteoglycan (PG40) core protein mRNA, complete cds. //4.6e-26//527//62//M14219

10 F-MAMMA1001252

F-MAMMA1002094

F-NT2RM4000634//DKFZp434D1813_r1 434 (synonym: hte s3) Homo sapiens cDNA clone DKFZp434D1813 5', mRNA sequence. //9.7e-16//226//69//AL040136

F-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds. //7.6e-179//817//99//AB028992

F-NT2RM4000783//wd82f06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338115 3', mRNA sequence. //1.8e-20//470//65//AI703299

20 F-NT2RM4000857//Homo sapiens KIAA0416 mRNA, partial cds. //1.9e-46//749//65//AB007876

F-NT2RM4001178//Homo sapiens protein tyrosine phosphatase (PAC-1) mRNA, complete cds. //0.0024//254//63//L11329

F-NT2RM4002420//wg39f11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367501 3' similar to contains element L1 L1 repetitive element ; , mRNA sequence. //1.4e-13//127//84//AI742251

F-NT2RP2000198//Human mRNA for platelet glycoprotein IX. //0.0033//241//62//X52997

F-NT2RP2000551//ze37d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361175 3', mRNA sequence. //5.0e-07//116//71//AA017066

F-NT2RP2000660//qx01g11.x1 NCI_CGAP_Br14 Homo sapiens cDNA clone IMAGE:1999364 3', mRNA sequence. //0.027//120//65//AI225283

F-NT2RP2001214

F-NT2RP2001460//wb50h10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309155 3', mRNA sequence. //0.0013//89//78//AI651878

F-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2H F8_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; , mRNA sequence. //2.3e-18//120//93//AA427992

F-NT2RP2002056//tw44g09.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2262592 3' similar to contains Alu repetitive element; , mRNA sequence. //2.4e-07//99//79//AI811687

F-NT2RP2002677

F-NT2RP2002755//zj83d10.s1 Soares_fetal_liver_sple

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en_INFLS_S1 Homo sapiens cDNA clone IMAGE:461491
3' similar to contains element TAR1 repetitive element ;, mRNA sequence.//1.9e-19//229//76//AA705059
F-NT2RP2002843//wt88d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2514551 3' similar to TR:P7952
2 P79522 MHC CLASS I REGION PROLINE RICH PROTEIN.
;, mRNA sequence.//8.2e-15//314//67//AI964055
F-NT2RP2003101//wi65a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398156 3', mRNA sequence.//0.38//106//68//AI763133
F-NT2RP2003799//Homo sapiens mRNA; cDNA DKFZp564C142 (from clone DKFZp564C142).//2.5e-29//124//91//AL049979
F-NT2RP2004095
F-NT2RP2004732//Homo sapiens mRNA for KIAA0884 protein, partial cds.//2.6e-109//533//96//AB020691
F-NT2RP2004920//wz68d10.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2563219 3' similar to TR:000172 000172 LINE-1 REVERSE TRANSCRIPTASE ;, mRNA sequence.//0.0020//220//61//AI969546
F-NT2RP2005454//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0.058//143//69//AB023194
F-NT2RP2005776//H. sapiens PAP mRNA.//4.3e-35//451//68//X76770
F-NT2RP2005806//HSZ78328 Human fetal brain S. Meier-Ewert Homo sapiens cDNA clone 2.48 (CEPH) 3', mRNA sequence.//2.0e-05//385//62//Z78328
F-NT2RP2005882//Human mRNA for KIAA0364 gene, complete cds.//7.3e-23//141//94//AB002362
F-NT2RP3001282
F-NT2RP3001723//ws73d05.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2503593 3' similar to contains MSRI.t1 TAR1 TAR1 repetitive element ;, mRNA sequence.//2.6e-07//245//66//AW008782
F-NT2RP3002099//yg49d01.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:36239 3', mRNA sequence.//0.58//164//64//R46086
F-NT2RP3003155
F-NT2RP3004028//Homo sapiens mRNA for KIAA1074 protein, complete cds.//1.3e-29//488//66//AB028997
F-OVARC1000008//Homo sapiens mRNA for KIAA0665 protein, complete cds.//0.00032//430//59//AB014565
F-OVARC1000724//Homo sapiens mRNA for KIAA0641 protein, complete cds.//0.0054//426//58//AB014541
F-OVARC1000751//Human Tis1ld gene, complete cds.//4.6e-12//527//62//U07802
F-OVARC1001029//qv29c05.x1 NCI_CGAP_Ov31 Homo sapiens cDNA clone IMAGE:1982984 3' similar to contains element L1 repetitive element ;, mRNA sequence.//0.0012//145//68//AI252422

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F-PLACE1000814//ak42f05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408641 3', mRNA sequence.//7.1e-31//275//76//AA868469
F-PLACE1003030
F-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//1.2e-57//737//67//AJ010046
F-PLACE1007218//yo34a08.s1 Soares adult brain N2b4 HB55Y Homo sapiens cDNA clone IMAGE:179798 3', mRNA sequence.//2.2e-21//216//76//H52716
【1132】 相同性検索結果データ11.
実施例16で選抜した54クローンの3'末端クローン配列に対するHuman Unigene相同性検索結果データ
各データは、クローン配列名、トップヒットデータのTitle、P値:比較配列の長さ(base):相同性(%):トップヒットデータのAccession No.の順に//で区切って記載した。なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。
20 R-HEMBA1000497//np09h02.s1 NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1115859 similar to contains Alu repetitive element; contains element MER22 repetitive element ;, mRNA sequence.//6.2e-38//185//83//AA614254
R-HEMBA1001750//yy71b10.s1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:278971 3', mRNA sequence.//0.0045//193//63//N63303
R-HEMBA1003854//Homo sapiens mRNA; cDNA DKFZp564F133 (from clone DKFZp564F133).//3.4e-72//310//80//AL049263
30 R-HEMBA1004193//tr01e08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2217062 3' similar to contains Alu repetitive element; contains element MER4 repetitive element ;, mRNA sequence.//1.5e-33//186//81//AI914747
R-HEMBA1004860//qh16b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844819 3', mRNA sequence.//0.017//118//69//AI218308
40 R-HEMBA1005572//wj16h05.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2403033 3', mRNA sequence.//4.6e-111//522//99//AI861830
R-HEMBA1006038//DKFZp434E1117_r1 434 (synonym: hte s3) Homo sapiens cDNA clone DKFZp434E1117 5', mRNA sequence.//1.2e-22//295//72//AL041450
R-HEMBA1006092//qt30d09.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1949489 3' similar to contains element PTR5 repetitive element ;, mRNA sequence.//1.4e-87//422//98//AI337963
50 R-HEMBA1006406//Homo sapiens mRNA for KIAA0752 pro

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tein, partial cds.//4.1e-30//291//76//AB018295
 R-HEMBA1006650//H.sapiens mRNA for serine/threonine protein kinase EMK.//3.6e-09//319//62//X97630
 R-HEMBA1006812//Human mRNA for KIAA0118 gene, partial cds.//3.1e-52//337//87//D42087
 R-HEMBA1000672//Homo sapiens mRNA; cDNA DKFZp434M011 (from clone DKFZp434M011).//3.2e-48//276//74//AL096734
 R-HEMBA1001197//zt35b11.r1 Soares ovary tumor NbH0 T Homo sapiens cDNA clone IMAGE:724317 5' similar to contains Alu repetitive element; , mRNA sequence.//9.9e-44//275//88//AA410788
 R-HEMBA1001871//wg20c02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2365634 3', mRNA sequence.//6.3e-104//501//98//AI741321
 R-MAMMA1001252//aa61h04.s1 NCI_CCAP_CCB1 Homo sapiens cDNA clone IMAGE:825463 3' similar to contains Alu repetitive element; contains element XTR repetitive element ; , mRNA sequence.//9.0e-19//127//91//AA504355
 R-MAMMA1002094//wd28h12.x1 Soares_NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329511 3', mRNA sequence.//2.5e-68//328//99//AI936520
 R-NT2RM4000634//DKFZp434F2016.s1 434 (synonym: hte s3) Homo sapiens cDNA clone DKFZp434F2016 3', mRNA sequence.//8.2e-20//185//81//AL041146
 R-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//5.7e-62//335//94//AB028992
 R-NT2RM4000783
 R-NT2RM4000857//Human megakaryocyte stimulating factor mRNA, complete cds.//0.00074//360//61//U70136
 R-NT2RM4001178//tk08e03.x1 NCI_CCAP_Lu24 Homo sapiens cDNA clone IMAGE:2150428 3', mRNA sequence.//0.77//96//62//AI457506
 R-NT2RM4002420//wl58b04.x1 NCI_CCAP_Brn25 Homo sapiens cDNA clone IMAGE:2429071 3', mRNA sequence.//2.4e-85//438//94//AI857508
 R-NT2RP2000198//nx19b11.s1 NCI_CCAP_GC3 Homo sapiens cDNA clone IMAGE:1256541 3', mRNA sequence.//1.9e-45//270//91//AA738352
 R-NT2RP2000551//tg80h11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2115141 3', mRNA sequence.//3.3e-53//311//85//AI417680
 R-NT2RP2000660//ns42a06.s1 NCI_CCAP_CCB1 Homo sapiens cDNA clone IMAGE:1186258 3', mRNA sequence.//4.3e-26//142//97//AA805691
 R-NT2RP2001214//tw65g08.x1 NCI_CCAP_Ut3 Homo sapiens cDNA clone IMAGE:2264606 3' similar to contains element MSR1 repetitive element ; , mRNA sequence.//1.5e-57//289//97//AI680174

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R-NT2RP2001460
 R-NT2RP2001756//zw54e12.s1 Soares_total_fetus_Nb2H F8_9w Homo sapiens cDNA clone IMAGE:773902 3' similar to TR:G456660 G456660 ZINC FINGER PROTEIN ZFP-1 ; , mRNA sequence.//6.0e-13//85//96//AA427992
 R-NT2RP2002056//yh26a12.s1 Soares_placenta_Nb2HP H omo sapiens cDNA clone IMAGE:130846 3', mRNA sequence.//0.0016//208//65//R22302
 R-NT2RP2002677//Homo sapiens mRNA for KIAA0524 protein, partial cds.//3.4e-26//339//71//AB011096
 R-NT2RP2002755//qd50d10.x1 Soares_fetal_heart_NbHH 19W Homo sapiens cDNA clone IMAGE:1732915 3', mRNA sequence.//1.5e-26//419//66//AI190698
 R-NT2RP2002843//at31f08.x1 Barstead_colon_HPLRB7 H omo sapiens cDNA clone IMAGE:2373639 3' similar to contains L1.t1 L1 repetitive element ; , mRNA sequence.//1.8e-45//463//74//AI749673
 R-NT2RP2003101//ty24h05.x1 NCI_CCAP_Ut3 Homo sapiens cDNA clone IMAGE:2280057 3', mRNA sequence.//7.5e-73//347//99//AI758824
 R-NT2RP2003799//Homo sapiens mRNA for KIAA0751 protein, complete cds.//0.0026//247//65//AB018294
 R-NT2RP2004095//zv08c02.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753026 3' similar to contains element MER32 repetitive element ; , mRNA sequence.//9.6e-07//188//66//AA436455
 R-NT2RP2004732//tu60a07.x1 NCI_CCAP_Gas4 Homo sapiens cDNA clone IMAGE:2255412 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; , mRNA sequence.//4.3e-25//414//68//AI678956
 R-NT2RP2004920//wd13h02.x1 NCI_CCAP_Co3 Homo sapiens cDNA clone IMAGE:2328051 3', mRNA sequence.//6.8e-91//483//93//AI694022
 R-NT2RP2005454//yy77g09.s1 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:279616 3', mRNA sequence.//0.0070//325//59//N48302
 R-NT2RP2005776//qq97d06.x1 Soares_total_fetus_Nb2H F8_9w Homo sapiens cDNA clone IMAGE:1939307 3', mRNA sequence.//7.5e-08//89//82//AI338419
 R-NT2RP2005806//wc29h01.x1 NCI_CCAP_Kid11 Homo sapiens cDNA clone IMAGE:2316625 3' similar to contains MER2.b3 MER2 repetitive element ; , mRNA sequence.//3.2e-16//235//71//AI671398
 R-NT2RP2005882//wo31f09.x1 NCI_CCAP_Gas4 Homo sapiens cDNA clone IMAGE:2456969 3', mRNA sequence.//0.00095//352//59//AI925528
 R-NT2RP3001282//wg35b03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367053 3', mRNA sequence.//1.7e-113//555//97//AI769199

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R-NT2RP3001723//wo48e06.x1 NCI_CGAP_Cas4 Homo sapiens cDNA clone IMAGE:2458594 3', mRNA sequence.//4.2e-98//471//98//AI926617

R-NT2RP3002099//DKFZp564L227_s1 564 (synonym: hfbr 2) Homo sapiens cDNA clone DKFZp564L227 3', mRNA sequence.//9.2e-50//329//87//AL037910

R-NT2RP3003155//zp07a07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595668 3', mRNA sequence.//1.4e-30//159//99//AA173172

R-NT2RP3004028//Homo sapiens protein kinase C-alpha mRNA, partial 3' UTR.//0.43//66//75//AF035594

R-OVARC1000008//wa69e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2301454 3', mRNA sequence.//1.0e-77//376//98//AI699393

R-OVARC1000724//tf94b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2106907 3', mRNA sequence.//0.71//27//100//AI380236

R-OVARC1000751//og93d04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455847 3', mRNA sequence.//3.5e-13//274//63//AA863306

R-OVARC1001029//yz96e02.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:290906 5' similar to contains Alu repetitive element; contains element PTR5 repetitive element ;, mRNA sequence.//3.5e-13//175//74//N99464

R-PLACE1000814//tg49a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112086 3' similar to contains L1.t2 L1 L1 repetitive element ;, mRNA sequence.//2.2e-18//285//69//AI424789

R-PLACE1003030//Homo sapiens snRNA activating protein complex 190kD subunit (SNAP190) mRNA, complete cds.//4.0e-34//225//90//AF032387

R-PLACE1005549//tm26b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157693 3', mRNA sequence.//0.91//127//66//AI480253

R-PLACE1007218//yq06e01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196152 5' similar to contains Alu repetitive element; contains LTR4 repetitive element ;, mRNA sequence.//2.4e-36//245//87//R92256

【1133】 相同性検索結果データ12. 全長塩基配列および推定アミノ酸配列に対する相同性検索結果データ各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LI GASE) (LEURS).//6.4E-99//457aa//45%/Q09996

C-HEMBA1000020//Homo sapiens beta 2 gene.//7.5E-264//1194bp//95%/X02344C-HEMBA1000129//HYPOTHETICAL

4268

HELICASE C8A4.08C IN CHROMOSOME I.//3.8E-25//166aa//36%/Q09884

C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B).//0//1612bp//99%/AJ011738

C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1E-86//146aa//56%/Q61221

C-HEMBA1000231

10 C-HEMBA1000264

C-HEMBA1000280

C-HEMBA1000282

C-HEMBA1000303//Mus musculus Plenty of SH3s (POS H) mRNA, complete cds.//7.1E-254//1440bp//87%/AF030131

C-HEMBA1000333//Homo sapiens mRNA for KIAA0874 protein, partial cds.//4.8E-253//1148bp//99%/AB020681

C-HEMBA1000351

20 C-HEMBA1000356//Homo sapiens mRNA; cDNA DKFZp566C243 (from clone DKFZp566C243).//3.3E-287//815bp//98%/AL050274

C-HEMBA1000396

C-HEMBA1000411//ANKYRIN.//5.7E-12//127aa//38%/Q02357

C-HEMBA1000442

C-HEMBA1000456

C-HEMBA1000504

C-HEMBA1000518//PECANEX PROTEIN.//2.1E-19//227aa//38%/P18490

30 C-HEMBA1000519

C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13.//2.4E-44//292aa//36%/Q01755

C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds.//2.2E-194//663bp//83%/D89340

C-HEMBA1000545

C-HEMBA1000557

C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX 6) mRNA, complete cds.//0//1465bp//99%/AF121856

C-HEMBA1000594

C-HEMBA1000604

C-HEMBA1000622

C-HEMBA1000637

C-HEMBA1000655

C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.2E-156//1366bp//76%/U35776

C-HEMBA1000749

50 C-HEMBA1000769

C-HEMBA1000773
 C-HEMBA1000774
 C-HEMBA1000822
 C-HEMBA1000843
 C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD).//1E-78//119aa//87%/P51689
 C-HEMBA1000870
 C-HEMBA1000908
 C-HEMBA1000934
 C-HEMBA1000972
 C-HEMBA1000986
 C-HEMBA1000991
 C-HEMBA1001008
 C-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 14.//4.8E-169//786bp//99%/U06088
 C-HEMBA1001094
 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.6E-258//682bp//94%/AF153686
 C-HEMBA1001330
 C-HEMBA1001497
 C-HEMBA1001569//SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2).//2.3E-53//110aa//100%/P19065
 C-HEMBA1001570
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.6E-166//506aa//60%/P42803
 C-HEMBA1001640
 C-HEMBA1001655
 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//1707bp//98%/AF072247
 C-HEMBA1001711
 C-HEMBA1001723//Rattus norvegicus G beta-like protein GBL mRNA, complete cds.//4.7E-172//1240bp//81%/AF051155
 C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//7.6E-59//998bp//64%/AF098066
 C-HEMBA1001781
 C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds.//0//1637bp//99%/AF125158
 C-HEMBA1001822//Mus musculus E2L protein mRNA, complete cds.//1.9E-235//1329bp//89%/AF132479
 C-HEMBA1001824
 C-HEMBA1001866//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUCT).//5.7E-51//234aa//41%/Q09332

C-HEMBA1001910
 C-HEMBA1001913//GCN20 PROTEIN.//2.3E-81//158aa//50%/P43535
 C-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//0//1850bp//99%/AF000145
 C-HEMBA1001939
 C-HEMBA1001950//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1974bp//99%/AB023188
 10 C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRNA, partial cds.//0//1721bp//99%/AF155114
 C-HEMBA1002035//Homo sapiens mRNA; cDNA DKFZp586E0518 (from clone DKFZp586E0518).//0//2149bp//99%/AL050089
 C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-271//1583bp//88%/U92703
 C-HEMBA1002102//ANKYRIN.//4.40E-10//106aa//35%/Q02357
 20 C-HEMBA1002150
 C-HEMBA1002151//Rattus norvegicus p34 mRNA, complete cds.//1.1E-153//1059bp//82%/AF178669
 C-HEMBA1002189
 C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//2.2E-199//392aa//89%/P47226
 C-HEMBA1002229
 C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//3.70E-06//95aa//33%/P46087
 30 C-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//0//1514bp//99%/AB018314
 C-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//1.4E-299//294bp//100%/AC005954
 C-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//0//1605bp//97%/AF016903
 C-HEMBA1002703
 C-HEMBA1002779
 C-HEMBA1002816
 40 C-HEMBA1002970
 C-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds.//1.4E-171//1552bp//75%/U20286
 C-HEMBA1003021
 C-HEMBA1003077//SLIT PROTEIN PRECURSOR.//2.6E-15//199aa//31%/P24014
 C-HEMBA1003079
 C-HEMBA1003273
 C-HEMBA1003304
 50 C-HEMBA1003309

C-HEMBA1003376	-166//416aa//72%/Q14141
C-HEMBA1003384	C-HEMBA1004138
C-HEMBA1003531	C-HEMBA1004143
C-HEMBA1003548	C-HEMBA1004150
C-HEMBA1003556	C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds. //3.9E-208//951bp//99%/AF067855
C-HEMBA1003571	C-HEMBA1004200
C-HEMBA1003579	C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13. //6.2E-30//208aa//37%/P51153
C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN). //2E-73//526aa//32%/Q13105	10 C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2. //1.5E-12//258aa//29%/P40991
C-HEMBA1003692	C-HEMBA1004238
C-HEMBA1003720	C-HEMBA1004248//Homo sapiens insulin induced protein 2 mRNA, complete cds. //8.20E-175//552bp//97%/AF125392
C-HEMBA1003725	C-HEMBA1004272
C-HEMBA1003729	C-HEMBA1004274
C-HEMBA1003758	C-HEMBA1004275//Homo sapiens mRNA for KIAA1111 protein, partial cds. //0//1341bp//99%/AB029034
C-HEMBA1003773//Mus musculus signal recognition particle receptor betasubunit mRNA, complete cds. //5.8E-81//511bp//86%/U17343	20 C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds. //0//1982bp//99%/AF022795
C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds. //1.1E-190//1204bp//84%/AF084259	C-HEMBA1004312
C-HEMBA1003799	C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT). //2.3E-93//357aa//42%/Q99676
C-HEMBA1003804	C-HEMBA1004323
C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds. //0//988bp//95%/AF090402	C-HEMBA1004327
C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1). //8.10E-31//134aa//52%/P40484	C-HEMBA1004330
C-HEMBA1003856	C-HEMBA1004341
C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds. //1.2E-105//1192bp//70%/AF030430	30 C-HEMBA1004366
C-HEMBA1003879	C-HEMBA1004372
C-HEMBA1003880	C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds. //0//1437bp//99%/AF125158
C-HEMBA1003893	C-HEMBA1004394
C-HEMBA1003908	C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10). //3.2E-32//148aa//52%/P52017
C-HEMBA1003937	C-HEMBA1004429
C-HEMBA1003942	40 C-HEMBA1004460
C-HEMBA1003958	C-HEMBA1004461
C-HEMBA1003976	C-HEMBA1004502
C-HEMBA1003978//Homo sapiens mRNA for KIAA0840 protein, partial cds. //0//1530bp//100%/AB020647	C-HEMBA1004554
C-HEMBA1003985	C-HEMBA1004560
C-HEMBA1004011	C-HEMBA1004610
C-HEMBA1004024	C-HEMBA1004629
C-HEMBA1004038	C-HEMBA1004632
C-HEMBA1004045	C-HEMBA1004637
C-HEMBA1004048	C-HEMBA1004670
C-HEMBA1004111//Homo sapiens mRNA for KIAA1276 protein, partial cds. //1.00E-163//751bp//99%/AB033102	50 C-HEMBA1004672
C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT). //1.6E	

- C-HEMBA1004697
 C-HEMBA1004711
 C-HEMBA1004725
 C-HEMBA1004730
 C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18
 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBI
 QUITIN CARRIER PROTEIN) (PM42).//9.9E-39//143aa//5
 2%/P42743
 C-HEMBA1004751
 C-HEMBA1004752
 C-HEMBA1004889//Human C3f mRNA, complete cds.//
 6.70E-24//341aa//26%/U72515
 C-HEMBA1004934
 C-HEMBA1004944
 C-HEMBA1004973
 C-HEMBA1004977
 C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRN
 A, complete cds.//0//1813bp//99%/AF041474
 C-HEMBA1005083
 C-HEMBA1005113
 C-HEMBA1005133
 C-HEMBA1005185
 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.3E-10//18
 9aa//25%/P39929
 C-HEMBA1005252//Homo sapiens mRNA for KIAA0585 pr
 otein, partial cds.//1.2E-268//1215bp//99%/AB011
 157
 C-HEMBA1005296
 C-HEMBA1005314
 C-HEMBA1005331
 C-HEMBA1005394
 C-HEMBA1005403
 C-HEMBA1005423//Homo sapiens cyclin-dependent kin
 ase inhibitor (CDKN2C)mRNA, complete cds.//2E-213
 //537bp//99%/AF041248
 C-HEMBA1005468
 C-HEMBA1005469
 C-HEMBA1005474
 C-HEMBA1005517
 C-HEMBA1005518
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//
 3.1E-154//285aa//99%/Q60809
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//1
 70aa//31%/P39929
 C-HEMBA1005576//Homo sapiens mRNA for KIAA0463 pr
 otein, partial cds.//1.1E-181//835bp//99%/AB0079
 32
 C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM
 (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN).//0.
 00000009//213aa//27%/P09492
- C-HEMBA1005583
 C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DY
 HC).//2.3E-54//562aa//29%/P34036
 C-HEMBA1005609//Homo sapiens mRNA; cDNA DKFZp564K1
 33 (from clone DKFZp564K133).//2.2E-315//1448bp//9
 9%/AL050012
 C-HEMBA1005621//Homo sapiens Mad2B protein (MAD2
 B) mRNA, complete cds.//2.9E-224//1031bp//99%/AF
 139365
 10 C-HEMBA1005666
 C-HEMBA1005680
 C-HEMBA1005685
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHO
 SPHATASE 2B REGULATORY SUBUNIT).//4.4E-17//167aa//3
 4%/P25296
 C-HEMBA1005746
 C-HEMBA1005755
 C-HEMBA1005813
 C-HEMBA1005822
 20 C-HEMBA1005834
 C-HEMBA1005884
 C-HEMBA1005891
 C-HEMBA1005909
 C-HEMBA1005911
 C-HEMBA1005931
 C-HEMBA1005963
 C-HEMBA1005991
 C-HEMBA1006005
 C-HEMBA1006031//Homo sapiens mRNA for putative ph
 ospholipase, complete cds.//0//1413bp//99%/AB0194
 35
 C-HEMBA1006067
 C-HEMBA1006081
 C-HEMBA1006091
 C-HEMBA1006100
 C-HEMBA1006108//Homo sapiens mRNA for KIAA0943 pr
 otein, partial cds.//4.8E-245//764bp//99%/AB0231
 60
 C-HEMBA1006121
 40 C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219a
 a//25%/Q93794
 C-HEMBA1006155
 C-HEMBA1006158//Homo sapiens transcription factor
 forkhead-like 7 (FKHL7) gene, complete cds.//0//
 1551bp//99%/AF048693
 C-HEMBA1006182
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSO
 R.//1.9E-19//215aa//39%/P05142
 C-HEMBA1006235//Homo sapiens clone 24422 mRNA sequ
 ence.//0//1615bp//99%/AF070557
 50

4275

4276

C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.0000002//62aa//53%/P42698
 C-HEMBA1006259
 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.3E-123//200aa//73%/P10265
 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1E-210//490aa//77%/P25500
 C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.000000012//176aa//30%/P32505
 C-HEMBA1006284
 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.2E-12//215aa//23%/P70473
 C-HEMBA1006293
 C-HEMBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ER P5-ORC6 INTERGENIC REGION.//1.4E-48//248aa//43%/P38821
 C-HEMBA1006349
 C-HEMBA1006364
 C-HEMBA1006381
 C-HEMBA1006398//Human L1 element L1.6 putative pl 50 gene, complete cds.//2E-277//1729bp//85%/U93563
 C-HEMBA1006445//Homo sapiens putative tumor suppressor NOEY2 mRNA, complete cds.//1.4E-270//1224bp//100%/U96750
 C-HEMBA1006483
 C-HEMBA1006492
 C-HEMBA1006497
 C-HEMBA1006502
 C-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//0//2334bp//99%/AB014566
 C-HEMBA1006535
 C-HEMBA1006559//Mus musculus PRAJA1 (Praj1) mRNA, complete cds.//2.8E-206//1107bp//83%/U06944
 C-HEMBA1006566
 C-HEMBA1006579
 C-HEMBA1006583
 C-HEMBA1006612
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%/Q58323
 C-HEMBA1006643
 C-HEMBA1006674
 C-HEMBA1006682
 C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEININ PMC1-TFC2 INTERGENIC REGION.//3.3E-22//241aa//31%/P53196
 C-HEMBA1006717
 C-HEMBA1006744

C-HEMBA1006754
 C-HEMBA1006767
 C-HEMBA1006789
 C-HEMBA1006832
 C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%/AB018566
 C-HEMBA1006900
 C-HEMBA1006926
 C-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.8E-226//1039bp//99%/AJ010841
 C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6E-143//740bp//94%/AF004828
 C-HEMBA1006993
 C-HEMBA1007002
 C-HEMBA1007062
 C-HEMBA1007080
 20 C-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//2E-45//304aa//32%/Q57626
 C-HEMBA1007112//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//1619bp//99%/AL117450
 C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6) mRNA, complete cds.//0//1588bp//99%/AF139658
 C-HEMBA1007206
 C-HEMBA1007256
 30 C-HEMBA1007267
 C-HEMBA1007281
 C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase10A1 (PDE10A) mRNA, splice variant 1, complete cds.//0//1519bp//99%/AF127479
 C-HEMBA1007301
 C-HEMBA1007319
 C-HEMBA1007320
 C-HEMBA1007327
 C-HEMBA1007347
 40 C-HEMBA1000005
 C-HEMBA1000030
 C-HEMBA1000048
 C-HEMBA1000099
 C-HEMBA1000141
 C-HEMBA1000198
 C-HEMBA1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%/AF090385
 C-HEMBA1000218
 50 C-HEMBA1000274

- C-HEM BB1000312 //266aa//33%/P27544
- C-HEM BB1000402 C-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA
- C-HEM BB1000420 A, complete cds. //0//1417bp//99%/AF089749
- C-HEM BB1000480 C-HEM BB1002607//Homo sapiens vitamin D3 receptor
- C-HEM BB1000530 interacting protein (DRIP80) mRNA, complete cds. //
- C-HEM BB1000550 /2E-136//660bp//98%/AF105421
- C-HEM BB1000556//Homo sapiens mRNA for KIAA0750 pr
- C-HEM BB1002684
- otein, complete cds. //6.3E-74//1213bp//64%/AB018
- C-HEM BB1002692
- 293 C-HEM BB1002697
- C-HEM BB1000586 10 C-HEM BB1002705//Homo sapiens CGI-27 protein mRNA,
- C-HEM BB1000592 complete cds. //7.80E-285//841bp//96%/AF132961
- C-HEM BB1000593//Homo sapiens transferrin receptor
- C-MAMMA1000019
- 2 alpha (TFR2) mRNA, complete cds. //1.3E-107//503
- C-MAMMA1000020//H. sapiens mRNA for flavin-containi
- bp//99%/AF067864 ng monooxygenase 5 (FM05). //8.2E-198//868bp//99%/
- C-HEM BB1000649 Z47553
- C-HEM BB1000693//Homo sapiens neuroanl mRNA, compl
- C-MAMMA1000025
- ete cds. //0//2952bp//94%/AF040723
- C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN
- C-HEM BB1000822 1 (TES1)]. //1.5E-90//323aa//48%/P47226
- C-HEM BB1000826 C-MAMMA1000069
- C-HEM BB1000890 20 C-MAMMA1000084
- C-HEM BB1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRE
- C-MAMMA1000139
- CURS0R (EC 3.4.21.-). //1.10E-08//129aa//31%/P2912
- C-MAMMA1000163
- 2 C-MAMMA1000171
- C-HEM BB1001008 C-MAMMA1000173//Homo sapiens src homology 3 domai
- C-HEM BB1001020//Homo sapiens mRNA for KIAA0889 pr
- n-containing protein HIP-55 mRNA, complete cds. //
- otein, complete cds. //0//1812bp//98%/AB020696
- 2.6E-164//1044bp//87%/AF197060
- C-HEM BB1001051 C-MAMMA1000277
- C-HEM BB1001112//Homo sapiens sec61 homolog mRNA,
- C-MAMMA1000278
- complete cds. //6E-145//961bp//83%/AF077032
- C-MAMMA1000284//P. walti mRNA for rnp associated pr
- C-HEM BB1001221 30 otein 55. //2.2E-109//864bp//76%/X99836
- C-HEM BB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP6
- C-MAMMA1000309
- 5). //5.4E-93//196aa//54%/P46938
- C-MAMMA1000312
- C-HEM BB1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2)
- C-MAMMA1000313
- (ERYTHROCYTE ANKYRIN). //7E-43//394aa//34%/P16157
- C-MAMMA1000361
- C-HEM BB1001302 C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiqi
- C-HEM BB1001335 tous Kruppel like factor, complete cds. //0//1466b
- C-HEM BB1001337 p//99%/AB015132
- C-HEM BB1001356 C-MAMMA1000395
- C-HEM BB1001364 C-MAMMA1000410
- C-HEM BB1001366 40 C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F
- C-HEM BB1001367 5.2 IN CHROMOSOME III. //2.00E-30//119aa//53%/Q092
- C-HEM BB1001527 32
- C-HEM BB1001537 C-MAMMA1000421
- C-HEM BB1002359 C-MAMMA1000422
- C-HEM BB1002415 C-MAMMA1000468
- C-HEM BB1002457 C-MAMMA1000472
- C-HEM BB1002492 C-MAMMA1000490
- C-HEM BB1002495 C-MAMMA1000524
- C-HEM BB1002502 C-MAMMA1000567
- C-HEM BB1002550//HYPOTHETICAL UOG-1 PROTEIN. //5E-28 50 C-MAMMA1000612//Rattus norvegicus G beta-like pro

4279

tein GBL mRNA, complete cds."//1E-95//1115bp//72%/AF051155
 C-MAMMA1000623
 C-MAMMA1000625//GYP7 PROTEIN.//2.1E-41//198aa//40%/P48365
 C-MAMMA1000664
 C-MAMMA1000670
 C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//4.4E-33//250aa//33%/P42660
 C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16).//7.7 10
 OE-17//246aa//29%/P94524
 C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1E-77//395aa//45%/O14646
 C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%/AJ011779
 C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G 8.09C IN CHROMOSOME I.//9E-299//1033aa//55%/P87115
 C-MAMMA1000746
 C-MAMMA1000775
 C-MAMMA1000824//ACTIN.//6.2E-20//284aa//28%/P53500
 C-MAMMA1000831
 C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.8E-40//101aa//54%/O27540
 C-MAMMA1000842
 C-MAMMA1000843
 C-MAMMA1000856
 C-MAMMA1000865
 C-MAMMA1000875
 C-MAMMA1000906
 C-MAMMA1000908
 C-MAMMA1000914
 C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%/AJ250711
 C-MAMMA1000968
 C-MAMMA1000979
 C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds."//2.50E-276//1263bp//99%/AF117892
 C-MAMMA1001021
 C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.6E-16//113aa//41%/Q01082
 C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%/AJ237946
 C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds."//1.3E-181//397bp//98%/AF151830
 C-MAMMA1001078
 C-MAMMA1001091

4280

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4E-49//125aa//68%/P51521
 C-MAMMA1001110
 C-MAMMA1001126
 C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%/Q09273
 C-MAMMA1001143
 C-MAMMA1001154
 C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%/Q92338
 C-MAMMA1001215
 C-MAMMA1001244
 C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds."//2.3E-271//1414bp//89%/AF184275
 C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D 3.4 IN CHROMOSOME III.//2.1E-52//630aa//30%/P34537
 C-MAMMA1001343
 20 C-MAMMA1001411//Homo sapiens mRNA; cDNA DKFZp56400823 (from clone DKFZp56400823).//0//2131bp//99%/AL080121
 C-MAMMA1001419
 C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//6.5E-129//260aa//92%/P52623
 C-MAMMA1001510
 C-MAMMA1001522
 C-MAMMA1001576//Human gamma-tubulin mRNA, complete cds."//7.5E-276//1561bp//90%/M61764
 30 C-MAMMA1001604
 C-MAMMA1001620
 C-MAMMA1001635
 C-MAMMA1001649
 C-MAMMA1001686
 C-MAMMA1001692
 C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRANSCRIPTION FACTOR).//8.5E-32//171aa//36%/P21573
 C-MAMMA1001754//Homo sapiens CGI-11 protein mRNA, complete cds."//0//1837bp//98%/AF132945
 40 C-MAMMA1001757
 C-MAMMA1001764
 C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOMOLOG MJ1156.//3.8E-45//351aa//38%/Q58556
 C-MAMMA1001771//M. musculus mRNA for semaphorin B.//2.60E-200//1272bp//79%/X85991
 C-MAMMA1001790
 C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29).//2.6E-77//507aa//38%/Q07230
 50 C-MAMMA1001858

4281

4282

- C-MAMMA1001868//TRICHOHYALIN.//2.7E-19//359aa//25%
//P22793
- C-MAMMA1001970
- C-MAMMA1002042
- C-MAMMA1002068
- C-MAMMA1002153
- C-MAMMA1002156
- C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLR
EP3 PROTEIN).//6E-66//157aa//70%/P15880
- C-MAMMA1002174
- C-MAMMA1002209
- C-MAMMA1002219//Homo sapiens mRNA for KIAA1067 pr
oteins, partial cds.//1.1E-181//861bp//98%/AB0289
90
- C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF-
2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).
//8.8E-217//310aa//86%/P70541
- C-MAMMA1002243
- C-MAMMA1002268//Mus musculus sphingosine kinase
(SPHK1a) mRNA, partial cds.//1E-190//1624bp//76%
AF068748
- C-MAMMA1002269
- C-MAMMA1002292
- C-MAMMA1002294
- C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase
activating protein.//1.1E-214//881bp//97%/AJ01167
9
- C-MAMMA1002312
- C-MAMMA1002329//M.musculus mRNA for semaphorin B./
/3.80E-45//332bp//84%/X85991
- C-MAMMA1002333
- C-MAMMA1002351//FERRI PYOCHELIN BINDING PROTEIN.//
0.000078//127aa//26%/P40882
- C-MAMMA1002353
- C-MAMMA1002355
- C-MAMMA1002356
- C-MAMMA1002362
- C-MAMMA1002380
- C-MAMMA1002384
- C-MAMMA1002427
- C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SY
NTHETASE (EC 6.3.5.1).//1E-11//128aa//36%/P47623
- C-MAMMA1002485//Homo sapiens stannocalcin-relate
d protein mRNA, complete cds.//0//1822bp//99%/AF
098462
- C-MAMMA1002494
- C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN S
TE2-FRS2 INTERGENIC REGION.//1.2E-34//337aa//31%/P
43571
- C-MAMMA1002530//Homo sapiens cytosolic phospholip
- ase A2 gamma (cPLA2 gamma) mRNA, complete cds.//0
//1910bp//99%/AF065214
- C-MAMMA1002554
- C-MAMMA1002585//Homo sapiens mRNA for KIAA0860 pr
oteins, complete cds.//0//1405bp//99%/AB020667
- C-MAMMA1002598
- C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMIN
AL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIO
LESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEAS
E) (DEUBIQUITINATING ENZYME).//9.5E-16//159aa//37%
//Q09931
- C-MAMMA1002655//Homo sapiens mRNA for ganglioside
sialidase, complete cds.//0//1515bp//99%/AB0081
85
- C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC
6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING EN
ZYME).//1.1E-45//618aa//26%/P27550
- C-MAMMA1002673
- C-MAMMA1002684//Homo sapiens mRNA for KIAA0214 pr
oteins, complete cds.//0//3174bp//99%/D86987
- C-MAMMA1002711
- C-MAMMA1002769//Homo sapiens cell cycle progressi
on restoration 8 protein (CPR8) mRNA, complete cd
s.//2.2E-25//330bp//77%/AF011794
- C-MAMMA1002775
- C-MAMMA1002782
- C-MAMMA1002796
- C-MAMMA1002807
- C-MAMMA1002838
- C-MAMMA1002842//Mus musculus c-Cbl associated pro
tein CAP mRNA, complete cds.//2.6E-58//373bp//81%
//U58883
- C-MAMMA1002869//PINCH PROTEIN (PARTICULARY INTERES
TING NEW CYS-HIS PROTEIN).//1.4E-160//305aa//85%/P
48059
- C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEI
N (RTVP-1 PROTEIN).//5.7E-30//214aa//35%/P48060
- C-MAMMA1002886
- C-MAMMA1002890
- C-MAMMA1002938//Homo sapiens mRNA for KIAA0698 pr
oteins, complete cds.//8.4E-252//1139bp//100%/AB0
14598
- C-MAMMA1002964
- C-MAMMA1003011//HISTONE MACRO-H2A.1.//2.7E-123//37
0aa//66%/Q02874
- C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7)./
/7.4E-46//332aa//36%/P06746
- C-MAMMA1003015
- C-MAMMA1003019
- C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURID

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INE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE). //1.9E-13//108aa//33%/P23851

C-MAMMA1003039

C-MAMMA1003044

C-MAMMA1003049

C-MAMMA1003056

C-MAMMA1003057//MD6 PROTEIN. //3.1E-225//419aa//97%/Q60584

C-MAMMA1003066

C-MAMMA1003099

C-MAMMA1003104

C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds. //1.1E-234//1178bp//86%/AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA). //2.2E-105//217aa//89%/P46735

C-MAMMA1003135

C-MAMMA1003146//Homo sapiens mRNA for GalT3 protein. //4.3E-218//996bp//99%/Y15062

C-MAMMA1003150//Homo sapiens mRNA for KIAA1096 protein, partial cds. //0//1342bp//99%/AB029019

C-MAMMA1003166//Homo sapiens MLL septin-like fusion protein (MSF) mRNA, complete cds. //3.10E-158//592bp//97%/AF123052

C-NT2RM1000032

C-NT2RM1000035//Human mRNA for KIAA0199 gene, partial cds. //0//2948bp//99%/D83782

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SRLQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2). //2.90E-14//299aa//25%/P37596

C-NT2RM1000055//Homo sapiens mRNA for KIAA0829 protein, partial cds. //0//3111bp//99%/AB020636

C-NT2RM1000059

C-NT2RM1000062

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT). //1.2E-10//150aa//28%/P87072

C-NT2RM1000119

C-NT2RM1000127

C-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete cds. //0//2980bp//99%/AB018335

C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. //7.8E-110//516bp//99%/AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5). //3.3E-38//469aa//27%/P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT). //1.2E-10//150aa//28%/P87072

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TORY SUBUNIT). //1.2E-10//150aa//28%/P87072

C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C. //1.1E-10//94aa//47%/042643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene). //0//2476bp//99%/AJ245820

C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds. //2E-126//592bp//99%/U81002

C-NT2RM1000252//H. sapiens E-MAP-115 mRNA. //9.7E-35//569bp//64%/X73882

C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds. //0//3012bp//99%/AB016789

C-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds. //0//3139bp//98%/D50920

C-NT2RM1000271

C-NT2RM1000300

20 C-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds. //0//4349bp//99%/D63880

C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds. //7.4E-245//2101bp//68%/AF111423

C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds. //0//1599bp//99%/AF152462

C-NT2RM1000365

30 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds. //3.2E-196//1016bp//94%/AF179212

C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CP T1-SPC98 INTERGENIC REGION. //0.00000019//67aa//31%/P53915

C-NT2RM1000399

C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds. //1.4E-185//1486bp//81%/AF084928

40 C-NT2RM1000555//Homo sapiens mRNA for KIAA0885 protein, complete cds. //0//2885bp//99%/AB020692

C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR. //0.0000068//199aa//30%/Q08372

C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-). //8.5E-75//301aa//39%/P43636

C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds. //4.3E-210//960bp//99%/AF038957

C-NT2RM1000666//DNA-BINDING PROTEIN A. //2.2E-09//165aa//34%/P16989

C-NT2RM1000672

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C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein. //0//3104bp//99%/AJ132440
 C-NT2RM1000699
 C-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds. //1.1E-295//1338bp//99%/AB011139
 C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds. //0//3524bp//99%/AF027208
 C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds. //6.70E-227//1043bp//99%/AF141310
 C-NT2RM1000770//DXS6673E PROTEIN. //1.4E-39//194aa//48%/Q14202
 C-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //7.3E-15//280aa//27%/Q00808
 C-NT2RM1000780
 C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene). //1.1E-98//571bp//89%/Z97207
 C-NT2RM1000802
 C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds. //0//3524bp//99%/AF027208
 C-NT2RM1000826//Homo sapiens mRNA for KIAA0885 protein, complete cds. //0//2885bp//99%/AB020692
 C-NT2RM1000829
 C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN). //9.7E-42//333aa//36%/P16157
 C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds. //0//2206bp//99%/AF077033
 C-NT2RM1000857//Homo sapiens mRNA for KIAA0962 protein, partial cds. //0//3716bp//99%/AB023179
 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds. //1.4E-244//1113bp//99%/AF043733
 C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds. //4.30E-122//1394bp//69%/AF126799
 C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D 3.4 IN CHROMOSOME III. //1.8E-56//630aa//30%/P34537
 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135). //0//1020aa//89%/P70700
 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR). //8.9E-26//229aa//29%/P02583
 C-NT2RM1000905//Homo sapiens HSPC021 mRNA, complete cds. //0//1480bp//99%/AF077207
 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E1

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0.2 IN CHROMOSOME III. //1E-15//266aa//26%/P46577
 C-NT2RM1000927
 C-NT2RM1000962
 C-NT2RM1000978
 C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds. //0//2230bp//99%/AF030233
 C-NT2RM1001043
 C-NT2RM1001066
 C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-II) (PLC-148). //8.3E-47//259aa//35%/P08487
 C-NT2RM1001085//Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds. //3.7E-32//460bp//64%/AF053768
 C-NT2RM1001102//Human HEM45 mRNA, complete cds. //2.3E-27//482bp//63%/U88964
 C-NT2RM1001105
 C-NT2RM1001139//Homo sapiens mRNA; cDNA DKFZp564F0522 (from clone DKFZp564F0522). //0//1756bp//99%/AL049943
 C-NT2RM2000420
 C-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds. //0//2519bp//96%/AF032108
 C-NT2RM2000609
 C-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds. //2.6E-106//1069bp//74%/U35776
 C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6). //2.9E-103//249aa//73%/P28160
 C-NT2RM2001588
 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein. //0//3114bp//99%/AJ132440
 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds. //0//2601bp//99%/AF084458
 C-NT2RM2001632//KES1 PROTEIN. //1.40E-31//342aa//34%/P35844
 C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds. //0//2421bp//99%/AF084458
 C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds. //0//2608bp//99%/AF111162
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN. //3.4E-39//161aa//34%/P20107
 C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds. //0//2471bp//99%/AF044195
 C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending

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in intron 11, complete cds."//6.2E-16//464bp//62%
//AF083391
C-NT2RM2001671//"*Oryctolagus cuniculus sarcolemmal*
associated protein (SLAP1) mRNA, complete cds."//
0//1843bp//94%//U21155
C-NT2RM2001675
C-NT2RM2001681
C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H1
0.01 IN CHROMOSOME 1.//4.60E-20//253aa//30%//Q0967
4
C-NT2RM2001695//Homo sapiens clone H63 unknown mRNA
A.//0//2016bp//99%//AF103804
C-NT2RM2001696
C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for gal
actosyltransferase I, complete cds."//6.2E-253//117
0bp//99%//AB028600
C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG
-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT)."
//5.7E-130//536aa//49%//P50544
C-NT2RM2001716
C-NT2RM2001723
C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMIN
AL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIO
LESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEAS
E) (DEUBIQUITINATING ENZYME).//7.2E-16//381aa//27%
//Q09931
C-NT2RM2001743//Homo sapiens cell cycle progressi
on 2 protein (CPR2) mRNA, complete cds."//0//1498b
p//99%//AF011792
C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//8.
8E-11//119aa//36%//Q92609
C-NT2RM2001760//Homo sapiens sec61 homolog mRNA,
complete cds."//0//2379bp//99%//AF084458
C-NT2RM2001768
C-NT2RM2001771//ZINC FINGER PROTEIN 135.//6.4E-154
//394aa//64%//P52742
C-NT2RM2001782//Homo sapiens GDP-mannose pyrophos
phorylase A (GMPPA) mRNA, complete cds."//0//1470b
p//99%//AF135422
C-NT2RM2001784
C-NT2RM2001785//Homo sapiens mRNA; cDNA DKFZp586C2
01 (from clone DKFZp586C201).//0//2146bp//99%//AL0
50118
C-NT2RM2001813
C-NT2RM2001823//CHD1 PROTEIN.//1.8E-106//631aa//39
%/P32657
C-NT2RM2001839//Homo sapiens calumein (Calu) mRN
A, complete cds."//0//2415bp//97%//AF013759
C-NT2RM2001840
C-NT2RM2001855

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C-NT2RM2001867//Homo sapiens mRNA for KIAA0943 pr
oteins, partial cds."//0//967bp//99%//AB023160
C-NT2RM2001879
C-NT2RM2001983//Homo sapiens RGS-GAIP interacting
protein GIPC mRNA, complete cds."//0//1658bp//98%
//AF089816
C-NT2RM2002145//Homo sapiens erythroblast macroph
age protein EMP mRNA, complete cds."//8.5E-191//152
4bp//81%//AF084928
10 C-NT2RM4000027
C-NT2RM4000030//LAS1 PROTEIN.//5.6E-12//184aa//32%
//P36146
C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.0
00008//112aa//31%//Q06003
C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLA
SMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRR
S)."/1.2E-157//321aa//61%//P26639
C-NT2RM4000156//H. sapiens HPBRII-7 gene.//3.6E-21/
/785bp//60%//X67336
20 C-NT2RM4000167//Homo sapiens kinesin superfamily
motor KIF4 mRNA, complete cds."//0//1946bp//99%//A
F071592
C-NT2RM4000199
C-NT2RM4000200
C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).
//4.9E-32//170aa//41%//Q16600
C-NT2RM4000233//Mus musculus semaphorin VIa mRNA,
complete cds."//3.4E-231//1395bp//86%//AF030430
C-NT2RM4000244
30 C-NT2RM4000251
C-NT2RM4000265
C-NT2RM4000324
C-NT2RM4000327
C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.9E-
80//213aa//75%//P35292
C-NT2RM4000425
C-NT2RM4000433//Mus musculus retinoic acid-respon
sive protein (Stra6) mRNA, complete cds."//4.1E-27
1//2085bp//77%//AF062476
40 C-NT2RM4000514
C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//
2.4E-89//389aa//43%//Q07230
C-NT2RM4000532
C-NT2RM4000534
C-NT2RM4000603
C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEI
N HET-E-1.//2.9E-09//108aa//31%//Q00808
C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC
6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING EN
ZYME).//2.7E-146//420aa//60%//P27550
50

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C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//
 1.2E-28//180aa//30%/P74168
 C-NT2RM4000689
 C-NT2RM4000698
 C-NT2RM4000700
 C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzin
 g enzyme I (UBH1) mRNA, partial cds."//1E-136//110
 4bp//77%/AF022789
 C-NT2RM4000717
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR R 10
 HO.//0.0000041//207aa//29%/P52154.
 C-NT2RM4000734//Homo sapiens mRNA for KIAA0760 pr
 otein, partial cds."//0//2273bp//99%/AB018303
 C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1
 p, complete cds."//0//2184bp//99%/D88208
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMEN
 T).//3.9E-125//301aa//53%/Q99676
 C-NT2RM4000764
 C-NT2RM4000778
 C-NT2RM4000787
 C-NT2RM4000790
 C-NT2RM4000795//Homo sapiens mRNA for KIAA0951 pr
 otein, complete cds."//0//1847bp//96%/AB023168
 C-NT2RM4000796
 C-NT2RM4000798//Homo sapiens brefeldin A-inhibite
 d guanine nucleotide-exchange protein 2 mRNA, comp
 lete cds."//0//2603bp//99%/AF084521
 C-NT2RM4000813
 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45
 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT)./ 30
 /1.10E-24//138aa//44%/P40682
 C-NT2RM4000833
 C-NT2RM4000848
 C-NT2RM4000852
 C-NT2RM4000855
 C-NT2RM4000887
 C-NT2RM4000895
 C-NT2RM4000950
 C-NT2RM4000979
 C-NT2RM4001002//Homo sapiens mRNA; cDNA DKFZp586G0 40
 518 (from clone DKFZp586G0518).//0//2259bp//100%/AL050092
 C-NT2RM4001032
 C-NT2RM4001047//M025 PROTEIN.//8E-140//333aa//80%/
 /Q06138
 C-NT2RM4001054//Homo sapiens sec61 homolog mRNA,
 complete cds."//3.1E-190//1315bp//81%/AF077032
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C
 9.06C IN CHROMOSOME I.//0.000000032//165aa//33%/Q
 09820

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C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F
 6.8 IN CHROMOSOME II.//5.9E-86//292aa//48%/Q09417
 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//1E-11//10
 3aa//38%/Q01704C-NT2RM4001151
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.
 1E-197//445aa//78%/Q27969
 C-NT2RM4001160
 C-NT2RM4001187
 C-NT2RM4001191//Homo sapiens clone 24963 mRNA seq
 uence, complete cds."//0//1950bp//99%/AF131737
 C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.5E-135
 //375aa//60%/P52742
 C-NT2RM4001203//Homo sapiens mRNA for KIAA0839 pr
 otein, partial cds."//0//3047bp//99%/AB020646
 C-NT2RM4001204//Homo sapiens mRNA for KIAA1089 pr
 otein, partial cds."//0//2349bp//99%/AB029012
 C-NT2RM4001217//Homo sapiens nuclear matrix prote
 in NRP/B (NRPB) mRNA, complete cds."//7.3E-148//140
 9bp//72%/AF059611
 20 C-NT2RM4001256//Xenopus laevis putative Zic3 bind
 ing protein mRNA, complete cds."//4.30E-55//289bp/
 //77%/AF129131
 C-NT2RM4001258
 C-NT2RM4001309
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS3
 4-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINAS
 E) (PI3K).//3.50E-35//124aa//65%/P54676
 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CH
 AIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD).//2.3E
 -31//334aa//30%/P08503
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblasto
 ma, complete cds."//1.8E-39//728bp//64%/D89016
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4
 PROTEIN).//1E-28//171aa//37%/P32626
 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN I
 N POP2-HOL1 INTERGENIC REGION.//8.1E-30//265aa//33%
 //P53742
 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mR
 NA, partial cds."//0//2300bp//99%/AF155103
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial c
 ds."//0//2524bp//99%/AB019494
 C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mR
 NA, complete cds."//2.2E-237//1079bp//99%/AF09879
 9
 C-NT2RM4001384
 C-NT2RM4001410
 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 do
 main-containing signaling mediator (PSM) mRNA, com
 plete cds."//0//1962bp//87%/AF020526
 50 C-NT2RM4001412//Homo sapiens nCAP mRNA, complete

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cds. "/0//1918bp//99%/AF047711
 C-NT2RM4001414
 C-NT2RM4001437
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNALIGASE) (ILERS).//1.4E-118//444aa//46%/P73505
 C-NT2RM4001454
 C-NT2RM4001455
 C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.1E-106//357aa//55%/P52737
 C-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds. "/0//1810bp//99%/AB014585
 C-NT2RM4001522
 C-NT2RM4001557//Homo sapiens mRNA for KIAA1040 protein, partial cds. "/0//1547bp//97%/AB028963
 C-NT2RM4001565
 C-NT2RM4001566//Homo sapiens mRNA for KIAA1114 protein, complete cds. "/0//1900bp//99%/AB029037
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds. "/1.5E-284//1082bp//90%/AF071317
 C-NT2RM4001592//Homo sapiens mRNA for KIAA1122 protein, partial cds. "/0//2170bp//99%/AB032948
 C-NT2RM4001594
 C-NT2RM4001597//M.musculus red-1 gene.//2.1E-171//1414bp//78%/X92750
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.6E-32//203aa//39%/Q12600
 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3). "/1.5E-93//278aa//38%/Q13368
 C-NT2RM4001650
 C-NT2RM4001662
 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.7E-84//410aa//42%/P37339
 C-NT2RM4001682
 C-NT2RM4001710
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.9E-141//354aa//72%/Q14141
 C-NT2RM4001715
 C-NT2RM4001731//Homo sapiens mRNA for KIAA1004 protein, partial cds. "/0//1922bp//100%/AB023221
 C-NT2RM4001746
 C-NT2RM4001754
 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.1E-186//639aa//58%/Q05512
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.9E-66//311aa//35%/Q03164

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C-NT2RM4001810//Homo sapiens mRNA for KIAA0863 protein, complete cds. "/0//2377bp//99%/AB020670
 C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%/P17346
 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.9E-55//325aa//37%/P28160
 C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.9E-161//481aa//56%/P51523
 C-NT2RM4001836
 10 C-NT2RM4001841//Homo sapiens mRNA for KIAA0920 protein, complete cds. "/0//1861bp//98%/AB023137
 C-NT2RM4001842
 C-NT2RM4001856
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBX6L (FRAGMENT).//6.5E-22//126aa//46%/P79779
 C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.3E-244//1248bp//94%/Y17711
 C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.5E-23//184aa//36%/Q15404
 20 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.9E-09//268aa//26%/P47486
 C-NT2RM4001922//Homo sapiens mRNA for KIAA0957 protein, complete cds. "/0//2165bp//99%/AB023174
 C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA A, complete cds. "/0//1930bp//99%/AF102851
 C-NT2RM4001940//Homo sapiens timeless homolog mRNA A, complete cds. "/0//2087bp//99%/AF098162
 30 C-NT2RM4001953
 C-NT2RM4001965
 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.6E-261//1563bp//84%/X99330
 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.8E-112//457aa//47%/P51523
 C-NT2RM4001984
 C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140].//3.2E-17//281aa//30%/P16170
 40 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEININ PWT6-PCT1 INTERGENIC REGION.//6.9E-94//589aa//35%/P42935
 C-NT2RM4002018
 C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds. "/1.9E-53//1585bp//60%/AF104260
 C-NT2RM4002044
 C-NT2RM4002054
 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds. "/0//1865bp//99%/U82267
 50

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C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71%/AF117755
 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.8E-105//556aa//41%/Q04652
 C-NT2RM4002128
 C-NT2RM4002140
 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//127aa//33%/P24014
 C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%/AF084535
 C-NT2RM4002174//MRP PROTEIN.//9.1E-68//264aa//51%/P21590
 C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.2E-33//688aa//27%/P08640
 C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3E-37//122aa//72%/Q07803
 C-NT2RM4002213//Homo sapiens protein phosphatase methylesterase-1 (PME-1) mRNA, complete cds.//0//2452bp//100%/AF157028
 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.7E-19//147aa//41%/P40809
 C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE I) (GNT- I) (GLCNAC-T I).//2.2E-36//320aa//38%/P27808
 C-NT2RM4002256
 C-NT2RM4002266
 C-NT2RM4002281
 C-NT2RM4002287
 C-NT2RM4002294
 C-NT2RM4002301
 C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.00000001//154aa//33%/P48778
 C-NT2RM4002339
 C-NT2RM4002344
 C-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//0//2666bp//99%/AB014549
 C-NT2RM4002374
 C-NT2RM4002383
 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL-ACTIVATING ENZYME).//1.3E-29//275aa//30%/P27095
 C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.1E-49//611bp//70%/AF129131

C-NT2RM4002446
 C-NT2RM4002452
 C-NT2RM4002457
 C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%/P51515
 C-NT2RM4002493
 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.9E-15//366aa//27%/Q00808
 10 C-NT2RM4002532//PROTEIN HOM1.//2E-16//276aa//28%/P55137
 C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%/AF055899
 C-NT2RM4002567
 C-NT2RM4002593
 C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.7E-68//236aa//58%/P54815
 C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNALIGASE) (ASPRS).//2.3E-101//488aa//45%/032038
 C-NT2RP1000324
 C-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//0//1345bp//99%/AB014538
 C-NT2RP1000418
 C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%/U47101
 C-NT2RP1000721
 C-NT2RP1000730
 30 C-NT2RP1000767
 C-NT2RP1000836
 C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F 6.4 IN CHROMOSOME III.//5.2E-20//306aa//33%/Q09531
 C-NT2RP1000943
 C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%/AF201333
 C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.1E-107//504bp//99%/AF182291
 40 C-NT2RP1001199
 C-NT2RP1001248
 C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%/AF029914
 C-NT2RP1001286
 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM 1.//1.80E-38//258aa//32%/Q12024
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM 1.//1.80E-38//258aa//32%/Q12024
 50 C-NT2RP1001310//Homo sapiens mitochondrial carrier

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r homolog 1 isoform mRNA, partial cds; nuclear gene for mitochondrial product. //0//1732bp//99%/AF176006

C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxidoreductase subunit B14.5B homolog mRNA, complete cds. //6.5E-116//541bp//100%/AF070652

C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SSU81-SCS2 INTERGENIC REGION. //2.7E-22//284aa//25%/P40074

C-NT2RP1001432

C-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds. //0//2648bp//99%/AB018290

C-NT2RP2000076//Homo sapiens partial mRNA for polyhomeotic 2 protein (PH2 gene). //7.9E-20//265bp//73%/AJ242730

C-NT2RP2000098

C-NT2RP2000108

C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL006W. //9.7E-41//278aa//36%/P40556

C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA). //7.1E-12//213aa//23%/P35251

C-NT2RP2000289

C-NT2RP2000327

C-NT2RP2000337

C-NT2RP2000420//ZINC FINGER PROTEIN 165. //8.5E-33//155aa//52%/P49910

C-NT2RP2000459

C-NT2RP2000498

C-NT2RP2000758

C-NT2RP2001137

C-NT2RP2001149

C-NT2RP2001168//VERPROLIN. //1.5E-09//143aa//33%/P37370

C-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds. //0//1780bp//99%/AB007949

C-NT2RP2001174//CASTRULA ZINC FINGER PROTEIN XLG46.1 (FRAGMENT). //6E-10//88aa//38%/P18722

C-NT2RP2001196

C-NT2RP2001226

C-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds. //0//3301bp//98%/AB018353

C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT). //4.4E-91//179aa//99%/P28663

C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN. //8.3E-39//161aa//34%/P20107

C-NT2RP2001312

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C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN). //5.5E-116//311aa//71%/Q13829

C-NT2RP2001328

C-NT2RP2001366

C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2). //2E-11//403aa//25%/Q02817

C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-). //8.4E-192//581aa//54%/P93647

C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein. //0//2068bp//99%/Y18004

C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds. //9E-112//742bp//82%/U76759

C-NT2RP2001450

C-NT2RP2001467

C-NT2RP2001506

C-NT2RP2001511//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds. //3.2E-297//2206bp//75%/AF093097

C-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALAR1. //0//2502bp//99%/Y14494

C-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3(XRCC3) mRNA, complete cds. //0//2326bp//99%/AF035586

C-NT2RP2001560//VAV2 PROTEIN. //0.00000015//219aa//27%/Q60992

C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.12C IN CHROMOSOME 1. //8.2E-29//294aa//31%/Q09837

30 C-NT2RP2001581

C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCLE. //0.000000036//127aa//36%/P30957

C-NT2RP2001628

C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT). //1.1E-47//126aa//53%/P42897

C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLLALLYLTRANSFERASE (EC 2.5.1.1) / GERANYLTRANSFERASE (EC 2.5.1.10)) (KIAA0032). //5.40E-47//96aa//97%/P14324

C-NT2RP2001813

C-NT2RP2001883//Homo sapiens CGI-01 protein mRNA, complete cds. //0//2306bp//99%/AF132936

C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5. //2.3E-38//395aa//30%/P53946

C-NT2RP2001947

C-NT2RP2001985//Homo sapiens high-risk human papilloma viruses E6 oncoproteins targeted protein E6T P1 alpha mRNA, complete cds. //2.00E-38//435bp//67

- %/AF090989
C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73. //6.5E-129//279aa//85%/Q08469
C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO). //1.7E-47//247aa//52%/P35331
C-NT2RP2002058//Homo sapiens WD repeat protein WD R3 (WDR3) mRNA, complete cds. //0//2510bp//99%/AF083217
C-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence. //1.5E-294//1334bp//99%/AF052183
C-NT2RP2002078//PECANEX PROTEIN. //1.8E-09//195aa//32%/P18490
C-NT2RP2002079//HISTONE H1, GONADAL. //4.4E-11//214aa//34%/P02256
C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein. //0//3389bp//99%/AJ007509
C-NT2RP2002185//Homo sapiens ubiquitin mRNA, complete cds. //0//1789bp//99%/AF176069
C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protein inhibitor of activated STAT3, complete cds. //0//2809bp//99%/AB021868
C-NT2RP2002231
C-NT2RP2002235
C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mRNA, complete cds. //0//3118bp//91%/L38621
C-NT2RP2002292
C-NT2RP2002408
C-NT2RP2002442//HES1 PROTEIN. //2.8E-14//163aa//30%/P46037
C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1. //6.50E-07//171aa//27%/P30620
C-NT2RP2002498
C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC174). //4.6E-144//537aa//49%/Q02386
C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds. //3.70E-34//668bp//61%/AF105427
C-NT2RP2002549
C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH). //2.80E-08//109aa//37%/P19076
C-NT2RP2002706
C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1. //4.9E-85//489aa//43%/P55194
C-NT2RP2002800
C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN. //0.000039//206aa//23%/P14922
C-NT2RP2002891
C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS TS CONTAINING PROTEIN D2013.2 IN CHROMOSOME 11. //4.1E-87//395aa//40%/Q18964
C-NT2RP2002939//ZINC FINGER PROTEIN 136. //5.4E-70//282aa//42%/P52737
C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135). //0//716aa//91%/P70700
C-NT2RP2003034
C-NT2RP2003099
C-NT2RP2003137//UBIQUITIN. //0.000026//70aa//30%/P13117
C-NT2RP2003157//Homo sapiens CGI-74 protein mRNA, complete cds. //0//2037bp//99%/AF151832
C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds. //0//2091bp//99%/D67025
C-NT2RP2003165
C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1. //0//1544bp//99%/AJ242978
C-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds. //0//3788bp//99%/AB014525
C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE). //4.1E-88//374aa//47%/Q23400
C-NT2RP2003297
C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC). //2.2E-199//550aa//70%/Q07866
C-NT2RP2003308//CROOKED NECK PROTEIN. //5.4E-244//622aa//67%/P17886
C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG. //0.000022//261aa//24%/P48754
C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor. //0//1509bp//99%/AJ133769
C-NT2RP2003393
C-NT2RP2003445
C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds. //0//2194bp//99%/AF126799
C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds. //0//3012bp//99%/AF125158
C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR). //5.4E-14//106aa//46%/P04175
C-NT2RP2003511
C-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds. //0//2137bp//97%/D87460
C-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds. //0//2343bp//99%/AB007931
C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds. //0//2442bp//9

- 9%//AF030233
C-NT2RP2003691
C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds. //0//2018bp//99%//AF073344
C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP). //0//869aa//80%//P53620
C-NT2RP2003764
C-NT2RP2003769
C-NT2RP2003777
C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B040 3.2 IN CHROMOSOME X. //3.7E-21//137aa//43%//Q11076
C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN). //0.00000016//117aa//29%//Q91955
C-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds. //0//3046bp//99%//AB018347
C-NT2RP2003984//Homo sapiens mRNA; cDNA DKFZp564A026 (from clone DKFZp564A026). //0//2514bp//99%//AL050367
C-NT2RP2004041//SYNAPSINS IA AND IB. //0.00000074//159aa//32%//P17599
C-NT2RP2004066//Human DNA sequence from clone 134019 on chromosome 1p36.11-36.33, complete sequence. //0//2410bp//99%//AL034555
C-NT2RP2004081
C-NT2RP2004124
C-NT2RP2004152
C-NT2RP2004165
C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTIONFACTOR RU49). //5.6E-31//424aa//28%//Q07231
C-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds. //0//3044bp//99%//AB015718
C-NT2RP2004245
C-NT2RP2004364
C-NT2RP2004365
C-NT2RP2004366//Homo sapiens mRNA for KIAA0986 protein, partial cds. //0//2790bp//97%//AB023203
C-NT2RP2004373
C-NT2RP2004476//Homo sapiens cyclin L ania-6a mRNA A, complete cds. //0//2075bp//99%//AF180920
C-NT2RP2004551
C-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03. //3E-117//625aa//40%//Q09903
C-NT2RP2004600
C-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds. //0//2368bp//99%//AB007929
C-NT2RP2004743
C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NR
- K1 (EC 2.7.1.-) (N-RICH KINASE 1). //1.3E-26//190aa//41%//P38692
C-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds. //0//2144bp//96%//AF054179
C-NT2RP2004861
C-NT2RP2004897
C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds. //0//2103bp//99%//AB007144
C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8. //3.3E-47//353aa//30%//Q12386
C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE). //4E-91//218aa//44%//Q92089
C-NT2RP2005162//Homo sapiens aspartyl aminopeptidase mRNA, complete cds. //0//1615bp//99%//AF005050
C-NT2RP2005204//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds. //0//1262bp//99%//AF090385
C-NT2RP2005227
C-NT2RP2005287
C-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds. //0//2992bp//99%//AF060219
C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA A, complete cds. //1.8E-175//1102bp//83%//AF053628
C-NT2RP2005539//Homo sapiens mRNA for KIAA0850 protein, complete cds. //0//1560bp//99%//AB020657
C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME). //8.2E-23//164aa//28%//032053
C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds. //0//2545bp//99%//AB011414
C-NT2RP2005732
C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds. //0//2191bp//92%//AF155120
C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION. //2.3E-39//318aa//31%//P40004
C-NT2RP2005859//Homo sapiens mRNA for KIAA0863 protein, complete cds. //0//1649bp//99%//AB020670
C-NT2RP2006023
C-NT2RP2006334//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154). //0//2318bp//99%//AL080155
C-NT2RP2006441
C-NT2RP3000002
C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER

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R PROTEIN HTF10) (HPF7). //2.2E-150//490aa//53%/Q05481
 C-NT2RP3000055
 C-NT2RP3000068
 C-NT2RP3000080
 C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BC CP)]. //1.9E-123//436aa//50%/P46401
 C-NT2RP3000092
 C-NT2RP3000109//P54 PROTEIN PRECURSOR. //0.000065//358aa//22%/P13692
 C-NT2RP3000134
 C-NT2RP3000149
 C-NT2RP3000197
 C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //2.9E-11//721aa//23%/P08640
 C-NT2RP3000233//Human DNA sequence from clone 22D 12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins. Contains ESTs and GSSs, complete sequence. //0//1462bp//99%/AL035424
 C-NT2RP3000235
 C-NT2RP3000247
 C-NT2RP3000267
 C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds. //0//2730bp//82%/D29766
 C-NT2RP3000324
 C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds. //1.5E-246//1124bp//99%/AF106622
 C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds. //5.8E-266//173bp//86%/AF061817
 C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds. //3.40E-42//645bp//67%/AF098066
 C-NT2RP3000449
 C-NT2RP3000451
 C-NT2RP3000456
 C-NT2RP3000542
 C-NT2RP3000561
 C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds. //0//2165bp//99%/AF093097

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C-NT2RP3000578//HES1 PROTEIN. //1.3E-22//229aa//27%/P35843
 C-NT2RP3000590//UVS-2 PROTEIN. //1.3E-22//458aa//24%/P33288
 C-NT2RP3000592
 C-NT2RP3000622
 C-NT2RP3000624
 C-NT2RP3000685
 C-NT2RP3000736//HYPOTHETICAL PROTEIN KIAA0140. //1.2E-166//305aa//99%/Q14153
 C-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT). //4.1E-165//371aa//49%/P10895
 C-NT2RP3000753
 C-NT2RP3000826
 C-NT2RP3000865
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK). //7.7E-87//175aa//98%/Q03426
 C-NT2RP3001007
 C-NT2RP3001055
 C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds. //1.50E-149//731bp//97%/AF097725
 C-NT2RP3001120//ZINC FINGER PROTEIN 136. //7.8E-170//512aa//58%/P52737
 C-NT2RP3001126
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO. //0.0000031//207aa//29%/P52154
 C-NT2RP3001232
 C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds. //0//3606bp//99%/AF198358
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein. //1.3E-99//669bp//83%/Y18101
 C-NT2RP3001274//Homo sapiens mRNA for KIAA1037 protein, partial cds. //0//2254bp//99%/AB028960
 C-NT2RP3001281
 C-NT2RP3001297
 C-NT2RP3001318
 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT). //2.4E-16//175aa//28%/P51508
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN). //3.6E-25//129aa//34%/P32089
 C-NT2RP3001374
 C-NT2RP3001428//NUCLEOPROTEIN TPR. //1.4E-128//152aa//99%/P12270

- C-NT2RP3001432
 C-NT2RP3001447
 C-NT2RP3001449// "Human DNA sequence from clone 283 E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the CNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs and GSSs, complete sequence."//0//1827bp//99%/AL031282
 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (HISTOCOMPATIBILITYANTIGEN MODIFIER 2).//3.2E-9 20 0//157aa//59%/P36371
 C-NT2RP3001459
 C-NT2RP3001527// "Human Sp140 protein (Sp140) mRNA, complete cds."//4.3E-290//793bp//93%/U63420
 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D 9.3 IN CHROMOSOME 11.//9.10E-10//158aa//31%/Q1002 2
 C-NT2RP3001580// "Mus musculus strain C57BL/J germ cell-less protein (Gcl) mRNA, complete cds."//0//1730bp//85%/AF163665
 C-NT2RP3001587// "Human anthracycline-associated resistance ARX mRNA, complete cds."//0//2617bp//99%/U35832
 C-NT2RP3001589
 C-NT2RP3001607
 C-NT2RP3001608
 C-NT2RP3001671// "Homo sapiens mRNA for KIAA0850 protein, complete cds."//0//2310bp//99%/AB020657
 C-NT2RP3001672// "Homo sapiens Sex comb on midleg homolog 1 isoform 2 (SCMH1) mRNA, complete cds."//0 40 //2836bp//99%/AF149046
 C-NT2RP3001678
 C-NT2RP3001688// "Homo sapiens glucocorticoid modulatory element binding protein-1 (GMEB1) mRNA, complete cds."//0//1695bp//99%/AF099013
 C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.00000024//481aa//21%/P25386
 C-NT2RP3001698
 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//3.4E-33//161aa//32%/P54356
 C-NT2RP3001716
 C-NT2RP3001752
 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.8E-117//462aa//55%/P52272
 C-NT2RP3001844
 C-NT2RP3001854//Homo sapiens mRNA; cDNA DKFZp564G013 (from clone DKFZp564G013).//0//1528bp//99%/AL050011
 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//8.1E-125//302aa//60%/P55347
 C-NT2RP3001898// "Homo sapiens mRNA for UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV, complete cds."//0//1587bp//100%/AB000624
 C-NT2RP3001931
 C-NT2RP3001969//TRICHOHYALIN.//2.7E-11//442aa//23%/P37709
 C-NT2RP3002002
 C-NT2RP3002004//H. sapiens mRNA for FAST kinase.//1.50E-192//475bp//94%/X86779
 C-NT2RP3002007//SAP1 PROTEIN.//1.1E-68//474aa//32%/P39955
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F 5.2 IN CHROMOSOME 11.//5.30E-25//139aa//48%/Q092 32
 C-NT2RP3002045// "Homo sapiens mRNA for KIAA0899 protein, partial cds."//0//3385bp//99%/AB020706
 C-NT2RP3002056// "Homo sapiens Rb binding protein homolog mRNA, partial cds."//0//2374bp//99%/AF0832 49
 C-NT2RP3002062// "Homo sapiens mRNA for KIAA0873 protein, partial cds."//0//3764bp//99%/AB020680
 C-NT2RP3002081//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds."//4.1E-233//1896bp//69%/AF111423
 C-NT2RP3002097
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.90E-09//181aa//22%/Q12387
 C-NT2RP3002142
 C-NT2RP3002146
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BINDINGPROTEIN GST1-HS).//2.8E-253//474aa//93%/P15170
 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP.//1.9E-151//223aa//91%/Q02614
 C-NT2RP3002166
 C-NT2RP3002181
 C-NT2RP3002244
 C-NT2RP3002248
 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28

- %/P45978
 C-NT2RP3002276
 C-NT2RP3002304
 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (E C 4.2.1.16) (THREONINE DEAMINASE).//3.70E-43//318aa//37%/P05792
 C-NT2RP3002529//Homo sapiens mRNA for leucocyte vacuolar protein sorting.//0//2276bp//99%/AJ133421
 C-NT2RP3002566
 C-NT2RP3002587
 C-NT2RP3002590
 C-NT2RP3002631
 C-NT2RP3002650//Mus musculus growth suppressor 1L (Gros1) mRNA, complete cds.//0//2109bp//87%/AF165163
 C-NT2RP3002663//Homo sapiens putative glycolipid transfer protein mRNA, complete cds.//8.10E-263//1243bp//97%/AF103731
 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E-73//179aa//36%/P13060
 C-NT2RP3002763
 C-NT2RP3002861
 C-NT2RP3002911
 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//2E-111//551aa//42%/Q04652
 C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds.//0//2388bp//99%/AF152498
 C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds.//1.8E-292//1325bp//99%/AF080158
 C-NT2RP3003008
 C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds.//3.6E-83//807bp//72%/D88315
 C-NT2RP3003204
 C-NT2RP3003278
 C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//0//2596bp//98%/L36983
 C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.5E-310//1468bp//82%/AB033922
 C-NT2RP3003302
 C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA, complete cds.//0//2476bp//99%/AF117657
 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//1.3E-35//178aa//44%/Q62191
 C-NT2RP3003344
- C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GD11-COX15 INTERGENIC REGION.//2.80E-07//161aa//28%/P40084
 C-NT2RP3003377
 C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%/U09874
 C-NT2RP3003433
 C-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//0//2437bp//99%/AB018268
 10 C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.6E-36//842bp//62%/AF091624
 C-NT2RP3004206//CROOKED NECK PROTEIN.//1.4E-220//567aa//67%/P17886
 C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%/AJ245820
 C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp//99%/AF126736
 20 C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.7E-13//118aa//33%/P52734
 C-NT2RP3004246
 C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%/AF065391
 C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.4E-248//1126bp//100%/AF088982
 30 C-NT2RP3004341
 C-NT2RP3004378
 C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1E-66//364bp//93%/AJ007798
 C-NT2RP3004428
 C-NT2RP3004451
 C-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//0//2875bp//99%/AB007917
 C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.6E-61//170aa//40%/Q01820
 C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2E-249//1777bp//80%/U83176
 C-NT2RP3004504//Mus musculus mRNA for CPEB protein.//1.9E-295//893bp//92%/Y08260
 C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.7E-37//190aa//39%/P40484
 C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%/L11316
 50 C-NT2RP4000528//NPL4 PROTEIN.//9.8E-86//515aa//37%

- //P33755
C-NT2RP4000907// "Mouse NLRR-1 mRNA for leucine-rich repeat protein, complete cds."//0//2127bp//86%//D45913
C-NT2RP4001029// "Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//0//1711bp//90%//U20086
C-NT2RP4001336// GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//186aa//29%//024076
C-NT2RP4001389// KES1 PROTEIN.//1.70E-31//342aa//34%//P35844
C-NT2RP4001442
C-NT2RP4001529// "Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds."//1.70E-255//1148bp//90%//U20086
C-NT2RP4001656// VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN).//1.10E-45//310aa//27%//P12868
C-OVARC1000106// "TROPOMYOSIN 1, FUSION PROTEIN 3.3."//0.000032//165aa//27%//P49455
C-OVARC1000198
C-OVARC1000682// "PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B)."//1.1E-209//293aa//95%//P39098
C-OVARC1000703
C-OVARC1000722// "Homo sapiens chromosome 1q21-q23 beta-1,4-galactosyltransferase mRNA, complete cds."//0//759bp//98%//AF038661
C-OVARC1000730
C-OVARC1000746// MATERNAL EFFECT PROTEIN STAUFEN.//0.000000017//78aa//48%//P25159
C-OVARC1000781
C-OVARC1000787
C-OVARC1000834// Homo sapiens mRNA for atopy related autoantigen CALC.//2.8E-258//1183bp//99%//Y17711
C-OVARC1000846// NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199
C-OVARC1000850// "Homo sapiens PB39 mRNA, complete cds."//0//2095bp//99%//AF045584
C-OVARC1000862// M.musculus mRNA for FT1.//5.9E-226//1498bp//81%//Z67963
C-OVARC1000876// MOB1 PROTEIN (HPS1 BINDER 1).//2.2E-50//206aa//52%//P40484
C-OVARC1000883
C-OVARC1000886
C-OVARC1000912
C-OVARC1000915// "Homo sapiens histone deacetylase 5 mRNA, complete cds."//1.60E-121//591bp//97%//AF132608
C-OVARC1000924
C-OVARC1000964
C-OVARC1000984
C-OVARC1001004
C-OVARC1001010
C-OVARC1001011
C-OVARC1001032
C-OVARC1001044
C-OVARC1001055// PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.9E-35//76aa//98%//P43490
10 C-OVARC1001068// "Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds."//0//1819bp//99%//AF082657
C-OVARC1001074
C-OVARC1001092// "Homo sapiens mRNA for JM5 protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin))."//2E-214//769bp//97%//AJ005897
C-OVARC1001107// "Homo sapiens protein methyltransferase (JBPI) mRNA, complete cds."//6.1E-276//594bp//98%//AF167572
20 C-OVARC1001154// "Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds."//2.3E-296//1561bp//93%//AF055008
C-OVARC1001161
C-OVARC1001167
C-OVARC1001170
C-OVARC1001171// "Homo sapiens translation initiation factor 3 47 kDa subunit mRNA, complete cds."//5.7E-151//436bp//92%//U94855
30 C-OVARC1001173
C-OVARC1001176
C-OVARC1001180// UBIQUITIN-LIKE PROTEIN DSK2.//1.1E-11//221aa//25%//P48510
C-OVARC1001188
C-OVARC1001232// "CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT)."//5.10E-22//83aa//37%//Q10568
C-OVARC1001270
C-OVARC1001271// NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1).//0.0000014//24aa//26%//P25976
C-OVARC1001306// N-MYC PROTO-ONCOGENE PROTEIN.//0.0000073//247aa//27%//P18444
C-OVARC1001344
C-OVARC1001369
C-OVARC1001372// "Homo sapiens mRNA for KIAA0897 protein, partial cds."//0//840bp//97%//AB020704
C-OVARC1001391
C-OVARC1001399
50 C-OVARC1001417// "Homo sapiens thyroid hormone receptor

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ptor-associated protein complex component TRAP170 mRNA, complete cds. "/0//1715bp//99%/AF135802
 C-OVARC1001419//Homo sapiens COK (STIM1) mRNA, complete cds. "/4.9E-48//586bp//69%/U52426
 C-OVARC1001436//ENL PROTEIN.//0.00000009//81aa//39%/Q03111
 C-OVARC1001453
 C-OVARC1001476//Mus musculus YGR163w mRNA homologue, complete cds. "/1.80E-187//510bp//89%/AB017616
 C-OVARC1001480
 C-OVARC1001489
 C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1).//0//777aa//91%/P98161
 C-OVARC1001525
 C-OVARC1001555//NGG1-INTERACTING FACTOR 3.//4.4E-19//130aa//40%/P53081
 C-OVARC1001577//Homo sapiens SRp46 splicing factor transcribed retropseudogene.//0//1167bp//100%/AF031165
 C-OVARC1001600
 C-OVARC1001610//Homo sapiens choline/ethanolamine phosphotransferase (CEPT1) mRNA, complete cds. "/0//1870bp//99%/AF068302
 C-OVARC1001702
 C-OVARC1001703//Mus musculus ARL-6 interacting protein-2 (Aip-2) mRNA, complete cds. "/3.5E-16//399bp//61%/AF133670
 C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1B).//2.80E-10//106aa//38%/Q62267
 C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.4E-40//195aa//41%/P07106
 C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.3E-16//116aa//43%/Q13796
 C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4E-122//282aa//85%/P08942
 C-OVARC1001745
 C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLT RANSFERASE 1). "/6.4E-85//514aa//34%/P12945
 C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds. "/0//963bp//99%/U97670
 C-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds. "/0//2083bp//99%/AB014575
 C-OVARC1001768
 C-OVARC1001791

C-OVARC1001795
 C-OVARC1001802
 C-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds. "/2.7E-190//1624bp//76%/AF068748
 C-OVARC1001828
 C-OVARC1001846
 C-OVARC1001861
 C-OVARC1001879
 10 C-OVARC1001880
 C-OVARC1001883
 C-OVARC1001916
 C-OVARC1001928
 C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLT RANSFERASE 1). "/3.1E-81//497aa//35%/P12945
 C-OVARC1001943//Mus musculus DEBT-91 mRNA, complete cds. "/0//2035bp//87%/AF143859
 C-OVARC1001950
 20 C-OVARC1001987//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds. "/2.3E-220//652bp//84%/AF061817
 C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds. "/0//1019bp//99%/AB029290
 C-OVARC1002082
 C-OVARC1002107
 C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.4E-52//306aa//35%/O35913
 C-OVARC1002138//SAP1 PROTEIN.//7.6E-60//128aa//59%/P39955
 C-OVARC1002156
 C-OVARC1002158
 C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds. "/0//2365bp//99%/AB019602
 C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.4E-17//185aa//32%/P08643
 40 C-PLACE1000048
 C-PLACE1000050
 C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.9E-54//190bp//94%/L22154
 C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds. "/0//2077bp//99%/U63127
 C-PLACE1000094
 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.8E-62//158aa//81%/P20290
 50 C-PLACE1000214

- C-PLACE1000236
 C-PLACE1000246
 C-PLACE1000292
 C-PLACE1000308
 C-PLACE1000332
 C-PLACE1000453
 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%/P51522
 C-PLACE1000599
 C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//2 10 6%/P52918
 C-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1992bp//99%/AF180371
 C-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F18 57Q7 (RZPD Berlin)).//2.1E-277//1260bp//99%/AJ005896
 C-PLACE1000706//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//0//1 20 366bp//99%/AF119043
 C-PLACE1000712
 C-PLACE1000749
 C-PLACE1000769//Homo sapiens CGI-18 protein mRNA, complete cds.//0//1985bp//98%/AF132952
 C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%/P52734
 C-PLACE1000849
 C-PLACE1000856//Homo sapiens mRNA for KIAA0974 protein, partial cds.//0//1310bp//100%/AB023191
 C-PLACE1000931
 C-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//0//1749bp//99%/AB018267
 C-PLACE1001010
 C-PLACE1001015
 C-PLACE1001024
 C-PLACE1001062//Homo sapiens PAC clone DJ1049N15 from 7q31.2-7q32, complete sequence.//2.7E-32//47 40 0bp//71%/AC006020
 C-PLACE1001104
 C-PLACE1001168
 C-PLACE1001171//MYOTUBULARIN.//7.1E-84//198aa//73%/Q13496
 C-PLACE1001185//Homo sapiens mRNA for KIAA0943 protein, partial cds.//0//1668bp//99%/AB023160
 C-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2E-202//1333bp//80%/D14336
 C-PLACE1001280
 C-PLACE1001294//M. musculus GEG-154 mRNA.//4.3E-221//1057bp//78%/X71642
 C-PLACE1001304//Homo sapiens zinc finger protein dp mRNA, complete cds.//0//2421bp//99%/AF153201
 C-PLACE1001311
 C-PLACE1001323
 C-PLACE1001351
 C-PLACE1001414
 C-PLACE1001440
 C-PLACE1001456
 C-PLACE1001517//Homo sapiens gene for glycosylphosphatidylinositol anchor attachment 1 (GPAA1), complete cds.//4.60E-112//392bp//87%/AB002137C-PLAC E1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//5.7E-130//244aa//99%/Q60809
 C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-118//429aa//48%/P51523
 C-PLACE1001634
 C-PLACE1001640
 C-PLACE1001672//PROBABLE AMINOTRANSFERASE T01B11.2 (EC 2.6.1.-).//4.3E-66//174aa//45%/P91408
 C-PLACE1001705
 C-PLACE1001716
 C-PLACE1001720
 C-PLACE1001745
 C-PLACE1001748//Homo sapiens metalloprotease 1 (M P1) mRNA, complete cds.//0//2602bp//99%/AF061243
 C-PLACE1001771//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//2900bp//99%/AJ006276
 C-PLACE1001799
 C-PLACE1001845//Mus musculus cyclin ania-6a mRNA, complete cds.//3.30E-31//925bp//62%/AF159159
 C-PLACE1001897
 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//6.5E-58//112aa//100%/076094
 C-PLACE1002157
 C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TYE2).//0.00005//179aa//23%/P32591
 C-PLACE1002227
 C-PLACE1002259
 C-PLACE1002319
 C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//7.9E-100//966bp//75%/AB030505
 C-PLACE1002477
 C-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2A (STAM2) mRNA, complete cds.//

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1. 7E-113//545bp//98%/AF042273
 C-PLACE1002500
 C-PLACE1002514
 C-PLACE1002532//HOMEBOX PROTEIN DLX-5.//1.2E-152/
 /289aa//96%/P70396
 C-PLACE1002537
 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5E-99//38
 6aa//48%/P45890
 C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KA
 INATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6) 10
 (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMEN
 T). //5.6E-34//76aa//98%/P39087
 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//
 5.5E-17//76aa//56%/P45340
 C-PLACE1002625
 C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.5E-
 278//543aa//92%/Q28046
 C-PLACE1002768
 C-PLACE1002782//Rattus norvegicus zinc transporte
 r (ZnT-2) mRNA, complete cds. //3.8E-43//385bp//77 20
 %//U50927
 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-4
 8//217aa//46%/P53973
 C-PLACE1002853
 C-PLACE1002908//Homo sapiens XGalT-1 mRNA for gal
 actosyltransferase I, complete cds. //0//1654bp//99
 %//AB028600
 C-PLACE1002962
 C-PLACE1002968
 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1. 30
 4E-78//496aa//37%/Q49091
 C-PLACE1003025
 C-PLACE1003027//Homo sapiens mRNA for KIAA0516 pr
 otein, partial cds. //2.1E-314//1417bp//100%/AB01
 1088
 C-PLACE1003044//Homo sapiens mRNA for KIAA0829 pr
 otein, partial cds. //0//1382bp//96%/AB020636
 C-PLACE1003176
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTO
 R KIAA0001. //4.9E-76//309aa//47%/Q15391 40
 C-PLACE1003256
 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEI
 N. //7.9E-22//70aa//47%/P21541
 C-PLACE1003343
 C-PLACE1003361
 C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRN
 A, complete cds. //1.4E-78//542bp//67%/AF107403
 C-PLACE1003373
 C-PLACE1003375
 C-PLACE1003394//Sprague-Dawley (clone LRB13) RAB1 50
 4 mRNA, complete cds. //2.30E-150//774bp//94%/M83
 680
 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL
 006W. //1.3E-40//278aa//36%/P40556
 C-PLACE1003454
 C-PLACE1003478
 C-PLACE1003516
 C-PLACE1003519//H. sapiens hnRNP-E2 mRNA. //5.1E-218
 //905bp//99%/X78136
 C-PLACE1003521//HYPOTHETICAL HELICASE C28B8.3 IN C
 HROMOSOME III. //0.0000011//101aa//32%/Q09475
 C-PLACE1003528
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR
 (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACT
 OR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERM
 EDIATE COMPONENT). //7.7E-68//404aa//33%/P32802
 C-PLACE1003566
 C-PLACE1003584
 C-PLACE1003593
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR. //
 0.00000023//82aa//35%/Q02516
 C-PLACE1003618
 C-PLACE1003638
 C-PLACE1003738//ZINC FINGER PROTEIN 135. //9.6E-118
 //350aa//46%/P52742
 C-PLACE1003760//Homo sapiens tetraspanin TM4-A mR
 NA, complete cds. //5.2E-289//1313bp//97%/AF13342
 3
 C-PLACE1003768
 C-PLACE1003795
 C-PLACE1003886
 C-PLACE1003888//Homo sapiens mRNA for KIAA1092 pr
 otein, partial cds. //0//2057bp//99%/AB029015
 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AM
 MONIA LIGASE) (CTP SYNTHETASE). //1.4E-243//584aa//
 74%/P17812
 C-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE,
 CYTOPLASMIC (EC 6.1.1.19) (ARGININE- -TRNA LIGAS
 E) (ARGRS). //2.4E-108//581aa//40%/Q05506
 C-PLACE1004118
 C-PLACE1004256//Mus musculus short coiled coil pr
 otein SCOCO (Scoc) mRNA, complete cds. //2E-93//96
 0bp//76%/AF115778
 C-PLACE1004274
 C-PLACE1004284
 C-PLACE1005331
 C-PLACE1005739//Homo sapiens mRNA; cDNA DKFZp564A0
 32 (from clone DKFZp564A032). //0//2190bp//99%/AL0
 50267
 C-PLACE1005828

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C-PLACE1005876// "CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT). "/0//730aa//99%/Q10568
 C-PLACE1005890//BEM46 PROTEIN (FRAGMENT). //9.9E-42//224aa//43%/P54069
 C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE- ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E). //2E-28//236aa//30%/P98110
 C-PLACE1007053
 C-PLACE1007068
 C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN). //5.3E-26//309aa//30%/Q04652
 C-PLACE1009921
 C-PLACE1010401
 C-PLACE1010856
 C-PLACE1010857
 C-PLACE1010917
 C-PLACE1010925
 C-PLACE1010926// "Homo sapiens mRNA for KIAA0554 protein, partial cds. "/0//1160bp//100%/AB011126
 C-PLACE1010942// "Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds. "/0//1440bp//99%/AF114487
 C-PLACE1010944
 C-PLACE1010954
 C-PLACE1010960//ACTIN-LIKE PROTEIN 13E. //5.3E-98//297aa//48%/P45890
 C-PLACE1011026
 C-PLACE1011046// "1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-1) (PLC-154). "/0//646aa//97%/P10894
 C-PLACE1011054
 C-PLACE1011057
 C-PLACE1011109// "ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G). "/1.50E-22//63aa//88%/Q07803
 C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1. //2.9E-71//190aa//44%/Q03532
 C-PLACE1011133
 C-PLACE1011143
 C-PLACE1011165
 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INSB. //1.3E-89//167aa//100%/P03830
 C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-). //3.2E-12//212aa//29%/Q03326
 C-PLACE1011221
 C-PLACE1011263//Homo sapiens mRNA; cDNA DKFZp5640043 (from clone DKFZp5640043). //0//2487bp//99%/AL050390

C-PLACE1011325
 C-PLACE1011332// "Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds. "/7.2E-151//697bp//99%/AF102265
 C-PLACE1011340// "Homo sapiens IDN3-B mRNA, complete cds. "/1.20E-74//380bp//97%/AB019602
 C-PLACE1011399// "Homo sapiens CGI-72 protein mRNA, complete cds. "/3.2E-90//427bp//99%/AF151830
 C-PLACE1011433// "Homo sapiens mRNA for KIAA0530 protein, partial cds. "/0//1946bp//99%/AB011102
 C-PLACE1011452
 C-PLACE1011465
 C-PLACE1011472// "Homo sapiens mRNA for KIAA0712 protein, complete cds. "/0//2022bp//99%/AB018255
 C-PLACE1011477// "Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. "/0//2040bp//99%/AF065482
 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT). //4.90E-11//147aa//32%/P52178
 C-PLACE1011520
 C-PLACE1011563
 C-PLACE1011567
 C-PLACE1011576// "Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds. "/0//1791bp//82%/L11672
 C-PLACE1011586
 C-PLACE1011643
 C-PLACE1011649
 C-PLACE1011664//CROOKED NECK PROTEIN. //1.6E-187//505aa//64%/P17886
 C-PLACE1011682
 C-PLACE1011719
 C-PLACE1011729
 C-PLACE1011858//Homo sapiens mRNA; cDNA DKFZp586C021 (from clone DKFZp586C021). //0//1490bp//99%/AL050287
 C-PLACE1011874
 C-PLACE1011875// "Homo sapiens mRNA for KIAA0580 protein, partial cds. "/4.1E-112//524bp//100%/AB011152
 C-PLACE1011923// "Homo sapiens serum-inducible kinase mRNA, complete cds. "/0//2782bp//99%/AF059617
 C-PLACE1011982
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III. //2.6E-42//104aa//49%/Q09475
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN). //1.1E-116//364aa//45%/P42566
 C-PLACE2000017
 C-PLACE2000021// "Homo sapiens TRF1-interacting ank

4317

yrin-related ADP-ribose polymerase mRNA, complete cds."//2.7E-107//981bp//74%//AF082556
 C-PLACE2000047
 C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type lectin, complete cds, clone:HP01347."//6.3E-166//656bp//94%//AB015629
 C-PLACE2000100
 C-PLACE2000111
 C-PLACE2000172
 C-PLACE2000187
 C-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end."//3.2E-253//1799bp//83%//L02897
 C-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cds."//4.60E-172//796bp//99%//AB018338
 C-PLACE2000317
 C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds."//0//1554bp//99%//AF069307
 C-PLACE2000366
 C-PLACE2000373//F-SPONDIN PRECURSOR."//8.6E-16//371aa//28%//P35446
 C-PLACE2000394
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48)."//6.3E-37//90aa//98%//P10586
 C-PLACE2000411//Homo sapiens mRNA for KIAA1037 protein, partial cds."//0//2515bp//99%//AB028960
 C-PLACE2000425
 C-PLACE2000427//PROBABLE HELICASE MOT1."//1.2E-26//200aa//27%//P32333
 C-PLACE2000433
 C-PLACE2000438//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."//2.1E-86//348aa//41%//Q10472
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN)."//2.5E-25//165aa//40%//P33450
 C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds."//6.7E-127//671bp//94%//AF072733
 C-PLACE3000009
 C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds."//0//2253bp//99%//AF033861
 C-PLACE3000103

4318

C-PLACE3000142
 C-PLACE3000145//TENSIN."//1E-108//277aa//75%//Q04205
 C-PLACE3000156
 C-PLACE3000157
 C-PLACE3000197
 C-PLACE3000208
 C-PLACE3000226//Homo sapiens mRNA for KIAA0962 protein, partial cds."//0//4805bp//99%//AB023179
 10 C-PLACE3000242//Homo sapiens mRNA for KIAA1114 protein, complete cds."//0//2786bp//96%//AB029037
 C-PLACE3000363
 C-PLACE3000405
 C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds."//1.80E-141//565bp//98%//AB029290
 C-PLACE3000477
 C-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds."//0//6702bp//99%//AB007931
 20 C-PLACE4000323
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1)."//8.10E-24//319aa//31%//P30771
 C-PLACE4000369//Homo sapiens mRNA for KIAA1025 protein, partial cds."//0//4830bp//99%//AB028948
 C-PLACE4000445//Homo sapiens mRNA; cDNA DKFZp434C212 (from clone DKFZp434C212)."//0//2565bp//99%//AL080196
 C-PLACE4000558//Homo sapiens mRNA for KIAA0729 protein, partial cds."//0//1051bp//97%//AB018272
 30 C-PLACE4000581//FIBROPELLIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1)."//9.3E-70//226aa//52%//P10079
 C-PLACE4000593
 C-PLACE4000612//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE]."//7.1E-154//340aa//40%//P21414
 C-PLACE4000670
 C-THYR01000026
 40 C-THYR01000085//PAIRED BOX PROTEIN PAX-8, ISOFORM S 8A/8B."//2E-72//155aa//92%//Q06710
 C-THYR01000107
 C-THYR01000111
 C-THYR01000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds."//1.1E-159//824bp//95%//U97018
 C-THYR01000156
 C-THYR01000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds."//0//1713bp//99%//AF020797
 50

- C-THYR01000186
 C-THYR01000187
 C-THYR01000241
 C-THYR01000279
 C-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR)mRNA, complete cds.//0//1567 bp//99%/AF124145
 C-THYR01000452
 C-THYR01000471
 C-THYR01000484
 C-THYR01000502
 C-THYR01000505
 C-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%/AF075587
 C-THYR01000596
 C-THYR01000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341bp//99%/AB024313
 C-THYR01000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%/AJ132889
 C-THYR01000715
 C-THYR01000734
 C-THYR01000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%/P98171
 C-THYR01000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPH A-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACI I) (STY).//1.8E-55//243aa//42%/Q64686
 C-THYR01000777
 C-THYR01000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//2.4E-157//1656bp//70%/U37373
 C-THYR01000787
 C-THYR01000793
 C-THYR01000796
 C-THYR01000843
 C-THYR01000852//Human branched chain aminotransferase precursor (BCATm)mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.3E-147//790bp//93%/U68418
 C-THYR01000865
 C-THYR01000895
 C-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//0//2387 bp//99%/AF079529
 C-THYR01000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5E-83//566aa//37%/P43550
 C-THYR01000952
 C-THYR01000983//UBIQUITIN-CONJUGATING ENZYME E2-17
- KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%/P35132
 C-THYR01001003//UBIQUITIN-CONJUGATING ENZYME E2-2 1.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%/P52491
 C-THYR01001031
 C-THYR01001062
 10 C-THYR01001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.2E-67//245aa//62%/P98168
 C-THYR01001133
 C-THYR01001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%/AF151835
 C-THYR01001173
 C-THYR01001213
 C-THYR01001321
 C-THYR01001322
 C-THYR01001365
 C-THYR01001401
 C-THYR01001411
 C-THYR01001434
 C-THYR01001534
 C-THYR01001541
 C-THYR01001559
 C-THYR01001570
 C-THYR01001595
 C-THYR01001605
 C-THYR01001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//99%/AJ002190
 C-THYR01001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.1E-273//1947bp//82%/AF175968
 C-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59kDa isoform.//0//1820bp//99%/AJ225089
 C-THYR01001673
 C-THYR01001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%/P45672
 C-THYR01001706
 C-THYR01001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.4E-20//217aa//30%/P38584
 C-THYR01001745
 C-THYR01001793
 C-THYR01001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.4E-74//158aa//89%/P42128
 C-THYR01001895
 C-THYR01001907
 C-VESEN1000122

4321

C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.4E-3
0//80aa//60%/P25916
C-Y79AA1000059//Homo sapiens immunophilin homolog
ARA9 mRNA, complete cds.//2.9E-70//1040bp//65%//
U78521
C-Y79AA1000065
C-Y79AA1000131
C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA,
complete cds.//0//1858bp//99%/AF132936
C-Y79AA1000202
C-Y79AA1000214//Homo sapiens histone H2A.F/Z vari
ant (H2AV) mRNA, complete cds.//7.1E-71//345bp//1
00%/AF081192
C-Y79AA1000230
C-Y79AA1000258
C-Y79AA1000268//Mus musculus Nip2l mRNA, complete
cds.//2.10E-50//648bp//64%/AF035207
C-Y79AA1000313//CALPHOTIN.//0.000011//336aa//23%//
Q02910
C-Y79AA1000328//SEL-10 PROTEIN.//0.00000067//219a 20
a//25%/Q93794
C-Y79AA1000355
C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION
PROTEIN 161.//4E-20//261aa//27%/P25343
C-Y79AA1000420
C-Y79AA1000469//Mus musculus ancient ubiquitous 4
6 kDa protein AUP1 precursor (Aup1) mRNA, complete
cds.//8.30E-252//1207bp//85%/U41736
C-Y79AA1000480
C-Y79AA1000540
C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY
PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD CO
ATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR H
A2/AP2 ADAPTIN ALPHA C SUBUNIT).//0//652aa//98%/P
17427
C-Y79AA1000574//Homo sapiens clone H17 unknown mRN
A.//0//1932bp//99%/AF103801
C-Y79AA1000627//Homo sapiens zinc finger protein
(ZF5128) mRNA, complete cds.//2E-287//2031bp//82%//
AF060503
C-Y79AA1000705//M.musculus mRNA of enhancer-trap-l
ocus 1.//5.80E-254//1477bp//84%/X69942
C-Y79AA1000734//Homo sapiens peroxisomal biogenes
is factor (PEX11b) mRNA, complete cds.//0//1594bp
//99%/AF093670
C-Y79AA1000748//Homo sapiens CGI-05 protein mRNA,
complete cds.//1.9E-239//1367bp//91%/AF152097
C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIB
ONUCLEOPROTEIN X (HNRNP X) (CBP).//4.9E-91//200aa/
/64%/Q61990

4322

C-Y79AA1000774
C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE
(EC 3.1.3.5).//3E-37//469aa//27%/P49902
C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mR
NA, complete cds.//1.10E-236//1076bp//99%/AF0987
99
C-Y79AA1000794//Homo sapiens actin-associated pro
tein 2E4/kaptin (2E4)mRNA, 2E4-1 allele, complete
cds.//0//1610bp//99%/AF105369
10 C-Y79AA1000800//Homo sapiens putative secreted pr
otein (ZSIG11) mRNA, complete cds.//1.6E-284//128
8bp//99%/AF072733
C-Y79AA1000805
C-Y79AA1000824
C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//5E-173//22
0aa//79%/P05209
C-Y79AA1000850
C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (Z
IPPER PROTEIN) (MYOSINII).//4.2E-17//430aa//27%//
Q99323
C-Y79AA1000968//Rattus norvegicus initiation fact
or eIF-2B gamma subunit (eIF-2B gamma) mRNA, compl
ete cds.//3.9E-248//1468bp//87%/U38253
C-Y79AA1000976
C-Y79AA1001023
C-Y79AA1001041
C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG
-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD).//
/3.1E-138//583aa//47%/P45953
30 C-Y79AA1001077
C-Y79AA1001078
C-Y79AA1001145
C-Y79AA1001177
C-Y79AA1001185
C-Y79AA1001211//Homo sapiens origin recognition c
omplex subunit 6 (ORC6) mRNA, complete cds.//0//1
435bp//99%/AF139658
C-Y79AA1001228
C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1
40 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTER
OID DEHYDROGENASE 1).//7.7E-50//228aa//42%/P51657
C-Y79AA1001236//Homo sapiens mRNA for JM23 protei
n, complete coding sequence (clone IMAGE 34581 and
IMAGE 45355 and LLNLc110I133Q7 (RZPD Berlin)).//
0//1653bp//99%/AJ005892
C-Y79AA1001281
C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FI
NGER PROTEIN 46).//0.000000023//193aa//30%/Q03309
C-Y79AA1001323//Mus musculus mRNA for GSG1, compl
ete cds.//3.3E-172//1171bp//83%/D87325
50

4323

4324

- C-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J).
//1.2E-58//178aa//66%/P31271
- C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG
(EC 3.4.24.-)//1.2E-13//230aa//32%/O83746
- C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen(MA4) mRNA, partial cds."//
8.50E-65//784bp//62%/AF083115
- C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17
KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9)
(UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//3.80E-18 10
//151aa//38%/P35132
- C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds."//4.5E-193
//1333bp//80%/D14336
- C-Y79AA1001541
- C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA
(EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI
4K-ALPHA).//7.5E-76//85aa//90%/P42356
- C-Y79AA1001555
- C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 20
6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING EN
ZYME).//1.9E-40//482aa//27%/P27550
- C-Y79AA1001585
- C-Y79AA1001603//POLYPEPTIDE N-ACETYL GALACTOSAMINY
LTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYL GAL
ACTOSAMINYLTRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N
- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)."
//1.7E-84//313aa//48%/Q07537
- C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.8E-91/
/209aa//41%/P52740
- C-Y79AA1001665
- C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA,
complete cds."//3.4E-310//1430bp//98%/AF07704
9
- C-Y79AA1001696//Homo sapiens mRNA for KIAA1109 pr
oteins, partial cds."//0//1669bp//100%/AB029032
- C-Y79AA1001705//Homo sapiens p53 regulated PA26-T
2 nuclear protein (PA26) mRNA, complete cds."//3.4
E-47//626bp//68%/AF033120
- C-Y79AA1001711//Human 60-kdal ribonucleoprotein 40
(Ro) mRNA, complete cds."//1.2E-258//1185bp//99%/J04137
- C-Y79AA1001781
- C-Y79AA1001805
- C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase2 (IP6K2) mRNA, complete cds."
//0//1689bp//98%/AF177145
- C-Y79AA1001846
- C-Y79AA1001923
- C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR 50
- ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1E-10//9
4aa//47%/O42643
- C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18
KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBI
QUITIN CARRIER PROTEIN) (PW42).//9.9E-39//143aa//5
2%/P42743
- C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//
5E-163//752bp//99%/X86018
- C-Y79AA1002089
- C-Y79AA1002115
- C-Y79AA1002125
- C-Y79AA1002204
- C-Y79AA1002208//ANKYRIN.//8.1E-34//188aa//38%/Q02
357
- C-Y79AA1002209//Homo sapiens CGI-04 protein mRNA,
complete cds."//0//1617bp//99%/AF132939
- C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PS02
/SNM1.//7.10E-17//213aa//31%/P30620
- C-Y79AA1002246//SYNAPTOTAGMIN V.//1.6E-28//286aa//
32%/O00445
- C-Y79AA1002298
- C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2)
mRNA, complete cds."//0//1209bp//99%/AF116574
- C-Y79AA1002311//R.norvegicus mRNA for cytosolic re
sistinfatorxin-bindingprotein.//2.9E-186//1130bp//8
2%/X67877
- C-Y79AA1002351
- C-Y79AA1002407
- C-Y79AA1002433//Homo sapiens chromatin-specific t
ranscription elongation factor FACT 140 kDa subuni
t mRNA, complete cds."//0//1545bp//96%/AF152961
- C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGE
R PROTEIN HTF10) (HPF7).//1.5E-136//472aa//49%/Q0
5481
- 【1134】 相同性検索結果データ13.
全長塩基配列および推定アミノ酸配列に対する相同性検索結果データ
各データは、配列名、ヒットデータのDefinition、P
値、比較配列の長さ、相同性、ヒットデータのAccession
No.の順に//で区切って記載した。
- C-HEMBA1000042
- C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds."//0//1135bp//100%/AF196304
- C-HEMBA1000150//H.sapiens gene for U5 snRNP-specific 200kD protein.//2.50E-153//525bp//91%/Z70200
- C-HEMBA1000213
- C-HEMBA1000243
- C-HEMBA1000244
- C-HEMBA1000251

C-HEMBA1000338		C-HEMBA1001383	
C-HEMBA1000357		C-HEMBA1001391	
C-HEMBA1000376		C-HEMBA1001411	
C-HEMBA1000428		C-HEMBA1001432	
C-HEMBA1000469		C-HEMBA1001433	
C-HEMBA1000497		C-HEMBA1001435	
C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.40E-37//674aa//25%/Q05481		C-HEMBA1001442	
C-HEMBA1000569//GPI-ANCHORED PROTEIN P137.//6.50E-19//265aa//32%/Q60865C-HEMBA1000575	10	C-HEMBA1001463	
C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.20E-17//198aa//40%/P23246		C-HEMBA1001515	
C-HEMBA1000673		C-HEMBA1001522	
C-HEMBA1000702		C-HEMBA1001557	
C-HEMBA1000722		C-HEMBA1001566	
C-HEMBA1000726		C-HEMBA1001589	
C-HEMBA1000876		C-HEMBA1001608	
C-HEMBA1000942		C-HEMBA1001636	
C-HEMBA1000943		C-HEMBA1001647	
C-HEMBA1000960		C-HEMBA1001651	
C-HEMBA1000985		C-HEMBA1001658	
C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1).//3.10E-10//70aa//58%/P06493		C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATE	
C-HEMBA1001020		D PROTEIN VPS9.//5.40E-09//101aa//35%/P54787	20
C-HEMBA1001024		C-HEMBA1001712	
C-HEMBA1001026		C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//1.10E-38//87aa//96%/P55288	
C-HEMBA1001051		C-HEMBA1001745	
C-HEMBA1001060		C-HEMBA1001750	
C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%/P02461		C-HEMBA1001784	
C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%/AF119043		C-HEMBA1001791	
C-HEMBA1001099		C-HEMBA1001803	
C-HEMBA1001121		C-HEMBA1001820	30
C-HEMBA1001123		C-HEMBA1001835	
C-HEMBA1001208		C-HEMBA1001888	
C-HEMBA1001213		C-HEMBA1001912	
C-HEMBA1001226		C-HEMBA1001915	
C-HEMBA1001247		C-HEMBA1001918	
C-HEMBA1001299		C-HEMBA1001940	
C-HEMBA1001319		C-HEMBA1001942	
C-HEMBA1001323		C-HEMBA1001964	
C-HEMBA1001327		C-HEMBA1002022	
C-HEMBA1001361		C-HEMBA1002039	40
C-HEMBA1001375		C-HEMBA1002100	
C-HEMBA1001377		C-HEMBA1002113	
		C-HEMBA1002119	
		C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1 (MLN 50).//7.10E-05//51aa//49%/Q14847	
		C-HEMBA1002160	
		C-HEMBA1002162	
		C-HEMBA1002166	
		C-HEMBA1002185	
		C-HEMBA1002204	50

C-HEMBA1002328		C-HEMBA1003229	
C-HEMBA1002337		C-HEMBA1003276	
C-HEMBA1002348		C-HEMBA1003278	
C-HEMBA1002381		C-HEMBA1003328	
C-HEMBA1002486		C-HEMBA1003373	
C-HEMBA1002498		C-HEMBA1003597	
C-HEMBA1002538		C-HEMBA1003598	
C-HEMBA1002552		C-HEMBA1003656	
C-HEMBA1002555//Homo sapiens mSin3A associated polypeptide p30 mRNA, complete cds.//5.30E-51//768bp//68%/AF055993	10	C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-).//2.40E-92//423aa//47%/P34629	
C-HEMBA1002558		C-HEMBA1003733	
C-HEMBA1002621		C-HEMBA1003742	
C-HEMBA1002629		C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//3.70E-124//347aa//55%/Q16665	
C-HEMBA1002645		C-HEMBA1003803	
C-HEMBA1002659		C-HEMBA1003854	
C-HEMBA1002661		C-HEMBA1003926	20
C-HEMBA1002666		C-HEMBA1003939	
C-HEMBA1002678		C-HEMBA1003987	
C-HEMBA1002679		C-HEMBA1004012	
C-HEMBA1002712		C-HEMBA1004015	
C-HEMBA1002716		C-HEMBA1004193	
C-HEMBA1002742		C-HEMBA1004225	
C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7).//5.00E-37//268aa//34%/P06746		C-HEMBA1004241	
C-HEMBA1002748		C-HEMBA1004267	
C-HEMBA1002780		C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//9.40E-31//381bp//65%/AF155103	30
C-HEMBA1002801		C-HEMBA1004354//CHL1 PROTEIN.//9.90E-26//130aa//42%/P22516	
C-HEMBA1002826		C-HEMBA1004356//H. sapiens MSSP-2 mRNA.//3.00E-243//573bp//98%/X77494	
C-HEMBA1002833		C-HEMBA1004396	
C-HEMBA1002921		C-HEMBA1004405	
C-HEMBA1002934		C-HEMBA1004433	
C-HEMBA1002944		C-HEMBA1004538	
C-HEMBA1002968		C-HEMBA1004542	
C-HEMBA1003034		C-HEMBA1004573	40
C-HEMBA1003037		C-HEMBA1004577	
C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACIDLABILE CHAIN PRECURSOR (ALS).//1.30E-09//121aa//40%/P35858		C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds.//0//1612bp//99%/AF193844	
C-HEMBA1003078		C-HEMBA1004617	
C-HEMBA1003083		C-HEMBA1004631	
C-HEMBA1003086		C-HEMBA1004705	
C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%/AF155096		C-HEMBA1004733	
C-HEMBA1003133		C-HEMBA1004748	
C-HEMBA1003142		C-HEMBA1004778	
C-HEMBA1003166		C-HEMBA1004803	50
C-HEMBA1003197			
C-HEMBA1003202			
C-HEMBA1003220			

C-HEMBA1004807		C-HEMBA1005426	
C-HEMBA1004820		C-HEMBA1005443	
C-HEMBA1004865		C-HEMBA1005447	
C-HEMBA1004880		C-HEMBA1005497	
C-HEMBA1004900		C-HEMBA1005500	
C-HEMBA1004909		C-HEMBA1005506	
C-HEMBA1004960		C-HEMBA1005508	
C-HEMBA1004978		C-HEMBA1005526	
C-HEMBA1004980		C-HEMBA1005530//Homo sapiens anaphase-promoting co	
C-HEMBA1004983	10	mplex subunit 7 (APC7)mRNA, complete cds.//0//1578	
C-HEMBA1004995		bp//98%/AF191340	
C-HEMBA1005019//Homo sapiens mRNA for KIAA0648 pro		C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic r	
tein, partial cds.//0//2212bp//99%/AB014548		egion/leucine zipper transcription factor (MAFB) m	
C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA,		RNA, complete cds.//1.00E-220//1014bp//99%/AF1341	
complete cds.//0//1487bp//99%/AF132947		57	
C-HEMBA1005035		C-HEMBA1005552	
C-HEMBA1005039		C-HEMBA1005568	
C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-1		C-HEMBA1005588	
6).//3.40E-101//106aa//98%/P35290		C-HEMBA1005593	
C-HEMBA1005050	20	C-HEMBA1005606	
C-HEMBA1005062		C-HEMBA1005616	
C-HEMBA1005066		C-HEMBA1005627	
C-HEMBA1005075		C-HEMBA1005670	
C-HEMBA1005079		C-HEMBA1005679	
C-HEMBA1005101//Homo sapiens SYT interacting prote		C-HEMBA1005699	
in SIP mRNA, completecds.//0//2762bp//99%/AF08056		C-HEMBA1005705	
1		C-HEMBA1005732//Human mRNA for KIAA1293 gene, comp	
C-HEMBA1005123		lete cds.//5.50E-102//317bp//98%/D14697	
C-HEMBA1005149		C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT	
C-HEMBA1005152	30	(EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEI	
C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA,		NASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%/P	
complete cds.//0//1608bp//99%/AF132941		00789	
C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD		C-HEMBA1005852	
PROTEIN (SRP68).//1.90E-179//361aa//95%/Q00004		C-HEMBA1005894	
C-HEMBA1005223		C-HEMBA1005921	
C-HEMBA1005232		C-HEMBA1006035	
C-HEMBA1005241		C-HEMBA1006036	
C-HEMBA1005275		C-HEMBA1006090	
C-HEMBA1005293		C-HEMBA1006138	
C-HEMBA1005311	40	C-HEMBA1006173	
C-HEMBA1005338//Homo sapiens mRNA for matrilin-4,		C-HEMBA1006252	
partial.//3.90E-241//1095bp//99%/AJ007581		C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complet	
C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85		e cds.//3.50E-157//845bp//92%/AF073836	
//206aa//69%/P52743		C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN	
C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1)		(EC 2.3.1.-).//1.60E-130//332aa//62%/002193	
mRNA, complete cds.//9.00E-77//620bp//74%/AF07178		C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTE	
7		IN HTF6).//3.50E-105//381aa//54%/P28160	
C-HEMBA1005374		C-HEMBA1006380	
C-HEMBA1005382		C-HEMBA1006416	
C-HEMBA1005411	50	C-HEMBA1006421	

C-HEMBA1006424		tein, complete cds.//0//1212bp//98%/D86987
C-HEMBA1006426		C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%/AF196304
C-HEMBA1006446		C-HEMBA1007243//Chinese hamster hpert mRNA, complete cds.//2.00E-58//650bp//70%/J00060
C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%/P55786		C-HEMBA1007251
C-HEMBA1006486		C-HEMBA1007288
C-HEMBA1006494		C-HEMBA1007322
C-HEMBA1006546		10 C-HEMBA1007341
C-HEMBA1006562		C-HEMBA1000050
C-HEMBA1006595		C-HEMBA1000054
C-HEMBA1006597		C-HEMBA1000059
C-HEMBA1006631		C-HEMBA1000089
C-HEMBA1006639		C-HEMBA1000113
C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%/P14148		C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINALGUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%/P51177
C-HEMBA1006659		C-HEMBA1000173
C-HEMBA1006665		20 C-HEMBA1000175
C-HEMBA1006676		C-HEMBA1000272
C-HEMBA1006695		C-HEMBA1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%/P37888
C-HEMBA1006709		C-HEMBA1000318
C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%/AF152492		C-HEMBA1000336
C-HEMBA1006780		C-HEMBA1000341
C-HEMBA1006807//Homo sapiens mRNA for SPOP.//5.70E-125//1109bp//75%/AJ000644		C-HEMBA1000343
C-HEMBA1006824		C-HEMBA1000354
C-HEMBA1006865		C-HEMBA1000374
C-HEMBA1006921		30 C-HEMBA1000434
C-HEMBA1006949		C-HEMBA1000441
C-HEMBA1006976//H. sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase.//1.90E-80//447bp//89%/X74570		C-HEMBA1000491
C-HEMBA1007051		C-HEMBA1000493
C-HEMBA1007052		C-HEMBA1000510
C-HEMBA1007066		C-HEMBA1000652
C-HEMBA1007073		C-HEMBA1000672
C-HEMBA1007078		C-HEMBA1000684
C-HEMBA1007085		C-HEMBA1000709
C-HEMBA1007113		C-HEMBA1000726
C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, completecds.//1.70E-252//1118bp//92%/AF125042		40 C-HEMBA1000770
C-HEMBA1007129		C-HEMBA1000827
C-HEMBA1007147		C-HEMBA1000831
C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%/AF076929		C-HEMBA1000883
C-HEMBA1007178		C-HEMBA1000888
C-HEMBA1007203//Homo sapiens mRNA for KIAA0214 pro	50	C-HEMBA1000893
		C-HEMBA1000913
		C-HEMBA1000996
		C-HEMBA1001004
		C-HEMBA1001047
		C-HEMBA1001060

C-HEM BB1001114	1.70E-16//84aa//47%/Q03330
C-HEM BB1001119	C-HEM BB1001753
C-HEM BB1001133	C-HEM BB1001756
C-HEM BB1001142	C-HEM BB1001760
C-HEM BB1001177	C-HEM BB1001785
C-HEM BB1001208	C-HEM BB1001797
C-HEM BB1001209	C-HEM BB1001802//Human desmin mRNA, complete cds.//
C-HEM BB1001249	0//1523bp//98%/U59167
C-HEM BB1001253	C-HEM BB1001816
C-HEM BB1001254	10 C-HEM BB1001831//Homo sapiens PAM COOH-terminal int
C-HEM BB1001271	eractor protein 1 (PCIP1) mRNA, complete cds.//0//
C-HEM BB1001304	1514bp//99%/AF056209
C-HEM BB1001317	C-HEM BB1001839//CASTRULA ZINC FINGER PROTEIN XLGCF
C-HEM BB1001348	42.1 (FRAGMENT).//6.90E-11//87aa//35%/P18720
C-HEM BB1001394	C-HEM BB1001850
C-HEM BB1001410	C-HEM BB1001863
C-HEM BB1001424	C-HEM BB1001868
C-HEM BB1001426	C-HEM BB1001874
C-HEM BB1001429//Homo sapiens leucine aminopeptidas	C-HEM BB1001880
e mRNA, complete cds.//0//1933bp//99%/AF061738	20 C-HEM BB1001899
C-HEM BB1001436	C-HEM BB1001906
C-HEM BB1001443//Rattus norvegicus pyruvate dehydro	C-HEM BB1001910
genase phosphatase isoenzyme 1 mRNA, complete cds.	C-HEM BB1001911
//3.00E-130//553bp//86%/AF062740	C-HEM BB1001921
C-HEM BB1001449	C-HEM BB1001922
C-HEM BB1001458	C-HEM BB1001930
C-HEM BB1001521	C-HEM BB1001944
C-HEM BB1001531	C-HEM BB1001945
C-HEM BB1001535	C-HEM BB1001947
C-HEM BB1001536	30 C-HEM BB1001950//PROBABLE OXYGEN-INDEPENDENT COPRO
C-HEM BB1001564	ORPHYRINOGEN III OXIDASE (EC 1.-.-.) (COPROPORPHY
C-HEM BB1001565	RINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//
C-HEM BB1001585	31%/P54304
C-HEM BB1001588	C-HEM BB1001952
C-HEM BB1001603	C-HEM BB1001957
C-HEM BB1001618	C-HEM BB1001962
C-HEM BB1001635	C-HEM BB1001983
C-HEM BB1001653	C-HEM BB1001990
C-HEM BB1001668	C-HEM BB1001996
C-HEM BB1001673//Homo sapiens mRNA for KIAA0646 pro	C-HEM BB1002002
tein, complete cds.//0//2035bp//99%/AB014546	C-HEM BB1002005
C-HEM BB1001685	C-HEM BB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1)
C-HEM BB1001695	(CYPIVC1).//2.70E-49//139aa//55%/P29981
C-HEM BB1001707	C-HEM BB1002043
C-HEM BB1001735	C-HEM BB1002045
C-HEM BB1001736//EUKARYOTIC TRANSLATION INITIATION	C-HEM BB1002049
FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3 P110).//4.60E	C-HEM BB1002050
-15//391aa//25%/P55884	C-HEM BB1002068
C-HEM BB1001747	C-HEM BB1002092
C-HEM BB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//	50 C-HEM BB1002139

C-HEM BB1002142		PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//
C-HEM BB1002190		249aa//27%/P03396
C-HEM BB1002193		C-MAMMA1000057
C-HEM BB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-132//399aa//44%/Q05481		C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE-- TRNA LIGASE) (CYSRS).//2.10E-90//427aa//39%/Q09860
C-HEM BB1002218		C-MAMMA1000092
C-HEM BB1002232		C-MAMMA1000103
C-HEM BB1002247		C-MAMMA1000117
C-HEM BB1002249	10	C-MAMMA1000129
C-HEM BB1002266//NEURONAL PROTEIN.//2.10E-46//121aa//76%/P41737		C-MAMMA1000133
C-HEM BB1002327		C-MAMMA1000155
C-HEM BB1002329		C-MAMMA1000175
C-HEM BB1002342//Homo sapiens mRNA for putative thioredoxin-like protein.//1.10E-274//1249bp//99%/AJ010841		C-MAMMA1000198
C-HEM BB1002358		C-MAMMA1000241
C-HEM BB1002371		C-MAMMA1000251
C-HEM BB1002387	20	C-MAMMA1000254
C-HEM BB1002409		C-MAMMA1000287
C-HEM BB1002425		C-MAMMA1000307
C-HEM BB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//31%/P34692		C-MAMMA1000331
C-HEM BB1002453		C-MAMMA1000339
C-HEM BB1002458		C-MAMMA1000340
C-HEM BB1002477//Human Grb2-associated binder-1 mRNA A, complete cds.//7.70E-258//774bp//99%/U43885		C-MAMMA1000348
C-HEM BB1002489		C-MAMMA1000356
C-HEM BB1002510//CYP7 PROTEIN.//3.10E-50//192aa//42 30 %//P48365		C-MAMMA1000360
C-HEM BB1002520		C-MAMMA1000402
C-HEM BB1002522		C-MAMMA1000414
C-HEM BB1002545		C-MAMMA1000431
C-HEM BB1002579		C-MAMMA1000444
C-HEM BB1002582		C-MAMMA1000458
C-HEM BB1002596		C-MAMMA1000500
C-HEM BB1002603		C-MAMMA1000522
C-HEM BB1002610		C-MAMMA1000576
C-HEM BB1002613		C-MAMMA1000583
C-HEM BB1002617		C-MAMMA1000594
C-HEM BB1002623		C-MAMMA1000605
C-HEM BB1002635		C-MAMMA1000616
C-HEM BB1002677		C-MAMMA1000643
C-HEM BB1002683		C-MAMMA1000684//Homo sapiens 7-60 mRNA, complete c
C-HEM BB1002699	40	ds.//0//2402bp//99%/AF109134
C-HEM BB1002702		C-MAMMA1000696
C-MAMMA1000009		C-MAMMA1000707
C-MAMMA1000043		C-MAMMA1000714
C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE 50		C-MAMMA1000720
		C-MAMMA1000744
		C-MAMMA1000761
		C-MAMMA1000776
		C-MAMMA1000798
		C-MAMMA1000839
		C-MAMMA1000851

C-MAMMA1000863		C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU-TYPE). //5.70E-55//86aa//97%/P07384
C-MAMMA1000867		C-MAMMA1001547
C-MAMMA1000876		C-MAMMA1001551
C-MAMMA1000880		C-MAMMA1001575
C-MAMMA1000883		C-MAMMA1001590
C-MAMMA1000921		C-MAMMA1001600
C-MAMMA1000931		10 C-MAMMA1001606
C-MAMMA1000941		C-MAMMA1001627//Homo sapiens mRNA for transcription factor TBX6. //5.20E-189//871bp//99%/AJ007989
C-MAMMA1000957		C-MAMMA1001663
C-MAMMA1000962		C-MAMMA1001670
C-MAMMA1000975		C-MAMMA1001671
C-MAMMA1000987		C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUNIT (CAPZ). //0.00000058//29aa//100%/P47756
C-MAMMA1001003		C-MAMMA1001711
C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT). //1.20E-26//276aa//28%/Q90674		C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN CLASS-V). //5.90E-240//445aa//97%/P09653
C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN]. //2.60E-107//190aa//95%/Q15746	20	C-MAMMA1001744
C-MAMMA1001082		C-MAMMA1001745
C-MAMMA1001162		C-MAMMA1001751//Homo sapiens tandem pore domain potassium channel TWIK-2(KCNK6) mRNA, complete cds. //0//2332bp//99%/AF117708
C-MAMMA1001186		C-MAMMA1001783
C-MAMMA1001191		C-MAMMA1001788
C-MAMMA1001206		C-MAMMA1001806
C-MAMMA1001220		C-MAMMA1001812
C-MAMMA1001243		30 C-MAMMA1001815
C-MAMMA1001249		C-MAMMA1001817
C-MAMMA1001256		C-MAMMA1001818
C-MAMMA1001268		C-MAMMA1001820//Rattus norvegicus mRNA for PAC608 gene. //1.30E-198//1157bp//80%/Y13148
C-MAMMA1001271		C-MAMMA1001824
C-MAMMA1001274		C-MAMMA1001851
C-MAMMA1001292		C-MAMMA1001854
C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP). //2.20E-98//283aa//63%/Q07960		C-MAMMA1001864
C-MAMMA1001324	40	C-MAMMA1001878
C-MAMMA1001341		C-MAMMA1001890
C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG). //1.40E-165//312aa//99%/P02750		C-MAMMA1001907
C-MAMMA1001397		C-MAMMA1001908
C-MAMMA1001408		C-MAMMA1001931
C-MAMMA1001420		C-MAMMA1001969
C-MAMMA1001442		C-MAMMA1002011
C-MAMMA1001452		C-MAMMA1002032
C-MAMMA1001465		C-MAMMA1002041
C-MAMMA1001487	50	C-MAMMA1002047
		C-MAMMA1002056
		C-MAMMA1002058

- C-MAMMA1002078
 C-MAMMA1002082
 C-MAMMA1002084
 C-MAMMA1002093
 C-MAMMA1002094
 C-MAMMA1002118
 C-MAMMA1002125
 C-MAMMA1002132
 C-MAMMA1002140
 C-MAMMA1002143//Homo sapiens Cdc42 effector protein 4 mRNA, complete cds.//1.70E-252//1170bp//99%//AF099664
 C-MAMMA1002145
 C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PEROXIDOREDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURALKILLER CELL ENHANCING FACTOR B) (NKEF-B).//5.20E-61//60aa//90%//P32119
 C-MAMMA1002230
 C-MAMMA1002250
 C-MAMMA1002282
 C-MAMMA1002293
 C-MAMMA1002298
 C-MAMMA1002299
 C-MAMMA1002308
 C-MAMMA1002310
 C-MAMMA1002311
 C-MAMMA1002322
 C-MAMMA1002339
 C-MAMMA1002352
 C-MAMMA1002359
 C-MAMMA1002360
 C-MAMMA1002392
 C-MAMMA1002411
 C-MAMMA1002413
 C-MAMMA1002417
 C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMALMEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2).//1.10E-24//96aa//68%//Q14108
 C-MAMMA1002434
 C-MAMMA1002446
 C-MAMMA1002454
 C-MAMMA1002461
 C-MAMMA1002475
 C-MAMMA1002556
 C-MAMMA1002566
 C-MAMMA1002612
 C-MAMMA1002622//VILLIN.//7.20E-35//53aa//64%//P02640
- C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC).//1.30E-198//550aa//70%//Q07866
 C-MAMMA1002650//Mus musculus ODA-8S protein mRNA, complete cds.//5.40E-57//480bp//68%//AF194030
 C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//4.3e-317//1942bp//85%//AF018261
 C-MAMMA1002727
 C-MAMMA1002748
 C-MAMMA1002758
 C-MAMMA1002780
 C-MAMMA1002820
 C-MAMMA1002833
 C-MAMMA1002843
 C-MAMMA1002895
 C-MAMMA1002937//ZINC FINGER PROTEIN 135.//8.30E-99//393aa//43%//P52742
 C-MAMMA1003004
 C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT proteinPIASy mRNA, complete cds.//0//1533bp//99%//AF077952
 C-NT2RM1000001//D.melanogaster sap47-2 mRNA.//1.50E-10//417bp//62%//X80110
 C-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//0//3376bp//99%//D31886
 C-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cds.//0//3551bp//99%//AB014590
 C-NT2RM1000086//Homo sapiens mRNA for KIAA0661 protein, complete cds.//0//3035bp//96%//AB014561
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR.//4.40E-21//372aa//30%//P10775
 C-NT2RM1000499
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4.//3.60E-11//180aa//28%//Q99383
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//3.60E-115//332aa//52%//Q05481
 C-NT2RM2001592//Homo sapiens mRNA for KIAA1067 protein, partial cds.//0//3471bp//99%//AB028990
 C-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds.//0//1632bp//99%//AB014518
 C-NT2RM2001637
 C-NT2RM2001641
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29).//6.50E-104//407aa//43%//Q07230
 C-NT2RM2001699
 C-NT2RM2001706
 C-NT2RM2001718
 C-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds.//0//2892bp//99%//AB007931

- C-NT2RM2001805
 C-NT2RM4000086
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//49%/P10962
 C-NT2RM4000414
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%/Q04652
 C-NT2RM4000634
 C-NT2RM4000657//Homo sapiens mRNA for KIAA1069 protein, partial cds.//0//1412bp//100%/AB028992 10
 C-NT2RM4000783
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRC).//6.70E-22//250aa//29%/P02750
 C-NT2RM4000971
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN-NTF10) (HPF7).//8.00E-211//738aa//50%/Q05481
 C-NT2RM4001092//ZINC FINGER PROTEIN GL03.//3.10E-24//265aa//33%/P38682
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%/Q03532 20
 C-NT2RM4001569
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//8.10E-300//1395bp//98%/M37712
 C-NT2RM4001905
 C-NT2RM4001938//Homo sapiens mRNA for KIAA0898 protein, partial cds.//0//2234bp//99%/AB020705
 C-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNALIGASE) (ASPRS).//1.90E-31//80aa//52%/P36419 30
 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%/AF072758
 C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%/AF176085
 C-NT2RM4002109//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2572bp//99%/AF071592
 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%/AF035940
 C-NT2RM4002194//Mus musculus semaphorin VIa mRNA, complete cds.//5.20E-297//1753bp//87%/AF030430
 C-NT2RM4002390
 C-NT2RM4002398
 C-NT2RM4002420
 C-NT2RM4002534
 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%/AF022962 50
- C-NT2RM4002571//H. sapiens mRNA for UDP-GalNAc:poly peptide N-acetylgalactosaminyltransferase (T2).//4.60E-78//921bp//69%/X85019
 C-NT2RP1000358//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//1938bp//88%/AL050019
 C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//8.20E-83//345aa//47%/Q61068C-NT2RP1000609//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2165bp//99%/AL050118
 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//1.20E-78//483aa//31%/P46721
 C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P)mRNA, complete cds.//0//1687bp//99%/AF145020
 C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%/AF047020
 C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%/AF064094
 C-NT2RP1000916
 C-NT2RP1000944
 C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%/U82267
 C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%/Q06218 30
 C-NT2RP1001113
 C-NT2RP1001173//Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone DKFZp566D1146).//0//2333bp//99%/AL080222
 C-NT2RP1001177//Rattus norvegicus histone macroH2A 1.2 mRNA, complete cds.//5.20E-108//1278bp//69%/U79139
 C-NT2RP1001185//Human isovaleryl-coA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%/M34192 40
 C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%/AF081513
 C-NT2RP1001311
 C-NT2RP1001313//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//7.50E-121//1394bp//69%/AF126799
 C-NT2RP2000001//Homo sapiens mRNA for KIAA1111 protein, partial cds.//0//3188bp//99%/AB029034 50

- C-NT2RP2000027
 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60).//3.30E-16//114aa//44%/002675
 C-NT2RP2000198
 C-NT2RP2000523//APOLIPOPROTEIN B MRNA EDITING PROTEIN (HEPR) (APOBEC-1).//6.00E-16//124aa//34%/P41238
 C-NT2RP2000551
 C-NT2RP2000644
 C-NT2RP2000660//SAP1 PROTEIN.//5.20E-68//474aa//32%/P39955
 C-NT2RP2000678
 C-NT2RP2000715
 C-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds.//0//1562bp//99%/U80811
 C-NT2RP2000970
 C-NT2RP2001347
 C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24%/P37709
 C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%/P24391
 C-NT2RP2001634//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//0//2445bp//99%/U97067
 C-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds.//0//1287bp//99%/AF058718
 C-NT2RP2001677
 C-NT2RP2001678
 C-NT2RP2001720
 C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//44%/Q61068
 C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.70E-49//411aa//32%/P51523
 C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24%/P53009
 C-NT2RP2001861
 C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26//126aa//52%/O14754
 C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//1.20E-45//141aa//65%/P55008
 C-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (5ptase) mRNA, 3' end.//0//2518bp//98%/M
 74161
 C-NT2RP2001936
 C-NT2RP2001943
 C-NT2RP2001946
 C-NT2RP2002032
 C-NT2RP2002033
 C-NT2RP2002041
 C-NT2RP2002047
 C-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//1.60E-226//1301bp//88%/U87306
 C-NT2RP2002124//Homo sapiens mRNA for KIAA1097 protein, partial cds.//0//1772bp//95%/AB029020
 C-NT2RP2002172
 C-NT2RP2002219
 C-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//0//1528bp//98%/AF005418
 C-NT2RP2002316
 C-NT2RP2002373
 C-NT2RP2002439
 C-NT2RP2002475
 C-NT2RP2002546
 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-155//562aa//50%/P51523
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//9.20E-147//874bp//87%/U19181
 C-NT2RP2002643
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//3.50E-74//727bp//72%/AF041107
 C-NT2RP2002736
 C-NT2RP2002740
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//9.90E-54//964bp//64%/D89016
 C-NT2RP2002752
 C-NT2RP2002753
 C-NT2RP2002857
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//1.90E-11//132aa//38%/Q13829
 C-NT2RP2003073
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase.//0//2313bp//99%/AJ132545
 C-NT2RP2003206
 C-NT2RP2003228//H. sapiens P1-Cdc21 mRNA.//0//2870bp//98%/X74794
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.60E-186//1551bp//77%/AF023657
 C-NT2RP2003237
 C-NT2RP2003272//Homo sapiens ubiquitin mRNA, compl

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ete cds.//0//1789bp//99%/AF176069
 C-NT2RP2003280
 C-NT2RP2003293
 C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PR
 OTEIN US01.//5.50E-13//302aa//26%/P25386
 C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROL
 ASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE D
 UB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-
 1) (DEUBIQUITINATING ENZYME 1).//9.60E-78//346aa//
 43%/Q61068
 C-NT2RP2003456
 C-NT2RP2003517//Human c-sis/platelet-derived growt
 h factor 2 (SIS/PDGF2)mRNA, complete cds.//0//1746
 bp//95%/M12783
 C-NT2RP2003522//Homo sapiens zinc finger DNA bindi
 ng protein 99 (ZNF281)mRNA, complete cds.//0//1764
 bp//99%/AF125158
 C-NT2RP2003559
 C-NT2RP2003564//52 KD RO PROTEIN (SJOGREN SYNDROME
 TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//2.10E-59//270
 aa//46%/P19474
 C-NT2RP2003581
 C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetyl
 neuraminic acid synthetase.//9.40E-243//1624bp//82
 %//AJ006215
 C-NT2RP2003702//Homo sapiens 17 beta-hydroxysterol
 d dehydrogenase type VII (HSD17B7) mRNA, complete
 cds.//2.1e-313//978bp//99%/AF098786
 C-NT2RP2003704//Homo sapiens mRNA for ATP-dependen
 t metalloprotease YME1L.//1.80E-72//350bp//100%/A
 J132637
 C-NT2RP2003727
 C-NT2RP2003751
 C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2
 IN CHROMOSOME II.//5.50E-63//253aa//50%/Q09201
 C-NT2RP2003825
 C-NT2RP2003871
 C-NT2RP2003885
 C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NE
 K1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1).//
 6.10E-183//387aa//87%/P51954
 C-NT2RP2003976//Homo sapiens mRNA for KIAA0447 pro
 tein, complete cds.//0//2866bp//98%/AB007916
 C-NT2RP2003988
 C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POL
 YMERASE B TRANSCRIPTION FACTOR 3).//2.30E-53//141a
 a//78%/P20290
 C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (AT
 P PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//5.40E-3
 0//319aa//31%/Q01513

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C-NT2RP2004142
 C-NT2RP2004170//Homo sapiens mRNA for transducin
 (beta) like 1 protein.//1.10E-138//1236bp//74%/Y1
 2781
 C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15
 mRNA, complete cds.//3.80E-52//397bp//82%/AF0039
 98
 C-NT2RP2004207
 C-NT2RP2004226
 10 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/
 threonine kinase, complete cds.//0//2272bp//99%/A
 B015982
 C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (2
 00 KD NEUROFILAMENT PROTEIN) (NF-H).//9.90E-12//42
 7aa//26%/P19246
 C-NT2RP2004270//PROTEIN PTM1 PRECURSOR.//1.40E-16/
 /334aa//24%/P32857
 C-NT2RP2004321
 C-NT2RP2004339
 20 C-NT2RP2004347
 C-NT2RP2004396//Homo sapiens mRNA for activator of
 S phase Kinase, complete cds.//5.40E-243//1108bp/
 /99%/AB028069
 C-NT2RP2004399
 C-NT2RP2004400
 C-NT2RP2004412
 C-NT2RP2004425//Mus musculus axotrophin mRNA, comp
 lete cds.//0//2321bp//86%/AF155739
 C-NT2RP2004490
 30 C-NT2RP2004523
 C-NT2RP2004538//Mus musculus kinesin-like protein
 KIF1B (Kif1b) mRNA, complete cds.//0//1387bp//86/
 /AF090190
 C-NT2RP2004580
 C-NT2RP2004587//Homo sapiens mRNA for KIAA0888 pro
 tein, partial cds.//0//2886bp//100%/AB020695
 C-NT2RP2004594
 C-NT2RP2004681
 C-NT2RP2004709
 C-NT2RP2004710//Homo sapiens mRNA for KIAA1014 pro
 tein, partial cds.//0//2587bp//100%/AB023231
 C-NT2RP2004732//Homo sapiens mRNA for KIAA0884 pro
 tein, partial cds.//0//1774bp//99%/AB020691
 C-NT2RP2004767
 C-NT2RP2004775
 C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger
 suppressor protein 1(KS1) mRNA, complete cds.//1.
 00E-228//1666bp//75%/U56732
 C-NT2RP2004962
 50 C-NT2RP2004982

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C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME
 TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//1.80E-99//376
 aa//43%/P19474
 C-NT2RP2005018
 C-NT2RP2005020
 C-NT2RP2005022
 C-NT2RP2005031
 C-NT2RP2005116//Homo sapiens mRNA for KIAA0664 pro
 tein, partial cds.//0//4069bp//99%/AB014564
 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3. 10
 1.26.-) (2-5A-DEPENDENT RNAASE) (RNASE L) (RIBONUC
 LEASE 4) (FRAGMENT).//0.00000022//139aa//35%/Q05
 921
 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-as
 sociated protein.//0//2769bp//98%/AJ007509
 C-NT2RP2005254
 C-NT2RP2005325//Homo sapiens LIM-homeodomain prote
 in HLX2 (LHX2) mRNA, complete cds.//0//1643bp//99%
 //AF124735
 C-NT2RP2005336//TRICHOHYALIN.//5.40E-10//545aa//22 20
 %//P37709
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPA
 SE 5 (EC 3.6.1.38).//2.10E-124//636aa//38%/P32660
 C-NT2RP2005360
 C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN.//5.30E-
 63//410aa//40%/P22059
 C-NT2RP2005454
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxido
 reductase subunit B14.5B homolog mRNA, complete cd
 s.//1.20E-130//608bp//99%/AF070652
 C-NT2RP2005476//Human p190-B (p190-B) mRNA, comple
 te cds.//3.40E-108//668bp//88%/U17032
 C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B).//0.0
 000015//279aa//26%/P35418
 C-NT2RP2005496//ZINC FINGER PROTEIN 135.//2.90E-14
 6//398aa//59%/P52742
 C-NT2RP2005501
 C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1).//5.
 50E-70//393aa//39%/P11171
 C-NT2RP2005600//Homo sapiens mRNA for KIAA1020 pro
 tein, partial cds.//0//2554bp//99%/AB028943
 C-NT2RP2005645
 C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPA
 SE REGULATOR.//2.60E-10//175aa//27%/Q92834
 C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGE
 R PROTEIN).//3.00E-63//323aa//39%/Q62158
 C-NT2RP2005741
 C-NT2RP2005806
 C-NT2RP2005815
 C-NT2RP2005841

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C-NT2RP2005882
 C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19)
 (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.50E
 -67//388aa//44%/P25500
 C-NT2RP2006103
 C-NT2RP2006166
 C-NT2RP2006258
 C-NT2RP2006261
 C-NT2RP2006321
 C-NT2RP2006454
 C-NT2RP2006598//Homo sapiens retinoid x receptor i
 nteracting protein mRNA, complete cds.//3.10E-295/
 //1193bp//99%/AF113538
 C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSO
 R.//4.60E-78//421aa//37%/P32559
 C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36
 %//P33755
 C-NT2RP3000418
 C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FF
 H-CRPE INTERGENIC REGION.//2.90E-15//319aa//26%/P
 37908
 C-NT2RP3000487
 C-NT2RP3000512//Human HOX2G mRNA from the Hox2 loc
 us.//0//1934bp//99%/X16667
 C-NT2RP3000526
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR
 1.//3.70E-11//90aa//42%/Q13562
 C-NT2RP3000605//Mus musculus mRNA for wizL, comple
 te cds.//0//2232bp//82%/AB012265
 C-NT2RP3000628
 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOL
 UYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%/Q1
 0149
 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN
 KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa//50%/P
 27448
 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E
 -46//73aa//98%/P39027
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGE
 R PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%/Q
 05481
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PR
 OTEIN US01.//2.90E-11//631aa//23%/P25386
 C-NT2RP3001245//Homo sapiens mRNA for KIAA0923 pro
 tein, complete cds.//0//2659bp//99%/AB023140
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SP
 ACER PROTEIN SPC110).//1.70E-10//540aa//23%/P3238
 0
 C-NT2RP3001356
 C-NT2RP3001383

4349

C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52
%/P53538
C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B
[CONTAINS: LIGHT CHAINLC1].//1.40E-76//388aa//32%/
/P46821
C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRN
A, complete cds.//0//1788bp//99%/AF113534
C-NT2RP3001724//Homo sapiens chromodomain-helicase
-DNA-binding protein mRNA, complete cds.//1.10E-24
0//902bp//99%/AF054177
C-NT2RP3001727//Rattus norvegicus implantation-ass
ociated protein (IAG2)mRNA, partial cds.//6.90E-13
2//774bp//88%/AF008554
C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10
E-132//294aa//84%/Q14141
C-NT2RP3001739
C-NT2RP3001777
C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEI
N HET-E-1.//1.20E-14//242aa//24%/Q00808
C-NT2RP3001943//Homo sapiens mRNA for KIAA0675 pro 20
tein, complete cds.//0//3747bp//99%/AB014575
C-NT2RP3001944
C-NT2RP3002033
C-NT2RP3002054
C-NT2RP3002063//Homo sapiens mRNA for KIAA1033 pro
tein, partial cds.//0//2830bp//99%/AB028956
C-NT2RP3002099
C-NT2RP3002102
C-NT2RP3002147
C-NT2RP3002163
C-NT2RP3002173
C-NT2RP3002255
C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHAT
E SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TR
ANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49/
/243aa//43%/Q58767
C-NT2RP3002343
C-NT2RP3002351//Human mRNA for NAD-dependent methy
lene tetrahydrofolatedehydrogenase cyclohydrolase
(EC 1.5.1.15).//4.20E-70//590bp//76%/X16396
C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR M
CM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//
34%/P33991
C-NT2RP3002455//Homo sapiens mRNA for KIAA0678 pro
tein, partial cds.//0//3811bp//99%/AB014578
C-NT2RP3002545//Homo sapiens mRNA; cDNA DKFZp586G0
518 (from clone DKFZp586G0518).//0//2499bp//99%/A
L050092
C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C
3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%/Q100 50

4350

10
C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERA
SE ER-60 PRECURSOR (EC5.3.4.1) (ERP60) (58 KD MICR
OSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//1
73aa//28%/P11598
C-NT2RP3002603
C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERA
SE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%
//P38660
C-NT2RP3002659
C-NT2RP3002660
C-NT2RP3002682//Homo sapiens CGI-145 protein mRNA,
complete cds.//0//1596bp//98%/AF151903
C-NT2RP3002687
C-NT2RP3002688//Mouse mRNA for kinesin-like protei
n (Kif1b), complete cds.//1.10E-93//1205bp//69%/D
17577
C-NT2RP3002701
C-NT2RP3002785//LETHAL(2)DENTICLELESS PROTEIN (DTL
83 PROTEIN).//2.50E-55//187aa//39%/Q24371
C-NT2RP3002869//Mus musculus semaphorin VIa mRNA,
complete cds.//2.50E-232//1282bp//85%/AF030430
C-NT2RP3002876
C-NT2RP3002877
C-NT2RP3002909//Homo sapiens mRNA for KIAA0771 pro
tein, partial cds.//0//2085bp//94%/AB018314
C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA syn
thetase 3, complete cds.//0//2722bp//99%/D89053
C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET
-1, complete cds.//3.90E-52//899bp//64%/AB029333
C-NT2RP3003032//Homo sapiens okadaic acid-inducibl
e and cAMP-regulated phosphoprotein 19 (ARPP-19) m
RNA, complete cds.//0//2656bp//99%/AF084555
C-NT2RP3003061//ANKYRIN.//1.40E-20//200aa//37%/Q0
2357
C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN.//1.1
0E-05//258aa//24%/P23645
C-NT2RP3003078
C-NT2RP3003139
C-NT2RP3003145//Mus musculus metallocarboxypeptida
se CPX-1 mRNA, complete cds.//0//2251bp//81%/AF07
7738
C-NT2RP3003150
C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H1
0.01 IN CHROMOSOME I.//5.70E-09//169aa//31%/Q0967
4
C-NT2RP3003203//Rattus norvegicus golgi stacking p
rotein homolog GRASP55mRNA, complete cds.//2.00E-2
10//1851bp//76%/AF110267
C-NT2RP3003210

4351

C-NT2RP3003212//Rattus norvegicus lamina associate
d polypeptide 1C (LAP1C) mRNA, complete cds.//4.30
E-187//1750bp//75%/U20286
C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, comp
lete cds.//0//2350bp//99%/AB030656
C-NT2RP3003242//Homo sapiens stanniocalcin-related
protein mRNA, complete cds.//0//2366bp//99%/AF09
8462
C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME
TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-86//366
aa//48%/P19474
C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG
1 PRECURSOR (EC 3.4.21.-).//1.10E-170//585aa//54%
//064948
C-NT2RP3003311
C-NT2RP3003409//Human DHHC-domain-containing cyste
ine-rich protein mRNA, complete cds.//9.20E-45//782
bp//65%/U90653
C-NT2RP3003427
C-NT2RP3003543
C-NT2RP3003552
C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN ME
T30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%
/P40529
C-NT2RP3003564
C-NT2RP3003589//Homo sapiens ras-related GTP-bindi
ng protein mRNA, complete cds.//0//3131bp//94%/AF
106681
C-NT2RP3003621
C-NT2RP3003625
C-NT2RP3003656
C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27
%/P35843
C-NT2RP3003686
C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//32
4aa//26%/P35446
C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10/
/150aa//34%/P24014
C-NT2RP3003726//Homo sapiens spermatogenesis assoc
iated PD1 mRNA, complete cds.//0//2568bp//99%/U28
164
C-NT2RP3003795
C-NT2RP3003805
C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41
%/Q07590
C-NT2RP3003819
C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTE
IN (PC-TP).//9.60E-19//174aa//31%/P02720
C-NT2RP3003831//Homo sapiens ENDOG-1 (alias ENGL-
a) mRNA for endonuclease G-like protein-1, complet

4352

e cds.//2.2e-316//1436bp//99%/AB020523
C-NT2RP3003833
C-NT2RP3003842
C-NT2RP3003846//Homo sapiens mRNA for putative pho
spholipase, complete cds.//4.80E-277//1255bp//99%
/AB019435
C-NT2RP3003870//Homo sapiens mRNA for KIAA0800 pro
tein, complete cds.//0//2557bp//99%/AB018343
C-NT2RP3003876
C-NT2RP3003914//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYL
TRANSFERASE PRECURSOR (EC 2.4.1.-) (DUCT).//2.20E-2
0//76aa//64%/Q09332
C-NT2RP3003918//Homo sapiens VAMP-associated prote
in B (VAP-B) mRNA, complete cds.//0//2191bp//99%
/AF086628
C-NT2RP3003989
C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR
1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATE
D PROTEIN 1).//1.50E-17//226aa//26%/Q13263
C-NT2RP3004070
C-NT2RP3004145
C-NT2RP3004215
C-NT2RP3004253
C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA,
complete cds.//5.10E-24//597bp//61%/AF007871
C-NT2RP3004348//R. norvegicus mRNA for cytosolic re
sistiferoxin-binding protein.//1.10E-185//1130bp//
82%/X67877
C-NT2RP3004490//Homo sapiens PAC clone 166H1 from
12q, complete sequence.//0//1778bp//99%/AC003982
C-NT2RP3004503
C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGE
R PROTEIN HPF2).//1.20E-95//434aa//43%/P51523
C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acet
ylglucosamine-6-O-sulfotransferase (GlcNAc6ST), c
omplete cds.//0//2393bp//99%/AB014679
C-NT2RP4000023
C-NT2RP4000218
C-NT2RP4000424
C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMEN
T).//5.70E-141//511aa//43%/Q99676
C-NT2RP4001447
C-NT2RP4001841
C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//1.40E-
85//489aa//43%/P55194
C-NT2RP4002047//GTP-BINDING PROTEIN LEPA.//1.50E-1
68//601aa//52%/067618
C-NT2RP4002075
C-NT2RP4002083
C-OVARC1000001//Homo sapiens mRNA for actin bindin

4353

4354

- g protein ABP620, complete cds.//7.00E-217//683bp/
/99%/AB029290
C-OVARC1000008
C-OVARC1000017
C-OVARC1000058
C-OVARC1000068
C-OVARC1000071//Homo sapiens NTF2-related export p
rotein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//
727bp//67%/AF156957
C-OVARC1000085//Human mRNA for proteasome subunit 10
HC5.//1.00E-151//699bp//100%/D00761
C-OVARC1000109
C-OVARC1000114
C-OVARC1000145
C-OVARC1000240
C-OVARC1000302
C-OVARC1000408
C-OVARC1000414
C-OVARC1000440
C-OVARC1000442
C-OVARC1000496
C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALP
HA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIB
OSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//
132aa//95%/Q15349
C-OVARC1000557
C-OVARC1000578
C-OVARC1000622
C-OVARC1000679//Homo sapiens myosin-IXa mRNA, comp
lete cds.//0//808bp//99%/AF117888
C-OVARC1000681
C-OVARC1000700
C-OVARC1000724
C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T2
3F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%/
/P49596
C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PR
ECURSOR (75 KD GLUCOSEREGULATED PROTEIN) (GRP 75).
//3.90E-46//78aa//98%/035501
C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).// 40
/1.30E-32//170aa//34%/P37440
C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP3
7).//0.0000054//135aa//28%/P03398
C-OVARC1000937//S-PHASE ENTRY CYCLIN 6.//4.90E-10/
/61aaaa//49%/P32943
C-OVARC1000960
C-OVARC1000971
C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR.//4.10E-
11//189aa//32%/Q06527
C-OVARC1001000
C-OVARC1001029
C-OVARC1001040
C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR S
UBSTRATE SUBSTRATE 15(PROTEIN EPS15) (AF-1P PROTEI
N).//1.10E-08//216aa//23%/P42566
C-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1)
mRNA, complete cds.//5.1e-310//1588bp//93%/AF0517
82
C-OVARC1001118
C-OVARC1001129
C-OVARC1001169
C-OVARC1001240
C-OVARC1001261
C-OVARC1001339
C-OVARC1001342//40S RIBOSOMAL PROTEIN S8.//1.40E-1
10//207aa//99%/P09058
C-OVARC1001357
C-OVARC1001442
C-OVARC1001611
20 C-OVARC1001813
C-OVARC1002112//Homo sapiens histone macroH2A1.2 m
RNA, complete cds.//0//1760bp//99%/AF054174
C-OVARC1002143
C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGEN
ASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2)
(SR TYPE 2).//7.60E-08//114aa//37%/P31213
C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-
CONTAINING PROTEIN) (BTRCP).//1.70E-09//207aa//30%
//Q91854
30 C-PLACE1000014
C-PLACE1000078
C-PLACE1000492//Rat vacuolar protein sorting homol
og r-vps33b mRNA, complete cds.//0//2041bp//87%/U
35245
C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.7
0E-07//251aa//24%/P23645
C-PLACE1000814
C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-15
3//326aa//64%/P52742
C-PLACE1001007
C-PLACE1001054//Homo sapiens mRNA for RuvB-like DN
A helicase TIP49b, complete cds.//4.00E-300//1355b
p//100%/AB024301
C-PLACE1001088
C-PLACE1001136
C-PLACE1001241
C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA,
complete cds.//5.90E-228//827bp//99%/AF009615
C-PLACE1001395
50 C-PLACE1001740

4355

4356

- C-PLACE1001746
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FF
 H-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%/P
 37908
 C-PLACE1002066
 C-PLACE1002115
 C-PLACE1002213
 C-PLACE1002342//Homo sapiens mRNA for KIAA0728 pro
 tein, partial cds.//0//1657bp//98%/AB018271
 C-PLACE1002450//Human zinc finger protein mRNA, co 10
 mplete cds.//0//2565bp//99%/U69274
 C-PLACE1002474//Mus musculus matrilin-2 precursor
 mRNA, complete cds.//0//2092bp//84%/U69262
 C-PLACE1002499
 C-PLACE1002578
 C-PLACE1002714
 C-PLACE1002772
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-1
 3//272aa//28%/P55201
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGE 20
 R PROTEIN HPF1).//5.50E-203//396aa//86%/P51522
 C-PLACE1002993
 C-PLACE1003030//Homo sapiens snRNA activating prot
 ein complex 190kD subunit (SNAP190) mRNA, complete
 cds.//8.50E-44//225bp//100%/AF032387
 C-PLACE1003205
 C-PLACE1003249
 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECUR
 SOR.//1.70E-23//594aa//33%/P28481
 C-PLACE1003553 30
 C-PLACE1003592
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SU
 BUNIT HOMOLOG.//2.60E-93//270aa//66%/P46975
 C-PLACE1003669//TRICHOHYALIN.//5.60E-09//219aa//30
 %//P22793
 C-PLACE1003709//Homo sapiens mitotic checkpoint ki
 nase Bub1 (BUB1) mRNA, complete cds.//6.20E-282//13
 16bp//98%/AF053305
 C-PLACE1003870
 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) 40
 (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//3.70E
 -222//651aa//66%/P25500
 C-PLACE1003892
 C-PLACE1003900
 C-PLACE1004336
 C-PLACE1004384
 C-PLACE1004425
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGE
 R PROTEIN HPF1).//2.90E-56//276aa//41%/P51522
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM 50
 domain protein (CLIM1) mRNA, complete cds.//2.10E
 -16//402bp//62%/U90878
 C-PLACE1004518
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA,
 complete cds.//3.50E-274//1305bp//97%/AF132954
 C-PLACE1004681
 C-PLACE1004693
 C-PLACE1004716//Homo sapiens HSPC038 protein mRNA,
 complete cds.//2.70E-103//586bp//91%/AF125099
 C-PLACE1004815
 C-PLACE1004836
 C-PLACE1004838
 C-PLACE1004840
 C-PLACE1004900
 C-PLACE1004985
 C-PLACE1005085
 C-PLACE1005086
 C-PLACE1005108
 C-PLACE1005146
 C-PLACE1005409
 C-PLACE1005453
 C-PLACE1005477
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27.//1.90E-
 11//60aa//48%/P46288
 C-PLACE1005595
 C-PLACE1005603
 C-PLACE1005639
 C-PLACE1005727//Homo sapiens STRIN protein (STRIN)
 mRNA, complete cds.//2.00E-118//378bp//98%/AF162
 680
 C-PLACE1005799
 C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX
 2) mRNA, complete cds.//0//2040bp//99%/AF065482
 C-PLACE1005884
 C-PLACE1005968
 C-PLACE1006002
 C-PLACE1006003//Homo sapiens CGI-94 protein mRNA,
 complete cds.//2.40E-177//829bp//99%/AF151852
 C-PLACE1006017
 C-PLACE1006037
 C-PLACE1006076
 C-PLACE1006143
 C-PLACE1006248//Homo sapiens mRNA for KIAA0648 pro
 tein, partial cds.//0//1489bp//100%/AB014548
 C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE
 CHANNEL PROTEIN 1 (VDAC1) (PLASMALEMAL PORIN) (OU
 TER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 3
 1HL) (PORIN 31HM).//4.60E-117//147aa//80%/P21796
 C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA,
 complete cds.//3.00E-07//376bp//59%/U76374

- C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//1.30E-18//460aa//24%/Q00547
- C-PLACE1006371
- C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//1.20E-83//313aa//49%/P27550
- C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4)mRNA, complete cds.//0//2170bp//99%/AF191338 10
- C-PLACE1006521
- C-PLACE1006534//Homo sapiens mRNA; cDNA DKFZp564G1964 (from clone DKFZp564G1964).//1.70E-192//883bp//99%/AL110144
- C-PLACE1006617
- C-PLACE1006640
- C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR (BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//191aa//43%/P13688
- C-PLACE1006760 20
- C-PLACE1006779
- C-PLACE1006805
- C-PLACE1006815
- C-PLACE1006867
- C-PLACE1007045
- C-PLACE1007097
- C-PLACE1007111
- C-PLACE1007112
- C-PLACE1007140//Homo sapiens mRNA for KIAA1009 protein, complete cds.//0//3492bp//99%/AB023226 30
- C-PLACE1007218
- C-PLACE1007454
- C-PLACE1007478
- C-PLACE1007677
- C-PLACE1007705//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds.//1.10E-184//1096bp//82%/AB033922
- C-PLACE1007737
- C-PLACE1007743
- C-PLACE1007852//Homo sapiens mRNA for KIAA0878 protein, complete cds.//1.00E-232//1174bp//94%/AB020685 40
- C-PLACE1007877
- C-PLACE1008045
- C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%/AB021179
- C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//3.00E-25//208aa//37%/Q03326
- C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%/L23077 50
- C-PLACE1008231
- C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%/Q00808
- C-PLACE1008330//EOSINOPHIL LYOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%/Q05315
- C-PLACE1008331
- C-PLACE1008369
- C-PLACE1008392
- C-PLACE1008405
- C-PLACE1008424
- C-PLACE1008584
- C-PLACE1008625
- C-PLACE1008630
- C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN B2).//5.20E-90//483aa//38%/002668
- C-PLACE1008715
- C-PLACE1008748
- C-PLACE1008757
- C-PLACE1008798
- C-PLACE1008851
- C-PLACE1008947
- C-PLACE1009039
- C-PLACE1009048
- C-PLACE1009050
- C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3(XRCC3) mRNA, complete cds.//0//2529bp//99%/AF035586
- C-PLACE1009150
- C-PLACE1009200
- C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%/P29675
- C-PLACE1009298//Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds.//0//2262bp//99%/AF191298
- C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%/P14922
- C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%/P52742
- C-PLACE1009410
- C-PLACE1009477//Homo sapiens mRNA for KIAA0684 protein, partial cds.//6.50E-148//592bp//99%/AB014584
- C-PLACE1009493
- C-PLACE1009539
- C-PLACE1009595
- C-PLACE1009637
- C-PLACE1009639

C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23
%/P53552
C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38
%/P43510
C-PLACE1009888
C-PLACE1009925//Homo sapiens RNA helicase (RIG-I)
mRNA, complete cds.//0//1730bp//99%/AF038963
C-PLACE1009947
C-PLACE1010069
C-PLACE1010089//Homo sapiens mRNA for KIAA1097 pro
tein, partial cds.//0//1554bp//100%/AB029020
C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRE
CURSOR (EMR1 HORMONE RECEPTOR).//5.10E-27//371aa//
28%/Q14246
C-PLACE1010270
C-PLACE1010562
C-PLACE1010579//Homo sapiens PTB domain adaptor pr
oteins CED-6 mRNA, complete cds.//9.30E-29//1362bp
//99%/AF200715
C-PLACE1010624
C-PLACE1010628//Homo sapiens S164 gene, partial cd
s; PS1 and hypothetical protein genes, complete cd
s; and S171 gene, partial cds.//7.50E-08//324bp//6
4%/AF109907
C-PLACE1010662//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYL
TRANSFERASE PRECURSOR (EC 2.4.1.-) (DUCT).//1.80E-2
22//808aa//52%/Q09332
C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTE
IN HTF6).//5.20E-15//427aa//55%/P28160
C-PLACE1010761
C-PLACE1010802
C-PLACE1010833//CALTRACTIN (CENTRIN).//0.000001//
154aa//28%/P41209
C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SP
ACER PROTEIN SPC110).//1.50E-25//583aa//23%/P3558
0
C-PLACE1010916
C-PLACE1010947
C-PLACE1010965
C-PLACE1011032
C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha p
rotein, complete cds.//0//1701bp//97%/AB015019
C-PLACE1011056//HISTONE H1, GONADAL.//6.80E-13//15
4aa//37%/P02256
C-PLACE1011090//Homo sapiens mRNA; cDNA DKFZp586A0
522 (from clone DKFZp586A0522).//0//880bp//99%/AL
050159
C-PLACE1011160//Homo sapiens HFB30 mRNA, complete
cds.//0//1691bp//99%/AB022663

C-PLACE1011214
C-PLACE1011229//Homo sapiens ubiquitin-specific pr
otease homolog (UPH) mRNA, complete cds.//2.30E-15
2//701bp//99%/AF153604
C-PLACE1011273
C-PLACE1011291
C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH
MUSCLE.//3.50E-20//496aa//25%/P10587
C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAV
Y CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//1.70E-
78//383aa//39%/Q61703
C-PLACE1011503
C-PLACE1011635//Homo sapiens heparan sulfate D-glu
cosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA,
complete cds.//0//1559bp//99%/AF105377
C-PLACE1011646//Homo sapiens clone 25059 mRNA sequ
ence.//5.00E-223//1035bp//99%/AF131752
C-PLACE1011650
C-PLACE1011675
20 C-PLACE1011725
C-PLACE1011749
C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE
B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-
B).//1.30E-15//409aa//27%/P35580
C-PLACE1012031//Homo sapiens mRNA for KIAA0713 pro
tein, partial cds.//0//1163bp//100%/AB018256
C-PLACE20000006
C-PLACE20000007//Homo sapiens mRNA for KIAA0913 pro
tein, partial cds.//0//1968bp//97%/AB020720
30 C-PLACE20000034//LAR PROTEIN PRECURSOR (LEUKOCYTE A
NTIGEN RELATED) (EC 3.1.3.48).//2.20E-29//212aa//3
5%/P10586
C-PLACE20000039//Rattus norvegicus cytoplasmic dyne
in heavy chain (MAP 1C), mRNA, complete cds.//4.60
E-291//1167bp//89%/L08505
C-PLACE20000061
C-PLACE20000072//Homo sapiens ZNF202 beta (ZNF202)
mRNA, complete cds.//0//3174bp//99%/AF027219
C-PLACE20000097
40 C-PLACE2000103
C-PLACE2000115
C-PLACE2000124
C-PLACE2000140
C-PLACE2000164//TIPD PROTEIN.//2.10E-59//481aa//33
%/O15736
C-PLACE2000176
C-PLACE2000223
C-PLACE2000235
C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//2.20E
-167//880aa//37%/P23098
50

C-PLACE2000302
 C-PLACE2000347
 C-PLACE2000359
 C-PLACE2000371//TENSIN. //2.90E-78//561aa//37%/Q04
 205
 C-PLACE2000379
 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRE
 CURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7). /
 /1.60E-14//180aa//39%/P14209
 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (E 10
 C 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS). //9.90E-
 229//821aa//54%/Q09996
 C-PLACE2000450
 C-PLACE2000455
 C-PLACE3000059//Mus musculus mRNA for ubiquitin co
 njugating enzyme. //0//1979bp//90%/Y17267
 C-PLACE3000070
 C-PLACE3000119
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN
 SEC15. //1.90E-08//281aa//22%/P22224
 C-PLACE3000136
 C-PLACE3000147//Homo sapiens metalloproteinase wit
 h thrombospondin type1 motifs ADAMTS1 (ADAMTS1) mR
 NA, complete cds. //0//2043bp//99%/AF170084
 C-PLACE3000148
 C-PLACE3000155//Homo sapiens mRNA for KIAA0672 pro
 tein, complete cds. //2.10E-75//382bp//99%/AB01457
 2
 C-PLACE3000160
 C-PLACE3000169//ZINC FINGER PROTEIN 135. //2.50E-90 30
 //358aa//47%/P52742
 C-PLACE3000194
 C-PLACE3000199
 C-PLACE3000218//Homo sapiens putative protein O-ma
 nnosyltransferase (POMT2) mRNA, complete cds. //0//
 1862bp//98%/AF105020
 C-PLACE3000230
 C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT
 REGULATOR). //0//1435aa//92%/P53995
 C-PLACE3000254//Homo sapiens transcriptional activ 40
 ator SRCAP (SRCAP) mRNA, complete cds. //0//4583bp/
 /83%/AF143946
 C-PLACE3000276
 C-PLACE3000310
 C-PLACE3000320
 C-PLACE3000331
 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC
 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPH
 A-D-GLUCAN GLUCOHYDROLASE). //9.60E-08//359aa//23%/
 /P08640

C-PLACE3000352
 C-PLACE3000353//Homo sapiens mRNA; cDNA DKFZp586H0
 623 (from clone DKFZp586H0623). //0//2456bp//99%/A
 L096739
 C-PLACE3000362
 C-PLACE3000365
 C-PLACE3000388
 C-PLACE3000413
 C-PLACE3000425
 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE
 B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-
 B). //2.90E-54//626aa//29%/P35580
 C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUC
 LEAR PROTEIN) (XNP). //3.10E-111//348aa//41%/P4610
 0
 C-PLACE4000052//Homo sapiens ATP cassette binding
 transporter 1 (ABC1) mRNA, complete cds. //0//4661b
 p//99%/AF165281
 C-PLACE4000089
 20 C-PLACE4000128//Mus musculus putative transcrip
 tion factor mRNA, complete cds. //1.60E-86//190aa//88%
 //AF091234
 C-PLACE4000129
 C-PLACE4000147
 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236)
 (HA4654). //7.00E-22//369aa//25%/P52746
 C-PLACE4000211//Homo sapiens TTF-I interacting pep
 tide 5 mRNA, partial cds. //1.70E-262//1217bp//98%/
 /AF000422
 C-PLACE4000222
 C-PLACE4000269//Homo sapiens mRNA for KIAA1067 pro
 tein, partial cds. //0//3787bp//99%/AB028990
 C-PLACE4000270
 C-PLACE4000300
 C-PLACE4000387
 C-PLACE4000392
 C-PLACE4000431//H.sapiens gene for U5 snRNP-specif
 ic 200kd protein. //0//5142bp//90%/Z70200
 C-PLACE4000450//Homo sapiens TTF-I interacting pep
 tide 5 mRNA, partial cds. //2.70E-261//1217bp//98%/
 /AF000422
 C-PLACE4000465
 C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING P
 ROTEIN ELF-1) (ELEMENT-1-BINDING ACTIVITY) (TRANSCR
 IPTION FACTOR NTF-1). //5.70E-60//254aa//44%/P1300
 2
 C-PLACE4000654//Mus musculus mRNA for ubiquitin co
 njugating enzyme. //0//6340bp//87%/Y17267
 C-SKNC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT
 50 (KARYOPHERIN BETA-4 SUBUNIT). //5.50E-35//431aa//29

- %/060100
C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%/AF034800
C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%/P17655
C-THYR01000034//TRICHOHYALIN.//9.40E-10//176aa//30%/P37709
C-THYR01000070
C-THYR01000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%/P11799
C-THYR01000092
C-THYR01000121//Homo sapiens mRNA for KIAA1116 protein, complete cds.//0//2159bp//99%/AB029039
C-THYR01000124
C-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%/AJ005698
C-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//0//1409bp//98%/AB014552
C-THYR01000206
C-THYR01000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%/P51523
C-THYR01000253
C-THYR01000270
C-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%/AB016068
C-THYR01000320
C-THYR01000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%/P17563
C-THYR01000368
C-THYR01000381
C-THYR01000387
C-THYR01000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%/AF072864
C-THYR01000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%/AF156857
C-THYR01000401
C-THYR01000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%/AB022663
C-THYR01000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-98//408aa//42%/P19474
C-THYR01000558
C-THYR01000570
C-THYR01000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%/AF140360
C-THYR01000625
C-THYR01000637
C-THYR01000676
C-THYR01000684//Homo sapiens mRNA for KIAA0872 protein, complete cds.//0//2131bp//99%/AB020679
C-THYR01000712
C-THYR01000805
C-THYR01000815
C-THYR01000855
C-THYR01000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%/P32322
C-THYR01000988
C-THYR01001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//8.40E-12//167aa//29%/P31948
C-THYR01001120//Mus musculus FX-induced thymoma transcript (FXI-T1) mRNA, complete cds.//1.90E-92//1479bp//66%/U38252
C-THYR01001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4, 5, and 6 and complete cds; a nd Th1 gene partial sequence.//3.80E-100//478bp//99%/AF136276
C-THYR01001262
C-THYR01001271
C-THYR01001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT).//3.40E-51//429aa//33%/P45701
C-THYR01001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%/AF121861
C-THYR01001347
C-THYR01001363//Homo sapiens mRNA; cDNA DKFZp56400423 (from clone DKFZp56400423).//0//2173bp//99%/AL080120
C-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//0//1700bp//99%/AB014607
C-THYR01001403
C-THYR01001405//PLECTIN.//6.90E-19//450aa//27%/P30427
C-THYR01001406//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//1676bp//98%/AF078850
C-THYR01001426
C-THYR01001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//2.70E-171//559aa//59%/P35580
C-THYR01001480
C-THYR01001487
C-THYR01001584

4365

4366

- C-THYR01001661
 C-THYR01001746
 C-THYR01001772
 C-THYR01001854
 C-Y79AA1000013//Mus musculus RING finger protein A
 07 mRNA, complete cds.//8.90E-205//1435bp//81%/AF
 171060
 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete
 cds.//0//2929bp//96%/AF126484
 C-Y79AA1000231//Homo sapiens nucleolar protein NOP 10
 5/NOP58 mRNA, completecds.//0//1515bp//99%/AF1235
 34
 C-Y79AA1000342//Homo sapiens Cizl mRNA, complete c
 ds.//0//2644bp//81%/AB030835
 C-Y79AA1000349//M.musculus Spnr mRNA for RNA bindi
 ng protein.//0//2048bp//93%/X84692
 C-Y79AA1000410
 C-Y79AA1000539
 C-Y79AA1000589//Homo sapiens clone 614 unknown mRN
 A, complete sequence.//1.00E-302//1375bp//99%/AF0 20
 91080
 C-Y79AA1000802
 C-Y79AA1000827
 C-Y79AA1000966//Homo sapiens COP9 complex subunit
 4 mRNA, complete cds.//0//1586bp//99%/AF100757
 C-Y79AA1000969
 C-Y79AA1000985//Human centrosomal protein kendrin
 mRNA, complete cds.//4.70E-151//985bp//87%/U52962
 C-Y79AA1001061
 C-Y79AA1001068
 C-Y79AA1001216
 C-Y79AA1001299//Homo sapiens mRNA for integrase in
 teractor 1b protein (INI1B).//0//996bp//99%/AJ011
 738
 C-Y79AA1001511
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEP
 TOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//
 24%/Q00547
 C-Y79AA1001692//Mus musculus strain C57BL/J germ c
 ell-less protein (Gcl)mRNA, complete cds.//1.40E-7 40
 8//227aa//40%/Q01820
 C-Y79AA1001866//Homo sapiens zinc finger protein Z
 NF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%
 //AF192913
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 AN
 TIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTE
 IN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//
 31%/P43489
 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//
 9.00E-17//120aa//45%/Q24133
 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUC
 ED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.000001
 8//140aa//25%/Q13829
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING P
 ROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%/016
 264
 C-Y79AA1002220
 C-Y79AA1002234//Homo sapiens mRNA for KIAA0692 pro
 tein, partial cds.//0//3168bp//99%/AB014592
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, compl
 ete cds.//0//2106bp//99%/AB013384
 C-Y79AA1002361//Rattus norvegicus mRNA for protein
 phosphatase 1 (GL-subunit).//6.90E-140//966bp//82
 %//Y18208
 C-Y79AA1002399//Homo sapiens mRNA for sperm protei
 n.//0//1163bp//95%/X91879
 C-Y79AA1002416//Mus musculus CTP synthetase homolo
 g (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//8
 6%/U49385
 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2
 (ESC2).//9.80E-62//318aa//35%/Q04725
 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGE
 R PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%/Q
 05481
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box pr
 otein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//1
 444bp//98%/AF129534
 C-HEMBA1000290
 C-HEMBA1000459
 C-HEMBA1000505
 C-HEMBA1001196//Human DNA topoisomerase II (top2)
 mRNA, complete cds.//1.60E-268//1213bp//100%/J040
 88
 C-HEMBA1002503
 C-HEMBA1002508
 C-HEMBA1002513//Homo sapiens mRNA for histone deac
 etylase-like protein (JM21).//0//2432bp//99%/AJ01
 1972
 C-HEMBA1003480
 C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR
 (EC 3.4.21.41).//2.40E-110//242aa//58%/P00736
 C-HEMBA1003645//TIPD PROTEIN.//2.40E-10//289aa//23
 %//015736
 C-HEMBA1003646//Homo sapiens mRNA for KIAA1013 pro
 tein, partial cds.//0//3049bp//99%/AB023230
 C-HEMBA1003667
 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINI
 DASE) (NA) (MAJOR SURFACE ANTIGEN).//1.00E-09//611
 aa//22%/P23253
 C-HEMBA1003827

- C-HEMBA1003838
 C-HEMBA1004055
 C-HEMBA1004056
 C-HEMBA1004086
 C-HEMBA1004335
 C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1.//3.00E-71//89aa//96%/Q99471
 C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//3.10E-51//152aa//40%/Q61221
 C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds.//3.40E-92//483bp//95%/AF201333
 C-HEMBA1004507
 C-HEMBA1004638
 C-HEMBA1004669//SON PROTEIN (SON3).//7.30E-17//288aa//36%/P18583
 C-HEMBA1004709
 C-HEMBA1004860
 C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%/AJ250308
 C-HEMBA1005472
 C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%/002193
 C-HEMBA1005572
 C-HEMBA1005780
 C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%/AF082516
 C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%/Q61001
 C-HEMBA1006124
 C-HEMBA1006461
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%/P25716
 C-HEMBA1006617
 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%/015509
 C-HEMBA1006779
 C-HEMBA1006796
 C-HEMBA1006812
 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%/U35832
 C-HEMBA1007174//Homo sapiens mRNA for KIAA1065 protein, complete cds.//0//1079bp//97%/AB028988
 C-HEMBB1000240
 C-HEMBB1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%/P22516
 C-HEMBB1000335
 C-HEMBB1000337
 C-HEMBB1000554
 C-HEMBB1000573
 C-HEMBB1000749
 C-HEMBB1000774
 C-HEMBB1000835
 C-HEMBB1001197
 C-HEMBB1001315
 C-HEMBB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//27%/Q05481
 C-HEMBB1001500
 C-HEMBB1001562//CYCLICIN II (MULTIPLE-BAND POLYPEPTIDE II).//1.40E-06//373aa//21%/Q28092
 C-HEMBB1001619
 C-HEMBB1001630
 C-HEMBB1001665
 C-HEMBB1001684//Homo sapiens mRNA for KIAA1108 protein, partial cds.//0//2348bp//99%/AB029031
 C-HEMBB1001812
 C-HEMBB1001834
 C-HEMBB1001869
 C-HEMBB1001871//BONE/CARTILAGE PROTEOGLYCAN I PRECURSOR (BIGLYCAN) (PG-S1).//5.40E-75//241aa//48%/P47853
 C-HEMBB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.90E-22//210aa//27%/Q61549
 C-HEMBB1001905//TRICHOHYALIN.//2.10E-10//268aa//27%/P37709
 C-HEMBB1001908//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds.//1.60E-131//874bp//86%/U47742
 C-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//6.90E-132//561aa//50%/Q24574
 C-HEMBB1001925
 C-HEMBB1002044//Mus musculus mRNA for vascular cadherin-2.//0//3562bp//81%/Y08715
 C-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.10E-56//176aa//67%/P56163
 C-HEMBB1002152
 C-HEMBB1002300
 C-HEMBB1002381
 C-HEMBB1002383
 C-HEMBB1002534
 C-MAMMA1000143
 C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.10E-57//941aa//27%/Q05481

4369

4370

R PROTEIN HPF2). //3.40E-134//359aa//63%/P51523

C-MAMMA1000227

C-MAMMA1000257

C-MAMMA1000264

C-MAMMA1000270

C-MAMMA1000279

C-MAMMA1000372

C-MAMMA1000559

C-MAMMA1000752

C-MAMMA1000760

C-MAMMA1000778

C-MAMMA1000855

C-MAMMA1000859

C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP). //1.00E-141//576aa//37%/Q06033

C-MAMMA1000940

C-MAMMA1001073

C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds. //1.6e-312//1596bp//94%/AF067420

C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds. //0//2253bp//99%/AB015346

C-MAMMA1001202

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN. //6.60E-09//255aa//29%/P12978

C-MAMMA1001252

C-MAMMA1001296

C-MAMMA1001502

C-MAMMA1001630

C-MAMMA1001633//ZINC FINGER PROTEIN 165. //6.30E-39//160aa//55%/P49910

C-MAMMA1001683

C-MAMMA1001715

C-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds. //0//1603bp//99%/AF095687

C-MAMMA1001760

C-MAMMA1001769

C-MAMMA1001785

C-MAMMA1001848

C-MAMMA1001874

C-MAMMA1001956

C-MAMMA1002009

C-MAMMA1002033

C-MAMMA1002155

C-MAMMA1002498

C-MAMMA1002545

C-MAMMA1002571

C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //2.60E-19//666aa//23%/P08640

C-MAMMA1002590

C-MAMMA1002617//ZINC FINGER PROTEIN 135. //7.60E-89//252aa//57%/P52742

C-MAMMA1002618

C-MAMMA1002636

10 C-MAMMA1002646

C-MAMMA1002665

C-MAMMA1002708

C-MAMMA1002728

C-MAMMA1002744

C-MAMMA1002764

C-MAMMA1002765

C-MAMMA1002830

C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT). //4.90E-10//334aa//22%/P52178

C-MAMMA1002858//Rat cMG1 mRNA. //3.70E-238//1147bp//92%/X52590

C-MAMMA1002880

C-MAMMA1002892

C-MAMMA1002909

C-MAMMA1002941

C-MAMMA1002947

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27. //1.10E-05//69aa//42%/P40343

30 C-MAMMA1002973

C-MAMMA1002987

C-MAMMA1003003

C-MAMMA1003026//Homo sapiens HSPC057 mRNA, complete cds. //0//1773bp//98%/AF161542

C-MAMMA1003031

C-MAMMA1003089

C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2). //1.00E-07//362aa//23%/P39843

40 C-NT2RM1000272

C-NT2RM1000341

C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein. //3.00E-158//733bp//99%/AJ238097

C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds. //3.40E-177//814bp//99%/AF103731

C-NT2RM1000623//RIBONUCLEASE INHIBITOR. //4.40E-21//372aa//30%/P10775

C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN

50 KINASE PKWA (EC 2.7.1.-). //5.60E-08//187aa//27%/P

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49695
 C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%/AF084458
 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//5107bp//99%/AF082516
 C-NT2RM1001082
 C-NT2RM1001112
 C-NT2RM2001105//Drosophila melanogaster eyelid (el d) mRNA, complete cds.//1.20E-28//805bp//61%/AF053091
 C-NT2RM2001360//Homo sapiens clone C40 unknown mRNA.//1.00E-250//1136bp//100%/AF103798
 C-NT2RM2001797//Homo sapiens mRNA; cDNA DKFZp572C163 (from clone DKFZp572C163); partial cds.//0//2300bp//100%/AL110217
 C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//2249bp//99%/AF044195
 C-NT2RM4002504
 C-NT2RP1000409
 C-NT2RP1000460//Homo sapiens mRNA for KIAA1068 protein, partial cds.//0//3199bp//99%/AB028991
 C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein P0 mRNA, complete cds.//9.70E-196//901bp//99%/AF173378
 C-NT2RP1000796
 C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%/P51522
 C-NT2RP2001214
 C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.00E-128//409aa//45%/Q05481
 C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds.//0//3712bp//99%/AB024334
 C-NT2RP2002056
 C-NT2RP2002105//H. sapiens MSH-R gene for melanocyte stimulating hormone receptor.//0//1644bp//98%/X65634
 C-NT2RP2002333
 C-NT2RP2002677
 C-NT2RP2002755
 C-NT2RP2002843
 C-NT2RP2003101
 C-NT2RP2003668
 C-NT2RP2003799
 C-NT2RP2004095
 C-NT2RP2004300
 C-NT2RP2004675
 C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-

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LINKED NUCLEAR PROTEIN) (HETEROCHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38PROTEIN).//4.20E-09//804aa//22%/Q61687
 C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.10E-308//1437bp//98%/AF045583
 C-NT2RP2005719//GPI-ANCHORED PROTEIN P137.//4.00E-14//99aa//43%/Q14444
 C-NT2RP2005726
 C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//4.40E-55//358aa//42%/P51005
 C-NT2RP2005980
 C-NT2RP2006184//Homo sapiens mRNA for KIAA0918 protein, partial cds.//0//4235bp//99%/AB020725
 C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN(EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%/Q13131
 C-NT2RP2006554
 C-NT2RP3000584
 C-NT2RP3001115
 C-NT2RP3001723//Homo sapiens cell recognition molecule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58//1138bp//63%/AF193613
 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-22//227aa//33%/P08458
 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete cds.//0//2443bp//99%/U87791
 C-NT2RP3002402
 C-NT2RP3002484//Homo sapiens mRNA for KIAA0998 protein, partial cds.//1.20E-124//597bp//98%/AB023215
 C-NT2RP3002512
 C-NT2RP3002713
 C-NT2RP3002770//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//1.00E-07//70aa//41%/P17564
 C-NT2RP3002799
 C-NT2RP3002810//HISTIDINE-RICH PROTEIN KE4.//2.20E-10//260aa//26%/Q31125
 C-NT2RP3002818//INSERTION ELEMENT IS2A HYPOTHETICAL 48.2 KD PROTEIN.//5.70E-226//303aa//97%/P51026
 C-NT2RP3002955
 C-NT2RP3002985
 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//3.80E-152//1007bp//82%/U78090
 C-NT2RP3003121
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-

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- type zinc finger protein, complete cds.//0//1998bp//91%/AB011414
- C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds.//0//2159bp//98%/AF071592
- C-NT2RP3003155
- C-NT2RP3003157
- C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33.//2.80E-06//402aa//23%/P49455
- C-NT2RP3003264
- C-NT2RP3003346
- C-NT2RP3003403
- C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%/AF071317
- C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%/P53009
- C-NT2RP3003572
- C-NT2RP3003576
- C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%/AB013885
- C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%/P14209
- C-NT2RP3003680//Homo sapiens mRNA; cDNA DKFZp434J154 (from clone DKFZp434J154); complete cds.//0//2047bp//95%/AL080155
- C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA A, complete cds.//9.00E-238//1529bp//84%/U71294
- C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%/AF130457
- C-NT2RP3003828
- C-NT2RP3003932
- C-NT2RP3003992//Homo sapiens mRNA; cDNA DKFZp564C186 (from clone DKFZp564C186).//0//2739bp//99%/AL050019
- C-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%/X84692
- C-NT2RP3004028
- C-NT2RP3004041
- C-NT2RP3004051
- C-NT2RP3004078//H.sapiens HRFX2 mRNA.//0//1806bp//99%/X76091
- C-NT2RP3004093
- C-NT2RP3004095
- C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%/AF126747
- C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%/P08640
- C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%/AF098948
- C-NT2RP3004189//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%/Q00808
- C-NT2RP3004332
- C-NT2RP3004349
- C-NT2RP3004470
- C-NT2RP4000035
- C-NT2RP4000049
- C-NT2RP4000102
- C-NT2RP4000167
- C-NT2RP4000515
- C-NT2RP4000517
- C-NT2RP4000519
- C-NT2RP5003512//Homo sapiens mRNA for KIAA1291 protein, partial cds.//0//1980bp//99%/AB033117
- C-OVARC1000092
- C-OVARC1000533
- C-OVARC1000678
- C-OVARC1000689//Homo sapiens mRNA; cDNA DKFZp434C1415 (from clone DKFZp434C1415); partial cds.//0//2032bp//99%/AL133014
- C-OVARC1000802
- C-OVARC1000890
- C-OVARC1000891
- C-OVARC1000945//Rattus norvegicus mRNA for atypical 1 PKC specific bindingprotein, complete cds.//0//1961bp//82%/AB005549
- C-OVARC1001072
- C-OVARC1001117
- C-OVARC1001200//Mus musculus mRNA for HS1 binding protein 3.//5.80E-88//658bp//80%/AJ132192
- C-OVARC1001244//H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue.//0//1467bp//99%/X62083
- C-OVARC1001329
- C-OVARC1001341
- C-OVARC1001376
- C-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, completecds.//0//1876bp//98%/AF016507
- C-OVARC1001873
- C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3(EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.60E-81//212aa//70%/P34547

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C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%/AF135421
 C-PLACE1001036//Homo sapiens mRNA for KIAA1017 protein, complete cds.//0//2117bp//99%/AB023234
 C-PLACE1001076
 C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-147//443aa//57%/P52742
 C-PLACE1001366
 C-PLACE1001545
 C-PLACE1001608
 C-PLACE1002004
 C-PLACE1002256
 C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.50E-76//180aa//83%/P41233
 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-70//208aa//66%/P31146
 C-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//0//2462bp//89%/AF079765
 C-PLACE1003383
 C-PLACE1003864
 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN.//5.20E-47//577aa//25%/P10267
 C-PLACE1004913
 C-PLACE1004979
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds.//6.6e-313//1413bp//99%/AF132950
 C-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2431bp//99%/AB011148
 C-PLACE1005128
 C-PLACE1005162
 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds.//3.90E-212//1040bp//96%/AF113539
 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*).//1.10E-09//93aa//31%/P32959
 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A.//7.60E-97//1287bp//67%/AJ010046
 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2.9/ER2.6).//6.80E-09//267aa//30%/P29128
 C-PLACE1005611//Mus musculus mRNA for mDj 10, complete cds.//2.00E-33//379bp//66%/AB028860
 C-PLACE1005802
 C-PLACE1005850
 C-PLACE1005898
 C-PLACE1005932
 C-PLACE1006129//Homo sapiens HSPC057 mRNA, complete cds.//0//2849bp//98%/AF161542

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e cds.//0//2849bp//98%/AF161542
 C-PLACE1006360
 C-PLACE1006795
 C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDONUCLEASE).//1.90E-08//122aa//36%/P16658
 C-PLACE1007557
 C-PLACE1007807
 C-PLACE1008181
 10 C-PLACE1008426//Homo sapiens mRNA for KIAA1288 protein, partial cds.//0//3311bp//99%/AB033114
 C-PLACE1008455
 C-PLACE1008941
 C-PLACE1009935
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%/P46804
 C-PLACE1011891
 C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds.//2.60E-287//1820bp//85%/U61969
 20 C-PLACE2000003
 C-PLACE2000132
 C-PLACE2000170
 C-PLACE2000335
 C-PLACE3000124
 C-PLACE3000158
 C-PLACE3000207
 C-PLACE3000221
 C-PLACE3000271
 C-PLACE3000304
 30 C-PLACE3000322
 C-PLACE3000341
 C-PLACE3000373
 C-PLACE3000399
 C-PLACE3000401
 C-PLACE3000402
 C-PLACE3000406
 C-PLACE3000475
 C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//1.70E-15//740aa//23%/P08640
 C-PLACE4000093
 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds.//0//4199bp//97%/AF146689
 C-PLACE4000131//Homo sapiens mRNA; cDNA DKFZp586J0917 (from clone DKFZp586J0917); partial cds.//0//1612bp//97%/AL117455
 C-PLACE4000247
 50 C-PLACE4000250

- C-PLACE4000252
 C-PLACE4000259//H.sapiens gene for U5 snRNP-specific 200kD protein.//0//5143bp//90%/Z70200
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN).//9.50E-10//128aa//34%/P55201
 C-PLACE4000320
 C-PLACE4000344
 C-PLACE4000367
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//7.20E-22//54aa//62%/Q01576
 C-PLACE4000411//Homo sapiens mRNA; cDNA DKFZp586D0624 (from clone DKFZp586D0624); partial cds.//0//2159bp//98%/AL117654
 C-PLACE4000487
 C-PLACE4000494
 C-PLACE4000521
 C-PLACE4000548//Homo sapiens mRNA for KIAA0947 protein, partial cds.//0//4864bp//99%/AB023164
 C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%/AF047690
 C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%/AB021663
 C-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//0//3711bp//99%/AB018333
 C-THYR01000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%/AF118566
 C-THYR01001142
 C-THYR01001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//62%/Q05481
 C-THYR01001320
 C-THYR01001537//Homo sapiens mRNA; cDNA DKFZp586A0522 (from clone DKFZp586A0522); partial cds.//0//1010bp//98%/AL050159
 C-THYR01001602
 C-THYR01001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%/Q04652
 C-THYR01001828
 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds.//0//2520bp//99%/AF157833
 C-Y79AA1001167
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds.//0//4708bp//99%/AF055084
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%/P51149
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%/P16415
 C-HEMBA1006092
 C-HEMBA1006406
 C-HEMBA1000790
 C-HEMBA1000917
 C-HEMBA1002280
 C-MAMMA1000802
 C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%/P20931
 C-MAMMA1002597
 C-MAMMA1002868
 C-NT2RP2003161
 C-NT2RP2003339
 C-NT2RP3001282
 C-PLACE1001761
 C-PLACE1004491
 C-PLACE1004686
 C-PLACE1005574
 C-PLACE1006382
 C-PLACE1006792
 C-PLACE3000455
 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//0//2567bp//88%/AF030430
 C-THYR01000916
 C-HEMBA1000327
 C-HEMBA1000637
 C-HEMBA1001967
 C-MAMMA1000266
 C-NT2RP2002979
 C-PLACE1007866
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE PAK-GAMMA (EC 2.7.1.-) (GAMMA-PAK) (P21-ACTIVATED KINASE 2) (PAK-2) (PAK65) (S6/H4 KINASE).//9.80E-25//155aa//45%/Q13177
 C-PLACE4000156//ZINC FINGER PROTEIN 132.//7.10E-151//476aa//46%/P52740
 C-THYR01001637
 C-MAMMA1002215
 C-MAMMA1002721
 C-NT2RP2002070
- 【1135】 相同性検索結果データ14.
 全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ。以下に示す検索結果には、比較配列の長さの単位にaaとbpが混在している。各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

4379

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1. //1.90E-250//554aa//85%/Q61712
 C-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS). //6.40E-99//457aa//45%/Q09996
 C-HEMBA1000020//Homo sapiens beta 2 gene. //7.50E-264//1194bp//95%/X02344
 C-HEMBA1000030//Homo sapiens ARF GTPase-activating protein GIT1 mRNA, complete cds. //0//1759bp//99%/AF124490
 C-HEMBA1000129//HYPOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I. //3.80E-25//166aa//36%/Q09884
 C-HEMBA1000141//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds. //0//1135bp//100%/AF196304
 C-HEMBA1000150//Homo sapiens putative RNA helicase mRNA, complete cds. //5.20E-213//525bp//99%/AF085356
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M). //1.90E-12//368aa//24%/P08553
 C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3-GAMMA (HNF-3G). //5.00E-16//166aa//36%/P35584
 C-HEMBA1000168//CYCLIN I (MULTIPLE-BAND POLYPEPTIDE I). //2.90E-14//303aa//25%/P35662
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A. //3.40E-12//125aa//31%/P48555
 C-HEMBA1000201//Homo sapiens mRNA for integrase interactor 1b protein (INI1B). //0//1612bp//99%/AJ011738
 C-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN). //1.00E-86//146aa//56%/Q61221
 C-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds. //7.10E-254//1440bp//87%/AF030131
 C-HEMBA1000304//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds. //5.10E-131//712bp//91%/U16802
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.20E-49//107aa//91%/O35594
 C-HEMBA1000333//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds. //0//1866bp//100%/AF174601
 C-HEMBA1000369//Homo sapiens mRNA for PICK1, complete cds. //0//1949bp//98%/AB026491
 C-HEMBA1000411//ANKYRIN. //5.70E-12//127aa//38%/Q02357
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN

4380

N). //3.30E-45//481aa//29%/Q04652
 C-HEMBA1000491//RAS-LIKE PROTEIN 2. //2.00E-22//188aa//31%/P22279
 C-HEMBA1000518//PECANEX PROTEIN. //2.10E-19//227aa//38%/P18490
 C-HEMBA1000523//TESTIS-SPECIFIC PROTEIN PBS13. //2.40E-44//292aa//36%/Q01755
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS). //2.60E-12//73aa//41%/P02826
 C-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase III, complete cds. //2.20E-194//663bp//83%/D89340
 C-HEMBA1000555//Mus musculus Mx2 interacting nuclear target protein mRNA, complete cds. //7.90E-226//1501bp//83%/AF156529
 C-HEMBA1000561//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //3.40E-37//674aa//25%/Q05481
 C-HEMBA1000569//GPI-ANCHORED PROTEIN P137. //6.50E-19//265aabb//32%/Q60865
 C-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds. //2.10E-144//602bp//77%/AF045573
 C-HEMBA1000591//PTB-ASSOCIATED SPLICING FACTOR (PSF). //2.20E-17//198aa//40%/P23246
 C-HEMBA1000592//Homo sapiens sorting nexin 6 (SNX6) mRNA, complete cds. //0//1465bp//99%/AF121856
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT). //1.80E-55//179aa//61%/O43295
 C-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds. //7.20E-156//1366bp//76%/U35776
 C-HEMBA1000851//Homo sapiens DNA binding protein p96PIF mRNA, complete cds. //0//1862bp//99%/AF173868
 C-HEMBA1000852//ARYLSULFATASE D PRECURSOR (EC 3.1.6.-) (ASD). //1.00E-78//119aa//87%/P51689
 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN) //1.60E-30//127aa//40%/P43366
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X. //1.00E-10//288aa//23%/Q19124
 C-HEMBA1001019//CELL DIVISION CONTROL PROTEIN 2 HOMOLOG (EC 2.7.1.-) (P34 PROTEIN KINASE) (CYCLIN-DEPENDENT KINASE 1) (CDK1). //3.10E-10//70aa//58%/P06493
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT). //1.40E-12//1

- 31aa//38%/Q01485
 C-HEMBA1001059//Human N-acetylglactosamine 6-sulphatase (GALNS) gene, exon 14.//4.80E-169//786bp//99%/U06088
 C-HEMBA1001071//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//1.50E-92//82aa//100%/P02461
 C-HEMBA1001077//Homo sapiens transcriptional intermediary factor 1 gamma mRNA, complete cds.//2.00E-80//432bp//94%/AF119043
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.50E-50//176aa//57%/P48059
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (K1AA0065) (HA0946) (FRAGMENT).//1.50E-116//197aa//58%/Q06730
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5.//6.80E-79//179aa//80%/P51646
 C-HEMBA1001197//Homo sapiens rap2 interacting protein x mRNA, complete cds.//0//1511bp//99%/AF112221
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%/AJ130733
 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.00000002//198aa//29%/Q60401
 C-HEMBA1001302//Homo sapiens calcium binding protein precursor, mRNA, complete cds.//9.60E-258//682bp//94%/AF153686
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33)mRNA, complete cds.//1.40E-133//614bp//99%/AF057358
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.90E-64//104aa//82%/P17081
 C-HEMBA1001405//Drosophila melanogaster eyelid (elid) mRNA, complete cds.//5.60E-25//863bp//60%/AF053091
 C-HEMBA1001446//Homo sapiens rap2 interacting protein x mRNA, complete cds.//9.20E-55//719bp//68%/AF112221
 C-HEMBA1001455//Mus musculus transposon-derived Buster2 transposase-like protein gene, partial cds.//4.20E-290//2008bp//81%/AF205599
 C-HEMBA1001476//Human DNA topoisomerase II (top2) mRNA, complete cds.//1.60E-268//1213bp//100%/J04088
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.70E-16//63aa//61%/P18850
 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.90E-37//399aa//29%/P29166
 C-HEMBA1001569//SYNAPTOSOMAL VESICLE ASSOCIATE D MEMBRANE PROTEIN 2) (VAMP-2).//2.30E-53//110aa//100%/P19065
 C-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//808bp//97%/AJ012449
 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.90E-156//348aa//83%/Q14141
 C-HEMBA1001620//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IPS).//1.60E-166//506aa//60%/P42803
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSCA).//1.60E-10//155aa//28%/Q63679
 C-HEMBA1001651//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1).//6.20E-07//362aa//24%/Q50365
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//4.60E-36//365aa//33%/P33450
 C-HEMBA1001672//Homo sapiens methyl-CpG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//1707bp//98%/AF072247
 C-HEMBA1001675//VACUOLAR PROTEIN SORTING-ASSOCIATE D PROTEIN VPS9.//5.40E-09//101aa//35%/P54787
 C-HEMBA1001714//Homo sapiens mRNA for ATPase inhibitor precursor, complete cds.//3.70E-78//200bp//100%/AB029042
 C-HEMBA1001723//Homo sapiens G protein beta subunit mRNA, partial cds.//3.10E-267//1212bp//99%/AF195883
 C-HEMBA1001734//CADHERIN-11 PRECURSOR (OSTEOBLAST-CADHERIN) (OB-CADHERIN) (OSF-4).//1.10E-38//87aa//96%/P55288
 C-HEMBA1001744//SCY1 PROTEIN.//9.90E-32//481aa//25%/P53009
 C-HEMBA1001746//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//7.60E-59//998bp//64%/AF098066
 C-HEMBA1001804//Homo sapiens zinc finger DNA binding protein 99 (ZNF281)mRNA, complete cds.//0//1637bp//99%/AF125158
 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.80E-11//206aa//36%/P11675
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.90E-135//459aa//52%/Q99676
 C-HEMBA1001822//Mus musculus E2F1 protein mRNA, complete cds.//1.90E-235//1329bp//89%/AF132479
 C-HEMBA1001824//Homo sapiens nuclear protein NP94 mRNA, complete cds.//1.40E-199//1180bp//89%/AF159025
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.60E-64//221aa//55%/Q07230
 C-HEMBA1001866//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYL

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RANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT). //5.70E-5
1//234aa//41%/Q09332
C-HEMBA1001869//TRITHORAX PROTEIN. //9.60E-05//166a
a//27%/P20659
C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRE
CURSOR (EC 1.5.99.2) (ME2GLYDH). //9.30E-36//395aa//
26%/Q63342
C-HEMBA1001913//GCN20 PROTEIN. //2.30E-81//158aa//5
0%/P43535
C-HEMBA1001921//Homo sapiens germinal center kinas
e related protein kinase mRNA, complete cds. //0//1
850bp//99%/AF000145
C-HEMBA1001967//Homo sapiens NY-REN-57 antigen mRN
A, partial cds. //0//1721bp//99%/AF155114
C-HEMBA1002035//Homo sapiens BAZ1A mRNA for bromod
omain adjacent to zincfinger domain 1A, complete c
ds. //0//2149bp//99%/AB032252
C-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 tran
scription factor (O/E-3) mRNA, complete cds. //1.30
E-271//1583bp//88%/U92703
C-HEMBA1002102//ANKYRIN. //4.40E-10//106aa//35%/Q0
2357
C-HEMBA1002139//LIM AND SH3 DOMAIN PROTEIN LASP-1
(MLN 50). //7.10E-05//51aa//49%/Q14847
C-HEMBA1002151//Rattus norvegicus p34 mRNA, comple
te cds. //1.10E-153//1059bp//82%/AF178669
C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE
BETA ISOFORM. //1.40E-51//180aa//56%/P79293
C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA
BINDING FACTOR-4). //6.00E-13//190aa//36%/P43694
C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.
1.112) (FRAGMENT). //3.00E-17//267aa//29%/P18161
C-HEMBA1002215//TESTIN 2 (TES2) [CONTAINS: TESTIN
1 (TES1)]. //2.20E-199//392aa//89%/P47226
C-HEMBA1002241//PROLIFERATING-CELL NUCLEOLAR ANTIG
EN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEI
N P120). //3.70E-06//95aa//33%/P46087
C-HEMBA1002267//Sus scrofa decorin mRNA, complete
cds. //1.10E-46//302bp//90%/AF125537
C-HEMBA1002341//P53-BINDING PROTEIN 2 (53BP2) (FRA
GMENT). //3.80E-55//109aa//96%/Q62415
C-HEMBA1002363//Homo sapiens chromosome-associated
protein-E (hCAP-E) mRNA, complete cds. //0//1847bp
//99%/AF092563
C-HEMBA1002417//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT
JUNCTION PROTEIN 1). //1.00E-121//489aa//52%/P394
47
C-HEMBA1002419//TRICHOHYALIN. //1.90E-09//299aa//24
%/P22793
C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PRO 50

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TEIN HCR74. //4.20E-24//109aa//55%/Q00994
C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT). //3.50
E-50//199aa//61%/P98175
C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURS
OR (APEG PROTEIN). //1.10E-12//285aa//31%/P17437
C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN
DET1. //6.80E-53//257aa//36%/P48732
C-HEMBA1002513//Homo sapiens mRNA for histone deac
etylase-like protein (JM21). //0//2432bp//99%/AJ01
1972
C-HEMBA1002547//Homo sapiens agrin precursor mRNA,
partial cds. //0//1605bp//97%/AF016903
C-HEMBA1002555//Homo sapiens mSin3A associated pol
ypeptide p30 mRNA, complete cds. //5.30E-51//768bp/
/68%/AF055993
C-HEMBA1002569//Homo sapiens protein associated wi
th Myc mRNA, complete cds. //6.80E-305//951bp//99%/A
F075587
C-HEMBA1002746//DNA POLYMERASE BETA (EC 2.7.7.7). /
20 /5.00E-37//268aa//34%/P06746
C-HEMBA1002768//Mus musculus formin binding protei
n 17 mRNA, partial cds. //7.80E-237//1522bp//85%/A
B011126
C-HEMBA1002770//Rattus norvegicus mRNA for TIP120,
complete cds. //2.90E-176//1024bp//88%/D87671
C-HEMBA1002777//Fugu rubripes BAW (BAW) mRNA, comp
lete cds. //3.40E-54//319bp//76%/AF153879
C-HEMBA1002810//Homo sapiens formin binding protei
n 21 mRNA, complete cds. //8.2E-314//1437bp//99%/A
30 F071185
C-HEMBA1002818//Homo sapiens mRNA for fibulin-4. //
2.00E-304//1383bp//99%/AJ132819
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EED
8.8 IN CHROMOSOME II. //1.50E-44//188aa//52%/Q0929
7
C-HEMBA1002935//ZINC FINGER PROTEIN 91 (ZINC FINGE
R PROTEIN HTF10) (HPF7). //1.30E-15//371aa//25%/Q0
5481
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2)
(ERYTHROCYTE ANKYRIN). //2.00E-34//300aa//34%/P161
57
C-HEMBA1002951//NUF1 PROTEIN (SPINDLE POLY BODY SP
ACER PROTEIN SPC110). //4.40E-06//324aa//24%/P3238
0
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPH
ODIESTERASE 4B (EC 3.1.4.17) (DPDE4). //1.20E-27//6
3aa//100%/P14646
C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROT
EIN). //3.80E-25//534aa//24%/Q02224
C-HEMBA1002999//Rattus norvegicus lamina associate

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d polypeptide 1C (LAP1C) mRNA, complete cds.//1.40E-171//1552bp//75%/U20286
 C-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, //0//1558bp//99%/AF054182
 C-HEMBA1003071//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACIDLABILE CHAIN PRECURSOR (ALS). //1.30E-09//121aa//40%/P35858
 C-HEMBA1003077//SLIT PROTEIN PRECURSOR. //2.60E-15//199aa//31%/P24014
 C-HEMBA1003096//Mouse 19.5 mRNA, complete cds.//5.60E-117//1139bp//72%/M32486
 C-HEMBA1003098//Homo sapiens NY-REN-6 antigen mRNA, partial cds.//6.20E-273//1253bp//99%/AF155096
 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE). //8.50E-51//221aa//33%/P41940
 C-HEMBA1003148//Homo sapiens mRNA for dachshund protein. //0//1583bp//99%/AJ005670
 C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61). //5.90E-74//134aa//53%/P44551
 C-HEMBA1003199//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//8.50E-87//285bp//90%/AF129534
 C-HEMBA1003235//TROPOMYOSIN. //2.30E-06//109aa//33%/Q02088
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-). //7.20E-41//245aa//42%/Q06548
 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR. //6.00E-11//239aa//32%/P32506
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds.//5.40E-229//1043bp//99%/AB024436
 C-HEMBA1003291//SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10). //6.20E-28//126aa//51%/Q38997
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN). //2.00E-08//248aa//23%/Q02224
 C-HEMBA1003408//DNA-DIRECTED RNA POLYMERASE II LARGE SUBUNIT (EC 2.7.7.6) (VERSION 1). //7.80E-13//297aa//30%/P18616
 C-HEMBA1003417//Homo sapiens BAG-family molecular chaperone regulator-2mRNA, complete cds.//1.50E-255//1179bp//99%/AF095192
 C-HEMBA1003418//TRICHOHYALIN. //8.70E-19//281aa//31%/P37709
 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511bp//94%/AB013139

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C-HEMBA1003538//COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41). //2.40E-110//242aa//58%/P00736
 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISLET-2 (ISLET-2). //8.80E-189//360aa//96%/P50480
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP). //2.10E-68//251aa//52%/P53384
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-1). //1.20E-31//71aa//100%/P16874
 10 C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //7.90E-49//279aa//32%/P19474
 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1. //6.90E-206//445aa//74%/Q13330
 C-HEMBA1003581//TALIN. //4.40E-45//52aa//98%/P26039
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP). //4.40E-10//118aa//35%/P19682
 C-HEMBA1003615//Homo sapiens ART-4 mRNA, complete cds.//0//1713bp//99%/AB026125
 20 C-HEMBA1003617//Homo sapiens ubiquitin-like product Chap1/Dsk2 mRNA, complete cds.//6.90E-178//501bp//97%/AB015344
 C-HEMBA1003645//TIPD PROTEIN. //2.40E-10//289aa//23%/Q015736
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2). //1.20E-75//151aa//99%/Q13207
 C-HEMBA1003679//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN). //1.00E-09//611aa//22%/P23253
 30 C-HEMBA1003680//PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III (EC 3.4.11.-). //2.40E-92//423aa//47%/P34629
 C-HEMBA1003684//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN). //2.00E-73//526aa//32%/Q13105
 C-HEMBA1003690//HISTONE DEACETYLASE HDA1. //2.10E-59//249aa//47%/P53973
 C-HEMBA1003742//Homo sapiens cleft lip and palate transmembrane protein1 (CLPTM1) mRNA, complete cds.//1.70E-44//501bp//67%/AF037339
 40 C-HEMBA1003760//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA). //3.70E-124//347aa//55%/Q16665
 C-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//5.80E-81//511bp//86%/U17343
 C-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.10E-190//1204bp//84%/AF084259
 50

- C-HEMBA1003805//Mus musculus KH domain RNA binding protein QKI-5A mRNA, complete cds. //0//988bp//95%/AF090402
- C-HEMBA1003836//MOB1 PROTEIN (MPS1 BINDER 1). //8.1 0E-31//134aa//52%/P40484
- C-HEMBA1003866//Mus musculus semaphorin VIa mRNA, complete cds. //1.20E-105//1192bp//70%/AF030430
- C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT). //3.80E-16//89aa//46%/P16372
- C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds. //8.50E-221//1188bp//78%/AF091234
- C-HEMBA1004131//SEPTIN 2 HOMOLOG (FRAGMENT). //1.60E-166//416aa//72%/Q14141
- C-HEMBA1004168//Homo sapiens geminin mRNA, complete cds. //3.90E-208//951bp//99%/AF067855
- C-HEMBA1004199//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III. //8.40E-60//243aa//39%/P34529
- C-HEMBA1004202//RAS-RELATED PROTEIN RAB-13. //6.20E-30//208aa//37%/P51153
- C-HEMBA1004203//NUCLEOLAR PROTEIN NOP2. //1.50E-12//258aa//29%/P40991
- C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds. //0//1892bp//99%/U50748
- C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds. //5.70E-217//1217bp//88%/AF095927
- C-HEMBA1004248//INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 (IMMEDIATE-EARLY PROTEIN CL-6). //2.00E-43//98aa//84%/Q08755
- C-HEMBA1004275//Homo sapiens PHD-finger protein (GRC5) mRNA, complete cds. //1.10E-152//1403bp//69%/AF043725
- C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds. //4.80E-257//738bp//99%/AF092094
- C-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds. //0//1982bp//99%/AF022795
- C-HEMBA1004295//Homo sapiens NY-REN-25 antigen mRNA, partial cds. //9.40E-31//381bp//65%/AF155103
- C-HEMBA1004321//ZINC FINGER PROTEIN 184 (FRAGMENT). //2.30E-93//357aa//42%/Q99676
- C-HEMBA1004353//C-MYC BINDING PROTEIN MM-1. //3.00E-71//89aa//96%/Q99471
- C-HEMBA1004354//CHL1 PROTEIN. //9.90E-26//130aa//42%/P22516
- C-HEMBA1004356//H. sapiens MSSP-2 mRNA. //3.00E-243/ 50
- /573bp//98%/X77494
- C-HEMBA1004389//Homo sapiens zinc finger DNA binding protein 99 (ZNF281) mRNA, complete cds. //0//1437bp//99%/AF125158
- C-HEMBA1004408//PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10). //3.20E-32//148aa//52%/P52017
- C-HEMBA1004479//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN). //3.10E-51//152aa//40%/Q61221
- C-HEMBA1004499//Homo sapiens delta-tubulin mRNA, complete cds. //3.40E-92//483bp//95%/AF201333
- C-HEMBA1004509//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG). //2.70E-12//200aa//28%/Q13107
- C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds. //1.2e-316//1445bp//99%/AF089841
- C-HEMBA1004573//Homo sapiens mRNA for HELG protein. //2.00E-59//483bp//68%/AJ277291
- C-HEMBA1004604//Homo sapiens COP9 complex subunit 7a mRNA, complete cds. //0//1612bp//99%/AF193844
- C-HEMBA1004669//SON PROTEIN (SON3). //7.30E-17//288aa//36%/P18583
- C-HEMBA1004697//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMHHC) (FRAGMENT). //2.90E-05//303aa//21%/P35749
- C-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42). //9.90E-39//143aa//52%/P42743
- C-HEMBA1004752//Homo sapiens mRNA for LAK-4p, complete cds. //4.60E-109//650bp//89%/AB002405
- C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds. //9.10E-34//515bp//66%/U49082
- C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds. //2.60E-246//1249bp//94%/L39060
- C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //5.40E-111//314aa//58%/P08547
- C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT). //3.80E-69//198aa//66%/P50851
- C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68). //8.20E-154//317aa//94%/Q00004
- C-HEMBA1004889//Human C3f mRNA, complete cds. //6.70E-24//341aabbp//26%/U72515
- C-HEMBA1004929//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01. //2.50E-05//148aa//24%/P25386

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C-HEMBA1004930//26S PROTEASOME SUBUNIT S5B (KIAA0072) (HA1357).//3.30E-27//65aa//100%/Q16401
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%/P12036
 C-HEMBA1004973//ZINC-BINDING PROTEIN A33.//4.10E-08//121aa//33%/Q02084
 C-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//0//1813bp//99%/AF041474
 C-HEMBA1005029//Homo sapiens CGI-13 protein mRNA, complete cds.//0//1487bp//99%/AF132947
 C-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16).//3.40E-101//106aa//98%/P35290
 C-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//0//2762bp//99%/AF080561
 C-HEMBA1005201//Homo sapiens CGI-07 protein mRNA, complete cds.//0//1608bp//99%/AF132941
 C-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.90E-179//361aa//95%/Q00004
 C-HEMBA1005206//Drosophila simulans anon73B1 gene and Su(P) gene.//1.90E-11//376bp//63%/AJ250308
 C-HEMBA1005219//NUCLEAR PROTEIN SNF7.//5.30E-10//189aa//25%/P39929
 C-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//3.90E-241//1095bp//99%/AJ007581
 C-HEMBA1005359//ZINC FINGER PROTEIN 137.//3.90E-85//206aa//69%/P52743
 C-HEMBA1005367//Homo sapiens melastatin 1 (MLSN1) mRNA, complete cds.//9.00E-77//620bp//74%/AF071787
 C-HEMBA1005394//Mus musculus pantothenate kinase 1 beta (panK1beta) mRNA, complete cds.//3.90E-126//1097bp//75%/AF200357
 C-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C)mRNA, complete cds.//2.00E-213//537bp//99%/AF041248
 C-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.90E-129//332aa//61%/002193
 C-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//3.10E-154//285aa//99%/Q60809
 C-HEMBA1005530//Homo sapiens anaphase-promoting complex subunit 7 (APC7)mRNA, complete cds.//0//1578bp//98%/AF191340
 C-HEMBA1005548//Homo sapiens MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB) mRNA, complete cds.//1.00E-220//1014bp//99%/AF134157
 C-HEMBA1005558//NUCLEAR PROTEIN SNF7.//6.40E-16//170aa//31%/P39929

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C-HEMBA1005576//Mus musculus mRNA for plexin 2, complete cds.//1.20E-122//870bp//82%/D86949
 C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%/AF133270
 C-HEMBA1005582//TROPOMYOSIN 1, NON-MUSCLE ISOFORM (TROPOMYOSIN II) (CYTOSKELETAL TROPOMYOSIN).//0.0000009//213aa//27%/P09492
 C-HEMBA1005595//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYH C).//2.30E-54//562aa//29%/P34036
 C-HEMBA1005621//Homo sapiens Mad2-like protein mRNA A, complete cds.//8.00E-211//962bp//99%/AF072933
 C-HEMBA1005666//Homo sapiens mRNA for DIPB protein.//8.60E-147//685bp//99%/AJ249128
 C-HEMBA1005699//EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIGAND ELK-L3).//2.10E-37//98aa//81%/Q15768
 C-HEMBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.40E-17//167aa//34%/P25296
 C-HEMBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (MU/M-TYPE).//2.00E-36//342aa//33%/P00789
 C-HEMBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//5.60E-15//76aa//51%/P51522
 C-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//2371bp//100%/AF082516
 C-HEMBA1006031//Homo sapiens mRNA for putative phospholipase, complete cds.//0//1413bp//99%/AB019435
 C-HEMBA1006038//LAMININ ALPHA-5 CHAIN (FRAGMENT).//3.10E-33//81aa//64%/Q61001
 C-HEMBA1006067//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//8.20E-12//297bp//64%/AF098066
 C-HEMBA1006130//SEL-10 PROTEIN.//0.000000043//219aa//25%/Q93794
 C-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//0//1551bp//99%/AF048693
 C-HEMBA1006198//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.90E-19//215aa//39%/P05142
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.60E-23//151aa//37%/P16372
 C-HEMBA1006253//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR.//0.00000002//62aa//53%/P4269

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C-HEMBA1006268//Homo sapiens HQ0024c mRNA, complete cds.//3.50E-157//845bp//92%//AF073836
 C-HEMBA1006272//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.30E-123//200aa//73%//P10265
 C-HEMBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE).//1.00E-210//490aa//77%//P25500
 C-HEMBA1006283//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB2.//0.00000012//176aa//30%//P32505
 C-HEMBA1006291//2-ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-.-).//4.20E-12//215aa//23%//P70473
 C-HEMBA1006309//Homo sapiens aspartyl aminopeptidase mRNA, complete cds.//5.30E-169//774bp//100%//AF005050
 C-HEMBA1006310//Rattus norvegicus cytosolic sortin g protein PACS-1a (PACS-1) mRNA, complete cds.//3.70E-225//1189bp//88%//AF076183
 C-HEMBA1006344//RADIXIN.//1.50E-31//333aa//28%//P26043
 C-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//1.60E-130//332aa//62%//002193
 C-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//3.50E-105//381aa//54%//P28160
 C-HEMBA1006398//Human L1 element L1.6 putative p150 gene, complete cds.//2.00E-277//1729bp//85%//U93563
 C-HEMBA1006445//Homo sapiens putative tumor suppressor NOY2 mRNA, complete cds.//1.40E-270//1224bp//100%//U96750
 C-HEMBA1006474//40 KD PROTEIN.//1.40E-39//292aa//34%//Q01552
 C-HEMBA1006485//PUROMYCIN-SENSITIVE AMINOPEPTIDASE (EC 3.4.11.-) (PSA).//1.90E-81//153aa//97%//P55786
 C-HEMBA1006507//DIAPHANOUS PROTEIN HOMOLOG 2.//1.40E-46//316aa//32%//060879
 C-HEMBA1006521//3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//4.00E-33//177aa//42%//P25716
 C-HEMBA1006559//Mus musculus PRAJA1 (Praj1) mRNA, complete cds.//2.80E-206//1107bp//83%//U06944
 C-HEMBA1006583//Drosophila melanogaster Scribble (scrib) mRNA, complete cds.//1.70E-63//1002bp//65%//AF190774
 C-HEMBA1006624//DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG.//0.00000069//109aa//38%//Q58323
 C-HEMBA1006650//ARP2/3 COMPLEX 20 KD SUBUNIT (P20-ARC).//9.00E-40//113aa//82%//015509
 C-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.40E-44//206aa//47%//P14148

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C-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEININ PMC1-TFG2 INTERGENIC REGION.//3.30E-22//241aa//31%//P53196
 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//0.000000043//111aa//40%//Q01485
 C-HEMBA1006758//Homo sapiens protocadherin beta 13 (PCDH-beta13) mRNA, complete cds.//0//1832bp//91%//AF152492
 C-HEMBA1006807//Homo sapiens mRNA for SPDP.//5.70E-125//1109bp//75%//AJ000644
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2.00E-59//378aa//39%//P16258
 C-HEMBA1006885//Homo sapiens gene for Proline synthetase associated, complete cds.//0//1467bp//96%//AB018566
 C-HEMBA1006914//Human anthracycline-associated resistance ARX mRNA, complete cds.//0//1837bp//99%//U35832
 C-HEMBA1006941//Homo sapiens PKCq-interacting protein PICOT (PICOT) mRNA, complete cds.//2.10E-271//1234bp//99%//AF118649
 C-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.60E-143//740bp//94%//AF004828
 C-HEMBA1006976//H. sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase.//1.90E-80//447bp//89%//X74570
 C-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A).//2.40E-188//391aa//89%//Q90828
 C-HEMBA1007087//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT).//8.30E-27//253aa//30%//Q10568
 C-HEMBA1007121//Homo sapiens bisphosphate 3'-nucleotidase mRNA, complete cds.//1.70E-252//1118bp//92%//AF125042
 C-HEMBA1007151//Homo sapiens synphilin 1 mRNA, complete cds.//0//1900bp//99%//AF076929
 C-HEMBA1007174//Homo sapiens epsin 2b mRNA, complete cds.//3.80E-271//642bp//99%//AF062085
 C-HEMBA1007194//Homo sapiens origin recognition complex subunit 6 (ORC6)mRNA, complete cds.//0//1588bp//99%//AF139658
 C-HEMBA1007224//Homo sapiens SUMO-1-specific protease (SSP1) mRNA, complete cds.//0//1590bp//99%//AF196304
 C-HEMBA1007243//Chinese hamster hprt mRNA, complete cds.//2.00E-58//650bp//70%//J00060
 C-HEMBA1007251//Homo sapiens F-box protein FBX29

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(FBX29) mRNA, partial cds.//5.00E-58//330bp//95%//AF176707

C-HEMBA1007300//Homo sapiens 3',5'-cyclic nucleotide phosphodiesterase 10A1 (PDE10A) mRNA, splice variant 1, complete cds.//0//1519bp//99%//AF127479

C-HEMBA1007301//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//6.20E-18//115aa//33%//P13941

C-HEMBA1000036//Homo sapiens CGI-51 protein mRNA, complete cds.//0//1665bp//99%//AF151809

C-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.80E-187//1582bp//80%//AF084928

C-HEMBA1000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.90E-22//426aa//25%//P11799

C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%//Y15521

C-HEMBA1000144//GUANYLATE CYCLASE ACTIVATING PROTEIN 2 (GCAP 2) (RETINALGUANYLYL CYCLASE ACTIVATOR PROTEIN P24).//1.40E-24//71aa//77%//P51177

C-HEMBA1000217//Homo sapiens SUMO-1-activating enzyme E1 N subunit (SUA1) mRNA, complete cds.//0//1038bp//99%//AF090385

C-HEMBA1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EED8.5.//2.70E-12//112aa//47%//Q09530

C-HEMBA1000264//CHL1 PROTEIN.//9.50E-19//104aa//45%//P22516

C-HEMBA1000266//HYPOTHETICAL 54.5 KD TRP-ASPEPTS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.10E-09//242aa//26%//Q23256

C-HEMBA1000317//FIBULIN-1, ISOFORM D PRECURSOR.//7.10E-62//458aa//35%//P37888

C-HEMBA1000593//Homo sapiens transferrin receptor 2 alpha (TFR2) mRNA, complete cds.//1.30E-107//503bp//99%//AF067864

C-HEMBA1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.10E-19//232aa//28%//P78970

C-HEMBA1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.20E-28//273aa//31%//P27671

C-HEMBA1000693//Homo sapiens neuroan1 mRNA, complete cds.//0//2952bp//94%//AF040723

C-HEMBA1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.20E-130//692bp//93%//U53475

C-HEMBA1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%//AF151847

C-HEMBA1000781//Homo sapiens mitogen-activated pro

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tein kinase kinase kinase MEKK2 mRNA, complete cds.//1.20E-126//613bp//97%//AF111105

C-HEMBA1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.10E-54//232aa//43%//P39956

C-HEMBA1000831//Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA, complete cds.//5.80E-60//301bp//99%//AF126008

C-HEMBA1000915//SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-).//1.10E-08//129aa//31%//P29122

C-HEMBA1000927//Homo sapiens A-type potassium channel modulatory protein2 (KCHIP2) mRNA, complete cds.//1.30E-126//592bp//99%//AF199598

C-HEMBA1000947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%//AF116910

C-HEMBA1000973//Mus musculus schlafen3 (Slfn3) mRNA, complete cds.//3.40E-120//580bp//67%//AF099974

C-HEMBA1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.60E-18//178aa//30%//P28575

C-HEMBA1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.40E-73//230aa//45%//P51523

C-HEMBA1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.90E-19//264aa//34%//P46087

C-HEMBA1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.60E-52//331bp//80%//AF010144

C-HEMBA1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.40E-307//1447bp//97%//AF034803

C-HEMBA1001112//Homo sapiens sec61 homolog mRNA, complete cds.//6.00E-145//961bp//83%//AF077032

C-HEMBA1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%//AB019435

C-HEMBA1001151//Rattus norvegicus golgi stacking protein homolog GRASP55mRNA, complete cds.//4.20E-210//1835bp//76%//AF110267

C-HEMBA1001175//ANKYRIN.//7.00E-11//169aa//31%//Q02357

C-HEMBA1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//5.40E-93//196aa//54%//P46938

C-HEMBA1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.80E-284//713bp//100%//AF089897

C-HEMBA1001282//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//7.00E-43//394aa//34%//P161

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C-HEM BB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//
7.80E-46//163aa//51%/P46719
C-HEM BB1001294//GTP-BINDING PROTEIN TC10.//1.20E-7
9//196aa//80%/P17081
C-HEM BB1001314//Mus musculus Olf-1/EBF-like-3 tran
scription factor (O/E-3) mRNA, complete cds.//1.30
E-129//724bp//86%/U92703
C-HEM BB1001331//Mus musculus mRNA for hepatoma-der
ived growth factor, complete cds, strain: BALB/c.//
2.10E-65//458bp//79%/D63850
C-HEM BB1001339//DXS8237E PROTEIN (FRAGMENT).//4.60
E-06//124aa//37%/P98175
C-HEM BB1001346//Homo sapiens phenylalanine-tRNA sy
nthesase (FARS1) mRNA, nuclear gene encoding mitoch
ondrial protein, complete cds.//1.10E-58//292bp//9
9%/AF097441
C-HEM BB1001384//Homo sapiens COP9 complex subunit
4 mRNA, complete cds.//0//1586bp//99%/AF100757
C-HEM BB1001429//Homo sapiens leucine aminopeptidas
e mRNA, complete cds.//0//1933bp//99%/AF061738
C-HEM BB1001443//Rattus norvegicus pyruvate dehydro
genase phosphatase isoenzyme 1 mRNA, complete cds.
//3.00E-130//553bp//86%/AF062740
C-HEM BB1001482//ZINC FINGER PROTEIN 91 (ZINC FINGE
R PROTEIN HTF10) (HPF7).//2.10E-57//941aa//27%/Q0
5481
C-HEM BB1001562//CYLICIN II (MULTIPLE-BAND POLYPEPT
IDE II).//1.40E-06//373aa//21%/Q28092
C-HEM BB1001564//VACUOLAR ATP SYNTHASE SUBUNIT H (E
C 3.6.1.34) (V-ATPASEH SUBUNIT) (V-ATPASE M9.2 SUB
UNIT) (9.2 KD MEMBRANE ACCESSORY PROTEIN).//9.60E-
32//80aa//78%/O15342
C-HEM BB1001673//Homo sapiens gene for new zinc fin
ger protein, completecds.//0//1919bp//99%/AB01277
0
C-HEM BB1001736//EUKARYOTIC TRANSLATION INITIATION
FACTOR 3 SUBUNIT 9 (EIF3 P116) (EIF3 P110).//4.60E
-15//391aa//25%/P55884
C-HEM BB1001749//TRANSCRIPTIONAL ACTIVATOR GCN5.//
1.70E-16//84aa//47%/Q03330
C-HEM BB1001802//Human desmin mRNA, complete cds.//
0//1523bp//98%/U59167
C-HEM BB1001831//Homo sapiens PAM COOH-terminal int
eractor protein 1 (PCIP1) mRNA, complete cds.//0//
1514bp//99%/AF056209
C-HEM BB1001839//CASTRULA ZINC FINGER PROTEIN XLGCF
42.1 (FRAGMENT).//6.90E-11//87aa//35%/P18720
C-HEM BB1001871//BONE/CARTILAGE PROTEOGLYCAN I PREC
URSOR (BIGLYCAN) (PG-S1).//5.40E-75//241aa//48%/P
47853

4396

C-HEM BB1001872//CELL SURFACE GLYCOPROTEIN EMR1 PRE
CURSOR (EMR1 HORMONE RECEPTOR) (CELL SURFACE GLYCO
PROTEIN F4/80).//1.90E-22//210aa//27%/Q61549
C-HEM BB1001905//TRICHOHYALIN.//2.10E-10//268aa//27
%/P37709
C-HEM BB1001908//Human monocytic leukaemia zinc fin
ger protein (MOZ) mRNA, complete cds.//1.60E-131//
874bp//86%/U47742
C-HEM BB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROL
ASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E)
10 (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEU
BIQUITINATING ENZYME 64E).//6.90E-132//561aa//50%/
Q24574
C-HEM BB1001950//PROBABLE OXYGEN-INDEPENDENT COPROP
ORPHYRINOGEN III OXIDASE (EC 1.-.-) (COPROPORPHY
RINOGENASE) (COPROGEN OXIDASE).//1.60E-41//370aa//
31%/P54304
C-HEM BB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1)
(CYP1VC1).//2.70E-49//139aa//55%/P29981
C-HEM BB1002044//Mus musculus mRNA for vascular cad
herin-2.//0//3562bp//81%/Y08715
C-HEM BB1002134//ZINC-FINGER PROTEIN NEURO-D4.//8.1
0E-56//176aa//67%/P56163
C-HEM BB1002193//TYROSINE-PROTEIN KINASE RECEPTOR T
YR03 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYRO
SINE-PROTEIN KINASE DTK) (TK19-2).//8.70E-61//77aa
//74%/P55144
C-HEM BB1002217//ZINC FINGER PROTEIN 91 (ZINC FINGE
R PROTEIN HTF10) (HPF7).//2.10E-132//399aa//44%/Q
30 05481
C-HEM BB1002266//NEURONAL PROTEIN.//2.10E-46//121aa
//76%/P41737
C-HEM BB1002342//Homo sapiens PKCq-interacting prot
ein PICOT (PICOT) mRNA, complete cds.//1.50E-229//
1045bp//99%/AF118649
C-HEM BB1002442//LIN-10 PROTEIN.//9.70E-14//121aa//
31%/P34692
C-HEM BB1002477//Human Grb2-associated binder-1 mRN
A, complete cds.//7.70E-258//774bp//99%/U43885
C-HEM BB1002510//GYP7 PROTEIN.//3.10E-50//192aa//42
40 %/P48365
C-HEM BB1002550//HYPOTHETICAL UOG-1 PROTEIN.//5.00E
-28//266aa//33%/P27544
C-HEM BB1002600//Homo sapiens tetraspan NET-5 mRNA,
complete cds.//0//1417bp//99%/AF089749
C-HEM BB1002607//Homo sapiens vitamin D3 receptor i
nteracting protein (DRIP80) mRNA, complete cds.//
2.00E-136//660bp//98%/AF105421
C-HEM BB1002705//Homo sapiens CGI-27 protein mRNA,
50 complete cds.//7.80E-285//841bp//96%/AF132961

4397

C-MAMMA1000020//H.sapiens mRNA for flavin-containing monooxygenase 5 (FM05).//8.20E-198//868bp//99%/Z47553

C-MAMMA1000045//ENV POLYPROTEIN [CONTAINS: SURFACE PROTEIN GP85; MEMBRANE PROTEIN GP37].//1.90E-07//249aa//27%/P03396

C-MAMMA1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//1.50E-90//323aa//48%/P47226

C-MAMMA1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) 10 74 (CYSRS).//2.10E-90//427aa//39%/Q09860

C-MAMMA1000173//Homo sapiens src homology 3 domain-containing protein HIP-55 mRNA, complete cds.//2.60E-164//1044bp//87%/AF197060

C-MAMMA1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.40E-134//359aa//63%/P51523

C-MAMMA1000284//P.walti mRNA for rnp associated protein 55.//2.20E-109//864bp//76%/X99836

C-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//0//1466bp//99%/AB015132

C-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN C09F 5.2 IN CHROMOSOME III.//2.00E-30//119aa//53%/Q09232

C-MAMMA1000612//Homo sapiens G protein beta subunit mRNA, partial cds.//8.30E-178//1992bp//84%/AF195883

C-MAMMA1000625//GYP7 PROTEIN.//2.10E-41//198aa//40%/P48365

C-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-).//4.40E-33//250aa//33%/P42660

C-MAMMA1000684//Homo sapiens opioid growth factor receptor mRNA, complete cds.//0//2391bp//99%/AF172451

C-MAMMA1000713//L-RIBULOKINASE (EC 2.7.1.16).//7.70E-17//246aa//29%/P94524

C-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//1.00E-77//395aa//45%/014646

C-MAMMA1000734//Homo sapiens mRNA for SEC63 protein.//0//1587bp//99%/AJ011779

C-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G 8.09C IN CHROMOSOME I.//9.00E-299//1033aa//55%/P87115

C-MAMMA1000824//ACTIN.//6.20E-20//284aa//28%/P53500

C-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//7.80E-40//101aa//54%/027540

C-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3) (SERUM-DERIVED HYALURONAN-ASSOCIATED PROTEIN) (SHAP).//1.0 50

4398

0E-141//576aa//37%/Q06033

C-MAMMA1000956//Homo sapiens CLDN8 gene for claudin-8.//0//1767bp//99%/AJ250711

C-MAMMA1001008//Homo sapiens aspartic-like protease mRNA, complete cds.//2.50E-276//1263bp//99%/AF117892

C-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CG-R) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//1.20E-26//276aa//28%/Q90674

C-MAMMA1001038//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//2.60E-107//190aa//95%/Q15746

C-MAMMA1001041//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETA CHAIN) (FODRIN BETA CHAIN) (SPTBN1).//1.60E-16//113aa//41%/Q01082

C-MAMMA1001059//Homo sapiens mRNA for DEAD Box Protein 5.//0//1440bp//99%/AJ237946

C-MAMMA1001075//Homo sapiens CGI-72 protein mRNA, complete cds.//1.30E-181//397bp//98%/AF151830

C-MAMMA1001080//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.6E-312//1596bp//94%/AF067420

C-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//4.00E-49//125aa//68%/P51521

C-MAMMA1001139//SRE-2 PROTEIN.//5.80E-35//239aa//38%/Q09273

C-MAMMA1001181//ABC1 PROTEIN HOMOLOG PRECURSOR.//1.30E-07//81aa//45%/Q92338

C-MAMMA1001198//Homo sapiens eps15R mRNA, partial cds.//0//2253bp//99%/AB015346

C-MAMMA1001222//EBNA-2 NUCLEAR PROTEIN.//6.60E-09//255aa//29%/P12978

C-MAMMA1001259//Mus musculus F-box protein FBX18 mRNA, partial cds.//2.30E-271//1414bp//89%/AF184275

C-MAMMA1001260//HYPOTHETICAL 97.1 KD PROTEIN R05D 3.4 IN CHROMOSOME III.//2.10E-52//630aa//30%/P34537

C-MAMMA1001305//RHO-GTPASE-ACTIVATING PROTEIN 1 (GTPASE-ACTIVATING PROTEIN RHOGAP) (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//2.20E-98//283aa//63%/Q07960

C-MAMMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.000000017//46aa//60%/P20931

C-MAMMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG).//1.40E-165//312aa//99%/P02750

C-MAMMA1001476//URIDINE KINASE (EC 2.7.1.48) (URID

4399

4400

- INE MONOPHOSPHOKINASE) (FRAGMENT). //6. 50E-129//260a
a//92%/P52623
- C-MAMMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUN
IT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTE
INASE) (CANP) (MU-TYPE). //5. 70E-55//86aa//97%/P07
384
- C-MAMMA1001576//Human gamma-tubulin mRNA, complete
cds. //7. 50E-276//1561bp//90%/M61764
- C-MAMMA1001627//Homo sapiens mRNA for transcriptio
n factor TBX6. //5. 20E-189//871bp//99%/AJ007989 10
- C-MAMMA1001633//ZINC FINGER PROTEIN 165. //6. 30E-39
//160aa//55%/P49910
- C-MAMMA1001679//F-ACTIN CAPPING PROTEIN BETA SUBUN
IT (CAPZ). //0. 00000058//29aa//100%/P47756
- C-MAMMA1001730//Homo sapiens brain and nasopharyng
eal carcinoma susceptibility protein NSG-x mRNA, p
artial cds. //0//1603bp//99%/AF095687
- C-MAMMA1001735//TUBULIN BETA-5 CHAIN (BETA-TUBULIN
CLASS-V). //5. 90E-240//445aa//97%/P09653
- C-MAMMA1001743//Y BOX BINDING PROTEIN-1 (Y-BOX TRA 20
NSCRIPTION FACTOR). //8. 50E-32//171aa//36%/P21573
- C-MAMMA1001751//Homo sapiens tandem pore domain po
tassium channel TWIK-2(KCNK6) mRNA, complete cds. /
/0//2332bp//99%/AF117708
- C-MAMMA1001754//Homo sapiens Vacuolar proton pump
subunit SFD alpha isoform mRNA, complete cds. //0//
1987bp//99%/AF112204
- C-MAMMA1001768//CELL DIVISION CYCLE PROTEIN 48 HOM
OLOG MJ1156. //3. 80E-45//351aa//38%/Q58556
- C-MAMMA1001771//M. musculus mRNA for semaphorin B. / 30
/2. 60E-200//1272bp//79%/X85991
- C-MAMMA1001820//Rattus norvegicus mRNA for PAG608
gene. //1. 30E-198//1157bp//80%/Y13148
- C-MAMMA1001837//ZINC FINGER PROTEIN 29 (ZFP-29). //
2. 60E-77//507aa//38%/Q07230
- C-MAMMA1001868//TRICHOHYALIN. //2. 70E-19//359aa//25
%/P22793
- C-MAMMA1002143//Homo sapiens Cdc42 effector protei
n 4 mRNA, complete cds. //1. 70E-252//1170bp//99%/A
F099664
- C-MAMMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLR
EP3 PROTEIN). //6. 00E-66//157aa//70%/P15880
- C-MAMMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDO
XIN-DEPENDENT PEROXIDREDUCTASE 1) (THIOL-SPECIFIC
ANTIOXIDANT PROTEIN) (TSA) (PRP) (NATURALKILLER C
ELL ENHANCING FACTOR B) (NKEF-B). //5. 20E-61//60aa/
/90%/P32119
- C-MAMMA1002219//Rattus norvegicus rexo70 mRNA, com
plete cds. //1. 30E-181//861bp//98%/AF032667
- C-MAMMA1002236//TRANSLATION INITIATION FACTOR EIF- 50
- 2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).
//8. 80E-217//310aa//86%/P70541
- C-MAMMA1002268//Mus musculus sphingosine kinase (S
PHK1a) mRNA, partial cds. //1. 00E-190//1624bp//76%/
/AF068748
- C-MAMMA1002297//Homo sapiens mRNA for Rab6 GTPase
activating protein. //1. 10E-214//881bp//97%/AJ0116
79
- C-MAMMA1002329//M. musculus mRNA for semaphorin B. /
/3. 80E-45//332bp//84%/X85991
- C-MAMMA1002351//Mus musculus dynactin subunit p25
(p25) mRNA, complete cds. //4. 30E-119//773bp//86%/
AF190795
- C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D. //1. 50E-07
//206aa//29%/Q02926
- C-MAMMA1002428//LYSOSOME MEMBRANE PROTEIN II (LIMP
II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN)
(LGP85) (CD36 ANTIGEN-LIKE 2). //1. 10E-24//96aa//68
%/Q14108
- C-MAMMA1002470//PROBABLE NH(3)-DEPENDENT NAD(+) SY
NTHETASE (EC 6.3.5.1). //1. 00E-11//128aa//36%/P476
23
- C-MAMMA1002485//Homo sapiens stanniocalcin-related
protein mRNA, complete cds. //0//1822bp//99%/AF09
8462
- C-MAMMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN S
TE2-FRS2 INTERGENIC REGION. //1. 20E-34//337aa//31%/
/P43571
- C-MAMMA1002530//Homo sapiens cytosolic phospholipa
se A2 gamma (cPLA2 gamma) mRNA, complete cds. //0//
1910bp//99%/AF065214
- C-MAMMA1002573//GLUCOAMYLASE S1/S2 PRECURSOR (EC
3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPH
A-D-GLUCAN GLUCOHYDROLASE). //2. 60E-19//666aa//23%/
/P08640
- C-MAMMA1002617//ZINC FINGER PROTEIN 135. //7. 60E-89
//252aa//57%/P52742
- C-MAMMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMIN
AL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIO
LESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEAS
E) (DEUBIQUITINATING ENZYME). //9. 50E-16//159aa//37
%/Q09931
- C-MAMMA1002622//VILLIN. //7. 20E-35//53aa//64%/P026
40
- C-MAMMA1002637//KINESIN LIGHT CHAIN (KLC). //1. 30E-
198//550aa//70%/Q07866
- C-MAMMA1002650//Mus musculus ODA-8S protein mRNA,
complete cds. //5. 40E-57//480bp//68%/AF194030
- C-MAMMA1002655//Homo sapiens mRNA for ganglioside
sialidase, complete cds. //0//1515bp//99%/AB008185

4401

C-MAMMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME). //1.10E-45//618aa//26%/P27550

C-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds. //4.3e-317//1942bp//85%/AF018261

C-MAMMA1002769//Homo sapiens cell cycle progression restoration 8 protein (CPR8) mRNA, complete cds. //2.20E-25//330bp//77%/AF011794

C-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds. //2.60E-58//373bp//81%/U58883

C-MAMMA1002844//TRIOSE PHOSPHATE/PHOSPHATE TRANSLATOR, NON-GREEN PLASTID PRECURSOR (CTPT). //4.90E-10//334aa//22%/P52178

C-MAMMA1002858//Rat cMG1 mRNA. //3.70E-238//1147bp//92%/X52590

C-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN). //1.40E-160//305aa//85%/P48059

C-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN). //5.70E-30//214aa//35%/P48060

C-MAMMA1002937//ZINC FINGER PROTEIN 135. //8.30E-99//393aa//43%/P52742

C-MAMMA1002972//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27. //1.10E-05//69aa//42%/P40343

C-MAMMA1003011//HISTONE MACRO-H2A.1. //2.70E-123//370aa//66%/Q02874

C-MAMMA1003013//DNA POLYMERASE BETA (EC 2.7.7.7). //7.40E-46//332aa//36%/P06746

C-MAMMA1003035//RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE C (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE). //1.90E-13//108aa//33%/P23851

C-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT protein PIASy mRNA, complete cds. //0//1533bp//99%/AF077952

C-MAMMA1003057//MD6 PROTEIN. //3.10E-225//419aa//97%/Q60584

C-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds. //1.10E-234//1178bp//86%/AF071316

C-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA). //2.20E-105//217aa//89%/P46735

C-MAMMA1003146//Homo sapiens mRNA for Galt3 protein. //4.30E-218//996bp//99%/Y15062

C-MAMMA1003150//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR. //5.00E-13//592aa//24%/P47179

C-MAMMA1003166//Homo sapiens NLL septin-like fusio

4402

n protein (MSF) mRNA, complete cds. //3.10E-158//592bp//97%/AF123052

C-NT2RM1000001//D.melanogaster sap47-2 mRNA. //1.50E-10//417bp//62%/X80110

C-NT2RM1000039//HYPOTHETICAL 41.4 KD PROTEIN IN SR LQ-HYPF INTERGENIC REGION (EC 1.18.1.-) (ORF4) (ORF2). //2.90E-14//299aa//25%/P37596

C-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds. //0//3106bp//89%/D87671

10 C-NT2RM1000080//UNC-1 PROTEIN. //5.90E-25//211aa//31%/Q21190

C-NT2RM1000086//HYPOTHETICAL 97.1 KD PROTEIN R05D 3.4 IN CHROMOSOME III. //8.40E-52//364aa//32%/P34537

C-NT2RM1000092//MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2). //1.00E-07//362aa//23%/P39843

C-NT2RM1000118//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT). //1.20E-10//150aa//28%/P87072

20 C-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUFS6 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds. //7.80E-110//516bp//99%/AF044959

C-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5). //3.30E-38//469aa//27%/P49902

C-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT). //1.20E-10//150aa//28%/P87072

30 C-NT2RM1000187//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C. //1.10E-10//94aa//47%/O42643

C-NT2RM1000199//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene). //0//2476bp//99%/AJ245820

C-NT2RM1000244//Homo sapiens TRAF4 associated factor 1 mRNA, partial cds. //2.00E-126//592bp//99%/U81002

C-NT2RM1000252//H.sapiens E-MAP-115 mRNA. //9.70E-35//569bp//64%/X73882

C-NT2RM1000256//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds. //0//3012bp//99%/AB016789

C-NT2RM1000257//MACO NASHI PROTEIN. //7.90E-69//143aa//91%/P49028

C-NT2RM1000260//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP100 mRNA, complete cds. //0//2766bp//99%/AF055995

C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE SUBUNIT) (V-ATPASE 28 KD A

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CESSORY PROTEIN). //1.50E-106//118aa//97%/P39942
 C-NT2RM1000354//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds. //7.40E-245//2101bp//68%/AF111423
 C-NT2RM1000355//Homo sapiens transmembrane protein BRI (BRI) mRNA, complete cds. //0//1599bp//99%/AF152462
 C-NT2RM1000377//Homo sapiens dual specificity phosphatase MKP5 (MKP5) mRNA, complete cds. //3.20E-196//1016bp//94%/AF179212
 C-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CP T1-SPC98 INTERGENIC REGION. //0.00000019//67aa//31%/P53915
 C-NT2RM1000421//RIBONUCLEASE INHIBITOR. //4.40E-21//372aa//30%/P10775
 C-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds. //1.40E-185//1486bp//81%/AF084928
 C-NT2RM1000499//Caenorhabditis elegans mRNA for centaurin gamma 1A. //3.00E-17//927bp//58%/AJ132700
 C-NT2RM1000539//Homo sapiens mRNA for Lsm5 protein. //3.00E-158//733bp//99%/AJ238097
 C-NT2RM1000553//Homo sapiens putative glycolipid transfer protein mRNA, complete cds. //3.40E-177//814bp//99%/AF103731
 C-NT2RM1000555//UNR PROTEIN. //0//678aa//98%/P18395
 C-NT2RM1000563//TRANSMISSION-BLOCKING TARGET ANTIGEN S230 PRECURSOR. //0.0000068//199aa//30%/Q08372
 C-NT2RM1000623//RIBONUCLEASE INHIBITOR. //4.40E-21//372aa//30%/P10775
 C-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-). //8.50E-75//301aa//39%/P43636
 C-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA, complete cds. //5.70E-210//960bp//99%/AF038957
 C-NT2RM1000666//DNA-BINDING PROTEIN A. //2.20E-09//165aa//34%/P16989
 C-NT2RM1000691//Homo sapiens mRNA for PLU-1 protein. //0//3104bp//99%/AJ132440
 C-NT2RM1000702//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-). //5.60E-08//187aa//27%/P49695
 C-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds. //0//3524bp//99%/AF027208
 C-NT2RM1000746//Homo sapiens polyamine modulated factor-1 (PMF1) mRNA, complete cds. //6.70E-227//1043bp//99%/AF141310
 C-NT2RM1000770//DXS6673E PROTEIN. //1.40E-39//194aa//48%/Q14202

4404

C-NT2RM1000772//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //7.30E-15//280aa//27%/Q00808
 C-NT2RM1000800//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene). //1.10E-98//571bp//89%/Z97207
 C-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds. //0//3524bp//99%/AF027208
 C-NT2RM1000826//UNR PROTEIN. //0//678aa//98%/P18395
 10 C-NT2RM1000833//Homo sapiens sec61 homolog mRNA, complete cds. //0//3541bp//99%/AF084458
 C-NT2RM1000850//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN). //9.70E-42//333aa//36%/P16157
 C-NT2RM1000852//Homo sapiens putative ATP-dependent RNA helicase ROK1 mRNA, complete cds. //0//2206bp//99%/AF077033
 C-NT2RM1000874//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds. //1.40E-244//1113bp//99%/AF043733
 20 C-NT2RM1000882//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds. //4.30E-122//1394bp//69%/AF126799
 C-NT2RM1000883//Homo sapiens I-1 receptor candidate protein mRNA, complete cds. //0//5107bp//99%/AF082516
 C-NT2RM1000885//HYPOTHETICAL 97.1 KD PROTEIN R05D 3.4 IN CHROMOSOME III. //1.80E-56//630aa//30%/P34537
 30 C-NT2RM1000894//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135). //0//1020aa//89%/P70700
 C-NT2RM1000898//ACTIN, CYTOPLASMIC (ACTIN, MICRONUCLEAR). //8.90E-26//229aa//29%/P02583
 C-NT2RM1000924//HYPOTHETICAL 39.7 KD PROTEIN C34E1 0.2 IN CHROMOSOME III. //1.00E-15//266aa//26%/P46577
 C-NT2RM1001003//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds. //0//2230bp//99%/AF030233
 40 C-NT2RM1001008//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME I. //1.60E-13//119aa//36%/Q09701
 C-NT2RM1001059//NUCLEAR POLYADENYLATED RNA-BINDING PROTEIN NAB4. //3.60E-11//180aa//28%/Q99383
 C-NT2RM1001072//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1 (EC 3.1.4.11) (PLC-GAMMA-1) (PHOSPHOLIPASE C-GAMMA-1) (PLC-11) (PLC-148). //8.30E-47//259aa//35%/P08487
 C-NT2RM1001092//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //3.60E-115//332aa//52%/Q

05481

C-NT2RM1001102//Human HEM45 mRNA, complete cds.//
2.30E-27//482bp//63%/U88964
C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.
1.14).//5.60E-06//239aa//27%/P54197
C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 12
8 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III
SUBUNIT 2).//2.20E-144//362aa//71%/P25167
C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOL
IC (DH IC) (CYTOPLASMIC)
C DYNEIN INTERMEDIATE CHAIN).//0.00000043//136aa//
31%/P54703
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROL
ASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (U
BIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUI
TINATING ENZYME 8).//1.30E-36//160aa//40%/P50102
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase
A1 (PDE9A) mRNA, complete cds.//0//1574bp//99%/AF067223
C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH G
LYCOPROTEIN).//3.60E-19//181aa//34%/P14918
C-NT2RM2000322//SPERMIDINE SYNTHASE (EC 2.5.1.16)
(PUTRESCINE AMINOPROPYLTRANSFERASE) (AMINOPROPYLTR
ANSFERASE).//8.10E-06//167aa//29%/O48660
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN.
//1.80E-14//245aa//29%/P11274
C-NT2RM2000368//Homo sapiens protein kinase C-bind
ing protein RACK7 mRNA, partial cds.//0//1506bp//9
9%/U48251
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRAN
SFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.70E-68//41
9aa//36%/P50849
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR
(70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACT
OR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTICINTERM
EDIATE COMPONENT).//1.60E-54//344aa//33%/P32802
C-NT2RM2000407//Mus musculus semaphorin VIa mRNA,
complete cds.//9.70E-201//826bp//84%/AF030430
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRA
NSPORTER NTT73.//1.00E-222//237aa//89%/Q08469
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YP
T52-GCN3 INTERGENIC REGION.//1.00E-07//157aa//28%/P36113
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROT
EIN (EC 2.7.1.-).//8.90E-06//377aa//24%/P22211
C-NT2RM2000490//SYNAPTOTAGMIN (P65).//1.80E-13//16
6aa//34%/P41823
C-NT2RM2000502//Rattus norvegicus W307 mRNA, compl
ete cds.//1.70E-58//381bp//86%/U78304
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP

10

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1) mRNA, complete cds.//0//1673bp//99%/AF061243
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURS
OR (APEG PROTEIN).//1.30E-12//282aa//32%/P17437
C-NT2RM2000566//Homo sapiens integrin alpha-7 mRN
A, complete cds.//0//2519bp//96%/AF032108
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.
1.5) (ISOLEUCINE--TRNALIGASE) (ILERS).//1.70E-187/
/741aa//46%/P73505
C-NT2RM2000588//HISTONE DEACETYLASE HDA1.//2.80E-6
0//384aa//40%/P53973
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyl
transferase 3 beta 3 (DNMT3B) mRNA, complete cds./
/0//2712bp//99%/AF156487
C-NT2RM2000599//Homo sapiens F-box protein Lilina
(LILINA) mRNA, complete cds.//4.90E-70//838bp//69%
//AF179221
C-NT2RM2000609//Homo sapiens CTL1 gene.//0//1559bp
//99%/AJ245620
C-NT2RM2000612//Rattus norvegicus ADP-ribosylation
factor-directed GTPase activating protein mRNA, c
omplete cds.//2.60E-106//1069bp//74%/U35776
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-R
ICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//4.40E-32/
/319aa//35%/Q08170
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//
3.70E-142//285aa//90%/P32391
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1)
(RSP-1 PROTEIN) (RSP-1).//3.80E-23//184aa//36%/Q1
5404
C-NT2RM2000718//Homo sapiens endocrine regulator m
RNA, complete cds.//0//1731bp//99%/AF121141
C-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTE
IN HTF6).//2.90E-103//249aa//73%/P28160
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTI
VATOR SNF2L.//5.70E-53//266aa//43%/P41877
C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT P
ROTEIN) (BETA-COP).//9.50E-279//545aa//98%/P23514
C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulok
inase, complete cds.//1.70E-200//927bp//99%/AB015
046
C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//
8.20E-154//285aa//99%/Q60809
C-NT2RM2001065//Homo sapiens COP9 complex subunit
4 mRNA, complete cds.//0//1554bp//99%/AF100757
C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E1
0.2 IN CHROMOSOME III.//2.40E-15//266aa//26%/P465
77
C-NT2RM2001105//Drosophila melanogaster eyelid (el
d) mRNA, complete cds.//1.20E-28//805bp//61%/AF05
3091

4407

C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //1.30E-20//267aa//35%/P05143
 C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5). //1.50E-07//95aa//35%/P48724
 C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10). //3.60E-10//177aa//32%/P97924
 C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE). //1.30E-180//328aa//99%/P13264
 C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR). //1.60E-166//312aa//98%/P53995
 C-NT2RM2001324//ZYXIN. //6.80E-55//200aa//41%/Q04584C-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //2.90E-08//334aa//22%/Q00808
 C-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein. //0//1621bp//99%/AJ007509
 C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2). //7.40E-121//437aa//57%/P52569
 C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). //6.90E-27//90aa//42%/P38660
 C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //4.30E-61//312aa//44%/P19474
 C-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds. //3.10E-156//909bp//88%/AF032667
 C-NT2RM2001605//Homo sapiens mRNA for PLU-1 protein. //0//3114bp//99%/AJ132440
 C-NT2RM2001613//Homo sapiens sec61 homolog mRNA, complete cds. //0//2601bp//99%/AF084458
 C-NT2RM2001632//KES1 PROTEIN. //1.40E-31//342aa//34%/P35844
 C-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145). //1.20E-142//566aa//56%/P52591
 C-NT2RM2001648//Homo sapiens sec61 homolog mRNA, complete cds. //0//2421bp//99%/AF084458
 C-NT2RM2001652//Homo sapiens guanine nucleotide exchange factor mRNA, complete cds. //0//2608bp//99%/AF111162
 C-NT2RM2001659//ZINC/CADMIUM RESISTANCE PROTEIN. //3.40E-39//161aa//34%/P20107
 C-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds. //0//2471bp//99%/AF044195
 C-NT2RM2001668//Homo sapiens putative WHSC1 protein (WHSC1) mRNA, alternative splice product ending in intron 11, complete cds. //6.20E-16//464bp//62%/

4408

/AF083391
 C-NT2RM2001670//ZINC FINGER PROTEIN 29 (ZFP-29). //6.50E-104//407aa//43%/Q07230
 C-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated protein (SLAP1) mRNA, complete cds. //0//1843bp//94%/U21155
 C-NT2RM2001688//HYPOTHETICAL 33.8 KD PROTEIN C5H10.01 IN CHROMOSOME I. //4.60E-20//253aa//30%/Q09674
 10 C-NT2RM2001698//Homo sapiens XGalT-1 mRNA for galactosyltransferase I, complete cds. //6.20E-253//1170bp//99%/AB028600
 C-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT). //5.70E-130//536aa//49%/P50544
 C-NT2RM2001716//Homo sapiens BPTF mRNA for bromodomain PHD finger transcription factor, complete cds. //0//1774bp//98%/AB032251
 20 C-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME). //7.20E-16//381aa//27%/Q09931
 C-NT2RM2001743//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds. //0//1498bp//99%/AF011792
 C-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210. //8.80E-11//119aa//36%/Q92609
 C-NT2RM2001760//Homo sapiens sec61 homolog mRNA, complete cds. //0//2379bp//99%/AF084458
 30 C-NT2RM2001771//ZINC FINGER PROTEIN 135. //6.40E-154//394aa//64%/P52742
 C-NT2RM2001782//Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA) mRNA, complete cds. //0//1470bp//99%/AF135422
 C-NT2RM2001785//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds. //0//2150bp//99%/AF126799
 C-NT2RM2001803//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds. //0//2249bp//99%/AF044195
 C-NT2RM2001823//CHD1 PROTEIN. //1.80E-106//631aa//39%/P32657
 C-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds. //0//2415bp//97%/AF013759
 C-NT2RM2001886//PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (EC 3.1.13.4) (PAB1P-DEPENDENT POLY(A)-NUCLEASE). //3.00E-54//337aa//39%/P53010
 50 C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ. //5.10E-

4409

-26//204aa//34%/P28692
 C-NT2RM2001930//M.musculus mRNA for semaphorin G./
 /5.20E-135//894bp//83%/X97818
 C-NT2RM2001935//Homo sapiens single-strand selecti
 ve monofunctional uracil DNA glycosylase mRNA, com
 plete cds.//0//1454bp//99%/AF125182
 C-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBR1 INTER
 GENIC REGION.//2.70E-27//216aa//34%/P28320
 C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN A
 AC3-RFC5 INTERGENIC REGION.//0.0000001//212aa//23% 10
 //P38250
 C-NT2RM2001983//Homo sapiens RGS-GAIP interacting
 protein GIPC mRNA, complete cds.//0//1658bp//98%/AF089816
 C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR
 PROTEIN NOP77).//1.90E-39//253aa//35%/P37838
 C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECUR
 SOR (PDI) (EC 5.3.4.1).//1.30E-10//232aa//28%/Q12
 730
 C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13C 20
 6.03 IN CHROMOSOME I.//3.10E-12//206aa//30%/Q0978
 2
 C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOP
 ROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.90E-08//83aa/
 /44%/P40796
 C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GR
 EB-FEOA INTERGENIC REGION.//1.10E-89//425aa//41%/P46837
 C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fr
 uctose-6-phosphate amidotransferase, complete cds. 30
 //0//1959bp//99%/AB016789
 C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATE
 D PROTEIN VPS13.//0.00000099//338aa//24%/Q07878
 C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIB
 ONUCLEOPROTEIN X (HNRNP X) (CBP).//5.00E-62//104aa
 //57%/Q61990
 C-NT2RM2002091//Drosophila melanogaster eyelid (el
 id) mRNA, complete cds.//7.10E-29//805bp//61%/AF05
 3091
 C-NT2RM2002100//Homo sapiens mRNA for ATP-dependen
 t RNA helicase, partial.//0//1807bp//99%/AJ010840
 C-NT2RM2002109//Homo sapiens glioma amplified on c
 hromosome 1 protein (GAC1) mRNA, complete cds.//0/
 /1868bp//99%/AF030435
 C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN
 KINASE PKWA (EC 2.7.1.-).//4.90E-13//487aa//26%/P
 49695
 C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.
 //8.00E-31//105aa//47%/P47805
 C-NT2RM2002145//Homo sapiens erythroblast macrophage 50

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ge protein EMP mRNA, complete cds.//8.50E-191//152
 4bp//81%/AF084928
 C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 12
 8 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III
 SUBUNIT 2).//7.10E-155//381aa//72%/P25167C-NT2RM4
 000030//LAS1 PROTEIN.//5.60E-12//184aa//32%/P3614
 6
 C-NT2RM4000046//GOLIATH PROTEIN (G1 PROTEIN).//0.0
 00008//112aa//31%/Q06003
 C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.50E-81
 //251aa//53%/P52742
 C-NT2RM4000139//R.norvegicus trg mRNA.//2.30E-114/
 /1161bp//72%/X68101
 C-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLAS
 MIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRRS).
 //1.20E-157//321aa//61%/P26639
 C-NT2RM4000156//H.sapiens HPBRII-7 gene.//3.60E-21
 //785bp//60%/X67336
 C-NT2RM4000167//Homo sapiens mRNA for Chromokinesi
 n (KIF 4 gene).//0//1946bp//99%/AJ271784
 C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PR
 OTEIN US01.//4.80E-13//686aa//23%/P25386
 C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICAS
 E PL10.//9.20E-75//439aa//41%/P16381
 C-NT2RM4000202//ZINC FINGER PROTEIN MOK-2 (HOK-2).
 //4.90E-32//170aa//41%/Q16600
 C-NT2RM4000215//MAK16 PROTEIN.//1.30E-68//295aa//4
 9%/P10962
 C-NT2RM4000229//Gallus gallus actin filament-assoc
 iated protein (AFAP-110) mRNA, complete cds.//1.10
 E-27//633bp//64%/L20303
 C-NT2RM4000233//Mus musculus semaphorin VIa mRNA,
 complete cds.//3.40E-231//1395bp//86%/AF030430
 C-NT2RM4000290//Human transducin-like enhancer pro
 tein (TLE3) mRNA, complete cds.//2.20E-276//1124bp
 //97%/M99438
 C-NT2RM4000344//Homo sapiens mRNA for ATP-dependen
 t metalloprotease YME1L.//0//2030bp//99%/AJ132637
 C-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL
 83 PROTEIN).//1.50E-21//208aa//35%/Q24371
 C-NT2RM4000356//RAS-RELATED PROTEIN RAB-17.//5.90E
 -80//213aa//75%/P35292
 C-NT2RM4000386//Mus musculus ODZ3 (Odz3) mRNA, par
 tial cds.//0//2156bp//87%/AF195418
 C-NT2RM4000421//Homo sapiens mRNA for nuclear tran
 sport receptor.//0//1730bp//99%/AJ133769
 C-NT2RM4000433//Mus musculus retinoic acid-respons
 ive protein (Stra6) mRNA, complete cds.//4.10E-271
 //2085bp//77%/AF062476
 C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H

4411

10.03C IN CHROMOSOME I.//8.00E-20//393aa//24%/Q10297
 C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2092bp//99%/AF097025
 C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 1B-6; PEPTIDE P-H].//4.80E-11//242aa//31%/P04280
 C-NT2RM4000496//SAP1 PROTEIN.//8.30E-53//434aa//2910%/P39955
 C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.10E-11//394aa//24%/P16884
 C-NT2RM4000531//ZINC FINGER PROTEIN 29 (ZFP-29).//2.40E-89//389aa//43%/Q07230
 C-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN).//1.00E-59//595aa//28%/Q04652
 C-NT2RM4000595//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//8.70E-15//403aa//30%/P26337
 C-NT2RM4000611//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//2.90E-09//108aa//31%/Q00808
 C-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//2.70E-146//420aa//60%/P27550
 C-NT2RM4000657//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).//3.00E-68//297aa//40%/P51178
 C-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374.//301.20E-28//180aa//30%/P74168
 C-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme I (UBH1) mRNA, partial cds.//1.00E-136//1104bp//77%/AF022789
 C-NT2RM4000733//TRANSCRIPTION TERMINATION FACTOR RH0.//0.00000041//207aa//29%/P52154
 C-NT2RM4000734//Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds.//0//2071bp//99%/AF221712
 C-NT2RM4000741//Homo sapiens hSGT1 mRNA for hSgt1 p, complete cds.//0//2184bp//99%/D88208
 C-NT2RM4000751//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-125//301aa//53%/Q99676
 C-NT2RM4000798//Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 mRNA, complete cds.//0//2603bp//99%/AF084521
 C-NT2RM4000820//VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).//1.10E-24//138aa//44%/P40682
 C-NT2RM4000857//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN 50

4412

(LRG).//6.70E-22//250aa//29%/P02750
 C-NT2RM4000996//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//8.00E-211//738aa//50%/Q05481
 C-NT2RM4001047//M025 PROTEIN.//8.00E-140//333aa//80%/Q06138
 C-NT2RM4001054//Homo sapiens sec61 homolog mRNA, complete cds.//3.10E-190//1315bp//81%/AF077032
 C-NT2RM4001084//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//0.000000032//165aa//33%/Q09820
 C-NT2RM4001092//ZINC FINGER PROTEIN GLO3.//3.10E-24//265aa//33%/P38682
 C-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME II.//5.90E-86//292aa//48%/Q09417
 C-NT2RM4001140//HOMEBOX PROTEIN MSH-D.//1.00E-11//103aa//38%/Q01704
 C-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN.//4.10E-197//445aa//78%/Q27969
 C-NT2RM4001178//PROBABLE ATP-DEPENDENT RNA HELICASE HAS1.//1.10E-48//218aa//43%/Q03532
 C-NT2RM4001200//ZINC FINGER PROTEIN 135.//9.50E-135//375aa//60%/P52742
 C-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//0//2310bp//99%/AF004828
 C-NT2RM4001217//Mus musculus actin-binding protein (ENC-1) mRNA, complete cds.//3.10E-148//1445bp//72%/U65079
 C-NT2RM4001256//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//4.30E-55//289bp//77%/AF129131
 C-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K).//3.50E-35//124aa//65%/P54676
 C-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD).//2.30E-31//334aa//30%/P08503
 C-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds.//1.80E-39//728bp//64%/D89016
 C-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN).//1.00E-28//171aa//37%/P32626
 C-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOL1 INTERGENIC REGION.//8.10E-30//265aa//33%/P53742
 C-NT2RM4001347//Homo sapiens NY-REN-25 antigen mRNA, partial cds.//0//2300bp//99%/AF155103
 C-NT2RM4001371//Homo sapiens IDN3 mRNA, partial cds.//0//2524bp//99%/AB019494

4413

C-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//2.20E-237//1079bp//99%/AF098799
 C-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds.//0//1962bp//87%/AF020526
 C-NT2RM4001412//Homo sapiens nGAP mRNA, complete cds.//0//1918bp//99%/AF047711
 C-NT2RM4001444//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNALIGASE) (ILERS).//1.40E-118//444aa//46%/P73505
 C-NT2RM4001483//ZINC FINGER PROTEIN 136.//5.10E-106//357aa//55%/P52737
 C-NT2RM4001566//NECDIN.//9.80E-44//227aa//41%/P25233
 C-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//1.50E-284//1082bp//90%/AF071317
 C-NT2RM4001592//HYPOTHETICAL 128.5 KD HELICASE IN ATS1-TPD3 INTERGENIC REGION.//7.60E-56//213aa//49%/P31380
 C-NT2RM4001597//M.musculus red-1 gene.//2.10E-171//1414bp//78%/X92750
 C-NT2RM4001611//SIS2 PROTEIN (HALOTOLERANCE PROTEIN HAL3).//2.60E-32//203aa//39%/Q12600
 C-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISCS, LARGE HOMOLOG 3).//1.50E-93//278aa//38%/Q13368
 C-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GABP INTERGENIC REGION.//2.70E-84//410aa//42%/P37339
 C-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT).//8.90E-141//354aa//72%/Q14141
 C-NT2RM4001731//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds.//0//1922bp//100%/AF179221
 C-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//4.10E-186//639aa//58%/Q05512
 C-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1).//7.90E-66//311aa//35%/Q03164
 C-NT2RM4001810//AGGRECAN CORE PROTEIN PRECURSOR (CARTILAGE-SPECIFIC PROTEOGLYCAN CORE PROTEIN) (CSPC P) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 1).//5.10E-07//263aa//30%/P16112
 C-NT2RM4001813//LECTIN BRA-2.//0.00000048//114aa//30%/P17346
 C-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//8.10E-300//1395bp//98%/M37712
 C-NT2RM4001823//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//2.90E-55//325aa//37%/P28160

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C-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.90E-161//481aa//56%/P51523
 C-NT2RM4001858//T-BOX CONTAINING PROTEIN TBXL (FRAGMENT).//6.50E-22//126aa//46%/P79779
 C-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC.//4.30E-244//1248bp//94%/Y17711
 C-NT2RM4001876//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.50E-23//184aa//36%/Q15404
 C-NT2RM4001880//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//5.90E-09//268aa//26%/P47486
 C-NT2RM4001930//Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase (ALG6) mRNA, complete cds.//0//1930bp//99%/AF102851
 C-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//0//2087bp//99%/AF098162
 C-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//2.60E-261//1563bp//84%/X99330
 C-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.80E-112//457aa//47%/P51523
 C-NT2RM4001987//NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR(N-CAM 180) [CONTAINS: N-CAM 140].//3.20E-17//281aa//30%/P16170
 C-NT2RM4002013//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEININ PMT6-PC1 INTERGENIC REGION.//6.90E-94//589aa//35%/P42935
 C-NT2RM4002034//Homo sapiens hiwi mRNA, partial cds.//1.90E-53//1585bp//60%/AF104260
 C-NT2RM4002062//ASPARYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNALIGASE) (ASPRS).//1.90E-31//80aa//52%/P36419
 C-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//1865bp//99%/U82267
 C-NT2RM4002066//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP230 mRNA, complete cds.//1.50E-211//1123bp//71%/AF117755
 C-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//9.30E-293//1751bp//83%/AF072758
 C-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//2.80E-105//556aa//41%/Q04652
 C-NT2RM4002093//Homo sapiens neural polypyrimidine tract binding protein (PTB) mRNA, complete cds.//0//2550bp//99%/AF176085
 C-NT2RM4002109//Homo sapiens mRNA for Chromokinesin (KIF 4 gene).//0//2572bp//99%/AJ271784
 C-NT2RM4002145//SLIT PROTEIN PRECURSOR.//1.40E-09//

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/127aa//33%/P24014
 C-NT2RM4002146//Homo sapiens MAGOH mRNA, complete cds.//6.90E-70//454bp//85%/AF035940
 C-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, complete cds.//0//2671bp//99%/AF084535
 C-NT2RM4002174//MRP PROTEIN.//9.10E-68//264aa//51%/P21590
 C-NT2RM4002189//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//6.20E-33//688aa//27%/P08640
 C-NT2RM4002194//Mus musculus semaphorin Via mRNA, complete cds.//5.20E-297//1753bp//87%/AF030430
 C-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G).//3.00E-37//122aa//72%/Q07803
 C-NT2RM4002213//Homo sapiens protein phosphatase m ethylesterase-1 (PME-1) mRNA, complete cds.//0//2452bp//100%/AF157028
 C-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//3.70E-19//147aa//41%/P40809
 C-NT2RM4002251//ALPHA-1,3-MANNOSYL-GLYCOPROTEIN BETA-1,2-N- ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.101) (N-GLYCOSYL- OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE 1) (GNT- 1) (GLCNAC-T 1).//2.20E-36//320aa//38%/P27808
 C-NT2RM4002323//ANTIGEN GOR (FRAGMENT).//0.00000001//154aa//33%/P48778
 C-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//1.30E-29//275aa//30%/P27095
 C-NT2RM4002438//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//1.10E-49//611bp//70%/AF129131
 C-NT2RM4002460//ENV POLYPROTEIN (COAT POLYPROTEIN) [CONTAINS: COAT PROTEINS GP70, GP20].//0.0000016//226aa//24%/P51515
 C-NT2RM4002527//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.90E-15//366aa//27%/Q00808
 C-NT2RM4002532//PROTEIN HOM1.//2.00E-16//276aa//28%/P55137
 C-NT2RM4002558//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//0//1797bp//99%/AF055899
 C-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//0//1915bp//87%/AF022962
 C-NT2RM4002571//H.sapiens mRNA for UDP-GalNAc:poly peptide N-acetylgalactosaminyl transferase (T2).//4.60E-78//921bp//69%/X85019
 C-NT2RM4002594//MSP1 PROTEIN HOMOLOG.//2.70E-68//236aa//58%/P54815

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C-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNALIGASE) (ASPRS).//2.30E-101//488aa//45%/032038
 C-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//0//1747bp//99%/AB013385
 C-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1652bp//99%/AJ012449
 C-NT2RP1000040//Mus musculus donson protein (Donson) mRNA, partial cds.//5.90E-150//1025bp//82%/AF193608
 C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%/X98834
 C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4.00E-116//296aa//51%/P93471
 C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDF).//4.50E-50//181aa//60%/P51859
 C-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//3.40E-270//951bp//98%/AF011792
 C-NT2RP1000202//ANKYRIN.//1.00E-25//302aa//34%/Q02357
 C-NT2RP1000272//Mus musculus mRNA for neural specific sr protein NSSR 2, complete cds.//1.40E-267//1155bp//87%/AB015895
 C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.30E-275//1249bp//99%/AF053551
 C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.70E-47//155aa//58%/P32447
 C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.70E-15//162aa//30%/P25343
 C-NT2RP1000363//R.norvegicus LL5 mRNA.//7.90E-262//1175bp//83%/X74226
 C-NT2RP1000376//Homo sapiens Ca²⁺-independent phospholipase A2 long isoform (iPLA2) mRNA, complete cds.//0//2252bp//96%/AF102989
 C-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.90E-153//230aa//99%/P55161
 C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCAP-G mRNA, complete cds.//1.80E-94//1019bp//63%/AF111423
 C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN).//2.40E-10//227aa//25%/Q08257
 C-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//3.80E-19//149aa//36%/P17624
 C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.60E-94//254aa//47%/P34580
 C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//

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4. 50E-240//445aa//97%/P09653
 C-NT2RP1000481//Homo sapiens antigen NY-CO-3 (NY-CO-3) mRNA, partial cds.//7.5e-315//1445bp//99%/AF039688
 C-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DBD).//3.60E-30//534aa//23%/P33194
 C-NT2RP1000513//Human NifU-like protein (hNifU) mRNA, partial cds.//6.50E-171//516bp//99%/U47101
 C-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//8.20E-83//345aa//47%/Q61068
 C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.10E-27//193aa//35%/P49020
 C-NT2RP1000574//HOMEODOMAIN PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.50E-75//151aa//94%/P97367
 C-NT2RP1000630//NECDIN.//2.40E-44//227aa//41%/P25233
 C-NT2RP1000677//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER (ORGANIC ANION TRANSPORTING POLYPEPTIDE).//1.20E-78//483aa//31%/P46721
 C-NT2RP1000701//Homo sapiens phospholipase A2 activating protein (PLA2P)mRNA, complete cds.//0//1687bp//99%/AF145020
 C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%/E14379
 C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%/AF101434
 C-NT2RP1000746//Homo sapiens 60S acidic ribosomal protein P0 mRNA, complete cds.//9.70E-196//901bp//99%/AF173378
 C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%/035566
 C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.20E-83//334aa//50%/Q07960
 C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%/AF067223
 C-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.80E-176//829bp//98%/AF047020
 C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANT

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IGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.20E-30//232aa//30%/035566
 C-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//0//1555bp//99%/AF064094
 C-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//5.20E-20//306aa//33%/Q09531
 C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.70E-19//343aa//25%/Q13823
 10 C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.60E-105//504bp//99%/U39317
 C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.40E-23//370aa//28%/Q04652
 C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.40E-19//343aa//25%/Q13823
 C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.50E-236//966bp//99%/M17885
 20 C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.90E-29//554aa//99%/P19338
 C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.20E-78//1529bp//61%/L01790
 C-NT2RP1001013//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.70E-253//425aa//98%/P51522
 C-NT2RP1001033//Homo sapiens delta-tubulin mRNA, complete cds.//2.10E-285//1290bp//100%/AF201333
 C-NT2RP1001073//Homo sapiens U6 snRNA-associated Sm-like protein LSm5 mRNA, complete cds.//8.10E-107//504bp//99%/AF182291
 30 C-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//0//2085bp//99%/U82267
 C-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.30E-116//319aa//46%/Q06218
 C-NT2RP1001113//Homo sapiens CTL2 gene.//0//2790bp//98%/AJ245621
 C-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//5.20E-108//1278bp//69%/U79139
 C-NT2RP1001185//Human isovaleryl-CoA dehydrogenase (IVD) mRNA, complete cds.//1.90E-158//729bp//99%/M34192
 C-NT2RP1001247//Homo sapiens TGF-beta type secreted signaling protein LEFTYA mRNA, complete cds.//0//2006bp//100%/AF081513
 C-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//0//2020bp//99%/AF029914
 50 C-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM

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1. //1.80E-38//258aa//32%/Q12024
 C-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM
 1. //1.80E-38//258aa//32%/Q12024
 C-NT2RP1001310//Homo sapiens mitochondrial carrier
 homolog 1 isoform a mRNA, partial cds; nuclear ge
 ne for mitochondrial product. //0//1732bp//99%/AF1
 76006
 C-NT2RP1001313//Homo sapiens delta-6 fatty acid de
 saturase mRNA, complete cds. //7.50E-121//1394bp//6
 9%/AF126799
 C-NT2RP1001361//Homo sapiens NADH-ubiquinone oxido
 reductase subunit B14.5B homolog mRNA, complete cd
 s. //6.50E-116//541bp//100%/AF070652
 C-NT2RP1001385//HYPOTHETICAL 48.8 KD PROTEIN IN SS
 U81-SCS2 INTERGENIC REGION. //2.70E-22//284aa//25%/
 /P40074
 C-NT2RP1001395//Homo sapiens COP9 complex subunit
 7a mRNA, complete cds. //0//1782bp//99%/AF210052
 C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E
 3.3. //8.90E-141//396aa//67%/P91917
 C-NT2RP1001449//Mus musculus Gng3lg mRNA, complete
 cds. //7.20E-165//800bp//87%/AF069954
 C-NT2RP1001457//Homo sapiens partial mRNA for beta
 -transducin family protein (putative). //1.20E-137/
 /629bp//100%/AJ005257
 C-NT2RP1001482//Mouse oncogene (ect2) mRNA, comple
 te cds. //2.10E-158//755bp//86%/L11316
 C-NT2RP1001494//MALE STERILITY PROTEIN 2. //7.20E-4
 0//261aa//27%/Q08891
 C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE
 (EC 5.5.1.4) (IPS). //1.60E-166//506aa//60%/P42803
 C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANT
 IGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-
 1) (CD151 ANTIGEN). //1.60E-30//232aa//30%/O35566
 C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPT
 OR BETA SUBUNIT (SR-BETA). //5.80E-121//271aa//89%/
 /P47758
 C-NT2RP1001665//CALMODULIN. //0.00000051//83aa//30%
 //P02594
 C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHA
 PERONE PROTEIN) (HSP40). //9.80E-17//79aa//55%/O34
 136
 C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGE
 R PROTEIN HPF2). //2.40E-177//726aa//47%/P51523
 C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1)
 (RSP-1 PROTEIN) (RSP-1). //1.80E-22//184aa//34%/Q0
 1730
 C-NT2RP2000045//Homo sapiens tumorous imaginal dis
 cs protein Tid56 homolog (TID1) mRNA, complete cd
 s. //0//1390bp//98%/AF061749

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C-NT2RP2000054//Homo sapiens putative ring zinc fi
 nger protein NY-REN-43antigen mRNA, complete cds. /
 /0//2245bp//99%/AF155109
 C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSIL
 ON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON). //9.40
 E-16//45aa//100%/P49446
 C-NT2RP2000067//Mus musculus ODZ3 (Odz3) mRNA, par
 tial cds. //0//3546bp//99%/AF195418
 C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR
 10 PRECURSOR (FAT PROTEIN). //3.40E-51//383aa//32%/P3
 3450
 C-NT2RP2000076//Homo sapiens partial mRNA for poly
 homeotic 2 protein (PH2 gene). //7.90E-20//265bp//7
 3%/AJ242730
 C-NT2RP2000114//Homo sapiens mRNA for GM3 synthas
 e, complete cds. //0//2244bp//99%/AB018356
 C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTI
 VATOR SNF2L. //2.50E-117//541aa//42%/P41877
 C-NT2RP2000133//Homo sapiens Leman coiled-coil pro
 20 tein (LCCP) mRNA, complete cds. //0//1490bp//99%/A
 F175966
 C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP4
 7 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI A
 DAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CL
 ATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1
 MEDIUM CHAIN). //4.40E-226//423aa//99%/P35585
 C-NT2RP2000153//GAR2 PROTEIN. //9.80E-23//311aa//28
 %//P41891
 C-NT2RP2000157//ML02 PROTEIN. //2.60E-11//62aa//40%
 30 //Q09329
 C-NT2RP2000161//DIS3 PROTEIN HOMOLOG. //4.10E-35//1
 84aa//44%/Q17632
 C-NT2RP2000183//DIHYDROPYRIMIDINASE RELATED PROTEI
 N-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60). //3.30
 E-16//114aa//44%/O02675
 C-NT2RP2000195//Homo sapiens androgen induced prot
 ein (AIG-1) mRNA, complete cds. //7.80E-152//704bp/
 /99%/AF153605
 C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-
 1). //0.000043//103aa//28%/P35568
 C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N
 -ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC
 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT). //3.4
 0E-21//210aa//33%/P56558
 C-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER YIL
 006W. //9.70E-41//278aa//36%/P40556
 C-NT2RP2000258//ACTIVATOR 1 140 KD SUBUNIT (REPLIC
 ATION FACTOR C LARGE SUBUNIT) (A1 140 KD SUBUNIT)
 (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT)
 50 (DNA-BINDING PROTEIN PO-GA). //7.10E-12//213aa//23%

- //P35251
C-NT2RP2000270//Human putative G-protein coupled receptor (SH120) mRNA, complete cds. //1.30E-242//1043bp//99%/U78723
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I. //1.60E-27//576aa//25%/Q10297
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT). //3.30E-186//256aa//60%/Q99676
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds. //4.30E-279//1193bp//99%/U82381
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3). //2.00E-111//226aa//92%/P08760
C-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds. //0//2331bp//99%/U83981
C-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds. //0//1886bp//99%/L28010
C-NT2RP2000420//ZINC FINGER PROTEIN 165. //8.50E-33//155aa//52%/P49910
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-6-phosphate mutase mRNA, complete cds. //0//1757bp//99%/AF102265
C-NT2RP2000448//KES1 PROTEIN. //8.70E-54//392aa//38%/P35844
C-NT2RP2000523//APOLOPOPROTEIN B mRNA EDITING PROTEIN (HEPR) (APOBEC-1). //6.00E-16//124aa//34%/P41238
C-NT2RP2000660//SAP1 PROTEIN. //5.20E-68//474aa//32%/P39955
C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-). //1.30E-27//349aa//32%/Q01577
C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNALLIGASE) //2.70E-100//488aa//44%/O32038
C-NT2RP2000764//NIFS PROTEIN. //6.60E-36//252aa//42%/P12623
C-NT2RP2000809//Homo sapiens BAG-family molecular chaperone regulator-5mRNA, complete cds. //0//3347bp//99%/AF095195
C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A). //5.60E-08//179aa//29%/Q99104
C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-120). //1.10E-07//96aa//29%/P13466
C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT. //7.90E-08//172aa//28%/P26174
C-NT2RP2000842//Human lysophosphatidic acid receptor or homolog mRNA, complete cds. //0//1562bp//99%/U80811
C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2. //0//694aa//99%/O60841
C-NT2RP2000892//Rattus norvegicus db83 mRNA, complete cds. //2.90E-191//1094bp//85%/AB006135
C-NT2RP2000931//MATRIN 3. //2.40E-289//467aa//95%/P43244
C-NT2RP2000943//Homo sapiens sec24D protein mRNA, complete cds. //0//2767bp//99%/AF130464
C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds. //0//1989bp//96%/AB024704
C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PMP OXIDASE). //5.80E-46//222aa//45%/Q20939
C-NT2RP2001081//SYNAPTOTAGMIN IV. //4.20E-118//430aa//54%/P50232
C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein. //0//2514bp//99%/AJ132440
C-NT2RP2001168//VERPROLIN. //1.50E-09//143aa//33%/P37370
C-NT2RP2001174//CASTRULA ZINC FINGER PROTEIN XLCGF46.1 (FRAGMENT). //6.00E-10//88aa//38%/P18722
C-NT2RP2001233//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //2.00E-128//409aa//45%/Q05481
C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMHC). //2.20E-10//366aa//28%/P14105
C-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (SNAP-ALPHA HOMOLOG) (BRAIN PROTEIN I47) (FRAGMENT). //4.40E-91//179aa//99%/P28663
C-NT2RP2001295//ZINC/CADMIUM RESISTANCE PROTEIN. //8.30E-39//161aa//34%/P20107
C-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN). //5.50E-116//311aa//71%/Q13829
C-NT2RP2001378//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2). //2.00E-11//403aa//25%/Q02817
C-NT2RP2001392//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-). //8.40E-192//581aa//54%/P93647
C-NT2RP2001394//Homo sapiens mRNA for SCML2 protein. //0//2068bp//99%/Y18004
C-NT2RP2001397//Homo sapiens mRNA for cyclin B2, complete cds. //1.9e-316//1428bp//100%/AB020981
C-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds. //9.00E-112//742bp//82%/U76759
C-NT2RP2001440//Homo sapiens mRNA for 14-3-3gamma, complete cds. //0//3712bp//99%/AB024334

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C-NT2RP2001460//TRICHOHYALIN.//1.00E-14//521aa//24
%/P37709
C-NT2RP2001511//Homo sapiens putative RNA-binding
protein Q99 mRNA, complete cds.//3.20E-297//2206bp
//75%/AF093097
C-NT2RP2001520//Homo sapiens mRNA for mitochondria
l carrier protein ARALAR1.//0//2502bp//99%/Y14494
C-NT2RP2001536//Homo sapiens X-ray repair cross-co
mplementing protein 3(XRCC3) mRNA, complete cds.//
0//2326bp//99%/AF035586
C-NT2RP2001560//VAV2 PROTEIN.//0.00000015//219aa//
27%/Q60992
C-NT2RP2001576//HYPOTHETICAL 62.2 KD PROTEIN C4G8.
12C IN CHROMOSOME I.//8.20E-29//294aa//31%/Q09837
C-NT2RP2001597//RYANODINE RECEPTOR, CARDIAC MUSCL
E.//0.000000036//127aa//36%/P30957
C-NT2RP2001601//Homo sapiens SUMO-1-specific prote
ase (SSP1) mRNA, complete cds.//0//1748bp//99%/AF
196304
C-NT2RP2001613//MITOCHONDRIAL IMPORT RECEPTOR SUBU
NIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER ME
MBRANE 40 KD SUBUNIT).//6.10E-12//184aa//31%/P243
91
C-NT2RP2001634//Homo sapiens alpha-catenin-like pr
otein mRNA, complete cds.//0//2445bp//99%/U97067
C-NT2RP2001660//Homo sapiens putative 13 S Golgi t
ransport complex 90kDsubunit brain-specific isofo
r mRNA, complete cds.//0//1287bp//99%/AF058718
C-NT2RP2001663//ENOLASE (EC 4.2.1.11) (2-PHOSPHOGL
YCERATE DEHYDRATASE) (2-PHOSPHO-D- GLYCERATE HYDRO
-LYASE) (FRAGMENT).//1.10E-47//126aa//53%/P42897
C-NT2RP2001740//UBIQUITIN CARBOXYL-TERMINAL HYDROL
ASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE D
UB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-
1) (DEUBIQUITINATING ENZYME 1).//7.90E-52//220aa//
44%/Q61068
C-NT2RP2001748//FARNESYL PYROPHOSPHATE SYNTHETASE
(FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTH
ETASE) (DIMETHYLLALLYLTRANSFERASE (EC 2.5.1.1) / GER
ANYLTRANSTRANSFERASE (EC 2.5.1.10)) (KIAA0032).//
5.40E-47//96aa//97%/P14324
C-NT2RP2001756//ZINC FINGER PROTEIN 84 (ZINC FING
ER PROTEIN HPF2).//1.70E-49//411aa//32%/P51523
C-NT2RP2001839//SCY1 PROTEIN.//5.40E-32//621aa//24
%/P53009
C-NT2RP2001869//ZINC FINGER PROTEIN 191.//7.10E-26
//126aa//52%/O14754
C-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (A
IF-1) (IONIZED CALCIUMBINDING ADAPTER MOLECULE 1).
//1.20E-45//141aa//65%/P55008

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C-NT2RP2001883//Homo sapiens CGI-01 protein mRNA,
complete cds.//0//2306bp//99%/AF132936
C-NT2RP2001898//Human inositol polyphosphate 5-ph
sphatase (5ptase) mRNA, 3' end.//0//2518bp//98%/M
74161
C-NT2RP2001900//ACTIN-LIKE PROTEIN ARP5.//2.30E-38
//395aa//30%/P53946C-NT2RP2001976//Mus musculus c
almodulin-binding protein SHA1 (Shal) mRNA, comple
te cds.//4.70E-177//1538bp//74%/AF062378
10 C-NT2RP2001985//Homo sapiens high-risk human papil
loma viruses E6 oncoproteins targeted protein E6TP
1 alpha mRNA, complete cds.//2.00E-38//435bp//67%
/AF090989
C-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRA
NSPORTER NTT73.//6.50E-129//279aa//85%/Q08469
C-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLEC
ULE PRECURSOR (NR-CAM) (BRAVO).//1.70E-47//247aa//5
2%/P35331
C-NT2RP2002046//Homo sapiens mRNA for transcriptio
n factor.//0//1664bp//99%/AJ130894
C-NT2RP2002058//Homo sapiens WD repeat protein WDR
3 (WDR3) mRNA, complete cds.//0//2510bp//99%/AF08
3217
C-NT2RP2002066//Rattus norvegicus transmembrane re
ceptor Unc5H2 mRNA, complete cds.//1.60E-226//1301
bp//88%/U87306
C-NT2RP2002078//PECANEX PROTEIN.//1.80E-09//195aa/
/32%/P18490
C-NT2RP2002079//HISTONE H1, GONADAL.//4.40E-11//21
4aa//34%/P02256
30 C-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-as
sociated protein.//0//3389bp//99%/AJ007509
C-NT2RP2002105//H. sapiens MSH-R gene for melanocyt
e stimulating hormonereceptor.//0//1644bp//98%/X6
5634
C-NT2RP2002124//UBIQUITIN CARBOXYL-TERMINAL HYDROL
ASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (U
BIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUI
TINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOM
OLOG).//4.30E-44//155aa//37%/Q13107
C-NT2RP2002185//Homo sapiens ubiquilin mRNA, compl
ete cds.//0//1789bp//99%/AF176069
C-NT2RP2002193//Homo sapiens PIAS3 mRNA for protei
n inhibitor of activated STAT3, complete cds.//0/
/2809bp//99%/AB021868
C-NT2RP2002252//Mus musculus (clone pVZmSin3A9) mS
in3A9 mRNA, complete cds.//0//3118bp//91%/L38621
C-NT2RP2002256//Homo sapiens retinoic acid hydroxy
lase mRNA, complete cds.//0//1528bp//98%/AF005418
50 C-NT2RP2002270//AF-9 PROTEIN.//1.20E-07//74aa//36%

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//P42568
 C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.
 n. //0//2333bp//99%/Y16521
 C-NT2RP2002325//Homo sapiens mRNA for Pex11p, complete cds. //8.40E-254//1158bp//99%/AB015594
 C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds. //4.30E-240//1105bp//99%/AF038958
 C-NT2RP2002408//Homo sapiens mRNA for TOLLIP protein. //3.20E-210//1136bp//93%/AJ242972
 C-NT2RP2002442//HESA PROTEIN. //2.80E-14//163aa//30%/P46037
 C-NT2RP2002464//DNA CROSS-LINK REPAIR PROTEIN PS02/SNM1. //6.50E-07//171aa//27%/P30620
 C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds. //0//2180bp//99%/AB005289
 C-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744). //4.60E-144//537aa//49%/Q02386
 C-NT2RP2002520//Homo sapiens transcription factor RFX-B (RFXB) mRNA, complete cds. //3.70E-34//668bp//61%/AF105427
 C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B041 6.5 IN CHROMOSOME X. //6.20E-19//288aa//26%/Q11073
 C-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2). //1.20E-155//562aa//50%/P51523
 C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257). //7.50E-35//181aa//42%/P12815
 C-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds. //9.20E-147//874bp//87%/U19181
 C-NT2RP2002609//2-HYDROXYMUCONIC SEMIALDEHYDE HYDROLASE (EC 3.1.1.-) (HMSH). //2.80E-08//109aa//37%/P19076
 C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-). //1.70E-51//326aa//38%/P55345
 C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F1 2.15C IN CHROMOSOME II. //1.90E-14//210aa//30%/O1345
 C-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1. //4.90E-85//489aa//43%/P55194
 C-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds. //3.50E-74//727bp//72%/AF041107
 C-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds. //9.90E-54//964bp//64%/D89016
 C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN). //8.80E-10//203aa//27%/P29764
 C-NT2RP2002880//GLUCOSE REPRESSION MEDIATOR PROTEIN. //0.000039//206aa//23%/P14922

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C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds. //1.90E-136//623bp//100%/AF038392
 C-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II. //4.10E-87//395aa//40%/Q18964
 C-NT2RP2002939//ZINC FINGER PROTEIN 136. //5.40E-70//282aa//42%/P52737
 C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2). //4.60E-80//147aa//100%/P51669
 C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10. //1.00E-08//98aa//36%/P10129
 C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds. //0//2209bp//99%/AB026190
 C-NT2RP2002993//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135). //0//716aa//91%/P70700
 C-NT2RP2003000//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN). //1.90E-11//132aa//38%/Q13829
 C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds. //2.30E-82//642bp//68%/AF079765
 C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN). //2.40E-38//539aa//25%/Q04652
 C-NT2RP2003137//UBIQUITIN. //0.000026//70aa//30%/P13117
 C-NT2RP2003157//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //1.30E-13//185aa//38%/Q08170
 C-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds. //0//2091bp//99%/D67025
 C-NT2RP2003164//Homo sapiens mRNA for protein kinase. //0//2313bp//99%/AJ132545
 C-NT2RP2003177//Homo sapiens recombination and sister chromatid cohesion protein homolog (hrec8) mRNA, partial cds. //0//1641bp//99%/AF006264
 C-NT2RP2003228//H. sapiens P1-Cdc21 mRNA. //0//2870bp//98%/X74794
 C-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds. //2.60E-186//1551bp//77%/AF023657
 C-NT2RP2003243//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1. //0//1544bp//99%/AJ242978
 C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds. //0//1580bp//99%/AF151811

- C-NT2RP2003272//Homo sapiens ubiquilin mRNA, complete cds. //0//1789bp//99%/AF176069
- C-NT2RP2003277//NAM7 PROTEIN (NONSENSE-MEDIATED mRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1). //1.90E-16//145aa//43%/P30771
- C-NT2RP2003286//PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (EC 6.5.1.4) (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE). //4.20E-88//374aa//47%/Q23400
- C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 methylating protein, complete cds. //0//1526bp//99%/AB006572
- C-NT2RP2003307//KINESIN LIGHT CHAIN (KLC). //2.20E-199//550aa//70%/Q07866
- C-NT2RP2003308//CROOKED NECK PROTEIN. //5.40E-244//622aa//67%/P17886
- C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN. //3.60E-14//332aa//32%/P26337
- C-NT2RP2003347//BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN HOMOLOG. //0.000022//261aa//24%/P48754
- C-NT2RP2003391//Homo sapiens mRNA for nuclear transport receptor. //0//1509bp//99%/AJ133769
- C-NT2RP2003394//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1. //5.50E-13//302aa//26%/P25386
- C-NT2RP2003401//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1). //9.60E-78//346aa//43%/Q61068
- C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT. //5.00E-131//269aa//91%/P38378
- C-NT2RP2003466//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds. //0//2194bp//99%/AF126799
- C-NT2RP2003480//Homo sapiens zinc finger DNA binding protein 99 (ZNF281)mRNA, complete cds. //0//3012bp//99%/AF125158
- C-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR). //5.40E-14//106aa//46%/P04175
- C-NT2RP2003513//Homo sapiens mRNA for paralemmin. //0//2137bp//97%/Y14770
- C-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2)mRNA, complete cds. //0//1746bp//95%/M12783
- C-NT2RP2003522//Homo sapiens zinc finger DNA binding protein 99 (ZNF281)mRNA, complete cds. //0//1764bp//99%/AF125158
- C-NT2RP2003543//HYPOTHETICAL tRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-). //1.70E-17//148aa//34%/P74261
- C-NT2RP2003564//52 KD RO PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //2.10E-59//270aa//46%/P19474
- C-NT2RP2003596//Mus musculus Fas-apoptosis inhibitory molecule (Faim) mRNA, complete cds. //4.80E-82//530bp//85%/AF130367
- C-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNAL1) mRNA, complete cds. //0//2442bp//99%/AF030233
- C-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase. //9.40E-243//1624bp//82%/AJ006215
- C-NT2RP2003702//Homo sapiens 17 beta-hydroxysteroid dehydrogenase type VII (HSD17B7) mRNA, complete cds. //2.1E-313//978bp//99%/AF098786
- C-NT2RP2003704//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L. //1.80E-72//350bp//100%/AJ132637
- C-NT2RP2003713//Homo sapiens ubiquitin-specific protease 3 (USP3) mRNA, complete cds. //0//2018bp//99%/AF073344
- C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //5.40E-29//85aa//72%/Q05481
- C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2). //1.70E-75//147aa//93%/P51669
- C-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP). //0//869aa//80%/P53620
- C-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II. //5.50E-63//253aa//50%/Q09201
- C-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B040 3.2 IN CHROMOSOME X. //3.70E-21//137aa//43%/Q11076
- C-NT2RP2003857//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN). //0.00000016//117aa//29%/Q91955
- C-NT2RP2003871//Homo sapiens transposon-derived Buser1 transposase-like protein gene, complete cds. //0//2807bp//99%/AF205601
- C-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1). //6.10E-183//387aa//87%/P51954
- C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B). //1.50E-23//200aa//30%/Q09175
- C-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8. //1.40E-16//664aa//20%/P39702
- C-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). //2.30E-53//141aa

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a//78%/P20290
 C-NT2RP2004041//SYNAPSINS IA AND IB.//0.0000074//
 159aa//32%/P17599
 C-NT2RP2004066//Mus musculus Msx2 interacting nucl
 ear target protein mRNA, complete cds.//2.70E-288/
 /1994bp//81%/AF156529
 C-NT2RP2004098//ADENYLATE CYCLASE (EC 4.6.1.1) (AT
 P PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//5.40E-3
 0//319aa//31%/Q01513
 C-NT2RP2004170//Homo sapiens mRNA for transducin 10
 (beta) like 1 protein.//1.10E-138//1236bp//74%/Y1
 2781
 C-NT2RP2004187//ZINC FINGER PROTEIN 38 (ZFP-38) (C
 TF1N51) (TRANSCRIPTIONFACTOR RU49).//5.60E-31//424
 aa//28%/Q07231
 C-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15
 mRNA, complete cds.//3.80E-52//397bp//82%/AF0039
 98
 C-NT2RP2004232//Homo sapiens EPK2 mRNA for serine/
 threonine kinase, complete cds.//0//2272bp//99%/A 20
 B015982
 C-NT2RP2004239//Homo sapiens lok mRNA for protein
 kinase, complete cds.//0//3044bp//99%/AB015718
 C-NT2RP2004242//NEUROFILAMENT TRIPLET H PROTEIN (2
 00 KD NEUROFILAMENT PROTEIN) (NF-H).//9.90E-12//42
 7aa//26%/P19246
 C-NT2RP2004245//Mus musculus pantothenate kinase 1
 beta (panK1beta) mRNA, complete cd
 s.//6.40E-117//1122bp//72
 %//AF200357 30
 C-NT2RP2004270//PROTEIN P
 TM1 PRECURSOR.//1.40E-16/
 /334aa//24%/P32857
 C-NT2RP2004366//VACUOLAR
 PROTEIN SORTING-ASSOCIATE
 D PROTEIN VPS13.//1.30E-5
 1//505aa//29%/Q07878
 C-NT2RP2004389//PROBABLE
 MITOCHONDRIAL 40S RIBOSOM
 AL PROTEIN S9 PRECURSOR. / 40
 /9.30E-15//126aa//39%/P3
 8120
 C-NT2RP2004392//MNN4 PROT
 EIN.//1.40E-11//143aa//27
 %//P36044
 C-NT2RP2004396//Homo sapi
 ens mRNA for activator of
 . S phase Kinase, complete
 cds.//5.40E-243//1108bp/
 /99%/AB028069

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C-NT2RP2004425//Mus muscu
 lus axotrophin mRNA, comp
 lete cds.//0//2321bp//86%
 //AF155739
 C-NT2RP2004476//Homo sapi
 ens cyclin L ania-6a mRN
 A, complete cds.//0//2075
 bp//99%/AF180920
 C-NT2RP2004538//Mus muscu
 lus kinesin-like protein
 KIF1B (Kif1b) mRNA, compl
 ete cds.//0//1387bp//86%/
 /AF090190
 C-NT2RP2004568//PUTATIVE
 ATP-DEPENDENT RNA HELICAS
 E C30D11.03.//3.00E-117//
 625aa//40%/Q09903
 C-NT2RP2004587//NEUROFILA
 MENT TRIPLET M PROTEIN (1
 60 KD NEUROFILAMENT PROTE
 IN) (NF-M).//7.30E-07//35
 2aa//23%/P07197
 C-NT2RP2004655//Homo sapi
 ens mRNA for leucine rich
 protein.//8.50E-233//106
 1bp//99%/AJ006291
 C-NT2RP2004681//NEUROFILA
 MENT TRIPLET H PROTEIN (2
 00 KD NEUROFILAMENT PROTE
 IN) (NF-H).//2.60E-07//42
 6aa//23%/P19246 30
 C-NT2RP2004689//HYPOTHETI
 CAL 192.5 KD PROTEIN C6G
 9.10C IN CHROMOSOME I.//
 5.60E-64//616aa//33%/Q92
 355
 C-NT2RP2004710//Mus muscu
 lus formin binding protei
 n 30 mRNA, complete cds. /
 /1.50E-280//1464bp//85%//
 U40750
 C-NT2RP2004732//NEUROFILA
 MENT TRIPLET M PROTEIN (1
 60 KD NEUROFILAMENT PROTE
 IN) (NF-M).//7.30E-07//35
 2aa//23%/P07197
 C-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NR
 K1 (EC 2.7.1.-) (N-RICH KINASE 1).//1.30E-26//190a
 a//41%/P38692
 50 C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, C

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YTOPLASMIC (EC 6.1.1.4) (LEUCINE-- TRNA LIGASE) (L EURS). //9.50E-73//153aa//59%/Q10490
 C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCI NYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA). //3.70E -135//414aa//62%/P53588
 C-NT2RP2004816//H58 PROTEIN. //9.00E-173//327aa//98 %//P40336
 C-NT2RP2004920//TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETEROCHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38PROTEI N). //4.20E-09//804aa//22%/Q61687
 C-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds. //0//2103bp//99%/AB007144
 C-NT2RP2004959//P54 PROTEIN PRECURSOR. //0.00000095 //297aa//20%/P13692
 C-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1(KS1) mRNA, complete cds. //1. 00E-228//1666bp//75%/U56732
 C-NT2RP2004978//ACTIN-LIKE PROTEIN ARP8. //3.30E-47 //353aa//30%/Q12386
 C-NT2RP2005003//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //1.80E-99//376 aa//43%/P19474
 C-NT2RP2005012//Homo sapiens mRNA for SEC63 protei n. //0//1693bp//99%/AJ011779
 C-NT2RP2005037//ANTI-SILENCING PROTEIN 1. //3.30E-4 7//155aa//59%/P32447
 C-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL ADDITION ENZYME) (TERMINAL DEO XYNUCLEOTIDYLTRANSFERASE) (TERMINAL TRANSFERASE). // 4.00E-91//218aa//44%/Q92089
 C-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION IN ITIATION FACTOR 3 ALPHA SUBUNIT (EIF-3 ALPHA). //2. 00E-173//273aa//57%/P34466
 C-NT2RP2005126//H.sapiens mRNA for RNA helicase (M yc-regulated dead boxprotein). //0//2388bp//98%/X9 8743
 C-NT2RP2005139//2-5A-DEPENDENT RIBONUCLEASE (EC 3. 1.26.-) (2-5A-DEPENDENT RNAASE) (RNAASE L) (RIBONUC LEASE 4) (FRAGMENT). //0.00000022//139aa//35%/Q05 921
 C-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, completecds. //0.00E-01//1437bp//98%/ AF045583
 C-NT2RP2005162//Homo sapiens aspartyl aminopeptida se mRNA, complete cds. //0//1615bp//99%/AF005050
 C-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-as sociated protein. //0//2769bp//98%/AJ007509
 C-NT2RP2005204//Homo sapiens SUMO-1-activating enz

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yme E1 N subunit (SUA1) mRNA, complete cds. //0//12 62bp//99%/AF090385
 C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifS) mRNA, completecds. //0//2087bp//99%/AF09702 5
 C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA syn thetase 3, complete cds. //0//2122bp//99%/D89053
 C-NT2RP2005288//Homo sapiens RCC1-like G exchangin g factor RLG mRNA, complete cds. //0//2992bp//99%/ AF060219
 C-NT2RP2005315//Homo sapiens meningioma-expressed antigen 5 (MEA5) mRNA, partial cds. //1.90E-170//780 bp//100%/AF036144
 C-NT2RP2005325//Homo sapiens LIM-homeodomain prote in HLEX2 (LHX2) mRNA, complete cds. //0//1643bp//99% //AF124735
 C-NT2RP2005336//TRICHOHYALIN. //5.40E-10//545aa//22 %//P37709
 C-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPA SE 5 (EC 3.6.1.38). //2.10E-124//636aa//38%/P32660
 C-NT2RP2005358//Homo sapiens methyl-CpG binding do main-containing protein MBD3 (MBD3) mRNA, complete cds. //0//2199bp//99%/AF072247
 C-NT2RP2005360//Homo sapiens sentrin/SUMO-specific protease (SENPI) mRNA, complete cds. //1.30E-52//7 53bp//67%/AF149770
 C-NT2RP2005393//AUTOANTIGEN NGP-1. //7.20E-39//224a a//35%/Q13823
 C-NT2RP2005407//OXYSTEROL-BINDING PROTEIN. //5.30E- 63//410aa//40%/P22059
 C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-R ICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //1.20E-13/ /185aa//38%/Q08170
 C-NT2RP2005441//Homo sapiens hypothalamus protein HT002 mRNA, complete cds. //4.10E-202//962bp//98%/ AF113540
 C-NT2RP2005457//Homo sapiens NADH-ubiquinone oxido reductase subunit B14.5B homolog mRNA, complete cd s. //1.20E-130//608bp//99%/AF070652
 C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM 2. //3.00E-44//252aa//41%/P38127
 C-NT2RP2005476//Human p190-B (p190-B) mRNA, comple te cds. //3.40E-108//668bp//88%/U17032
 C-NT2RP2005490//Mus musculus D3Mm3e (D3Mm3e) mRNA, complete cds. //1.80E-175//1102bp//83%/AF053628
 C-NT2RP2005491//PARAMYOSIN (PMY) (ANTIGEN B). //0.0 0000015//279aa//26%/P35418
 C-NT2RP2005496//ZINC FINGER PROTEIN 135. //2.90E-14 6//398aa//59%/P52742
 C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD RE

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CULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55). //5.20E-81//166aa//88%/P36876

C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds. //0//1825bp//99%/AF151803

C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds. //0//3994bp//99%/AF092563

C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds. //2.40E-304//1687bp//85%/AF035526

C-NT2RP2005531//PROTEIN 4.1 (BAND 4.1) (P4.1). //5.50E-70//393aa//39%/P11171

C-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP). //0//1560bp//98%/AJ012449

C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE). //2.00E-20//181aa//36%/Q39366

C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds. //1.00E-46//576bp//70%/AF062529

C-NT2RP2005605//QUEUINE TRNA-RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME). //8.20E-23//164aa//28%/032053

C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds. //8.9E-313//1455bp//98%/AF062085

C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1). //1.00E-11//128aa//36%/P47623

C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1). //1.20E-13//74aa//45%/P56101

C-NT2RP2005669//Homo sapiens death effector domain-containing testicular molecule mRNA, complete cds. //1.60E-248//1129bp//99%/AF043733

C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds. //4.40E-200//908bp//99%/AF089814

C-NT2RP2005694//X-LINKED RETINITIS PIGMENTOSA GTPASE REGULATOR. //2.60E-10//175aa//27%/Q92834

C-NT2RP2005701//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN). //3.00E-63//323aa//39%/Q62158

C-NT2RP2005712//Homo sapiens myosin X (MYO10) mRNA, partial cds. //0//2681bp//99%/AF132022

C-NT2RP2005719//GPI-ANCHORED PROTEIN P137. //4.00E-14//99aa//43%/Q14444

C-NT2RP2005722//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds. //0//2545bp//99%/AB011414

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C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODP1 PROTEIN). //3.00E-09//169aa//28%/P38074

C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds. //0//1968bp//99%/AF068868

C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds. //0//1966bp//99%/AF082516

10 C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A). //1.70E-61//374aa//38%/P47943

C-NT2RP2005767//G.gallus PB1 gene. //5.00E-163//1158bp//81%/X90849

C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2) mRNA, complete cds. //2.70E-180//656bp//99%/AF151351

C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP). //2.10E-213//249aa//85%/Q02038

C-NT2RP2005776//POLY(A) POLYMERASE TYPE 2 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE). //4.40E-55//358aa//42%/P51005

C-NT2RP2005784//Homo sapiens ubiquitin-conjugating enzyme variant Kua (UBE2V) mRNA, complete cds. //0//2191bp//92%/AF155120

C-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION. //2.30E-39//318aa//31%/P40004

C-NT2RP2005835//SHP1 PROTEIN. //1.80E-28//208aa//32%/P34223

C-NT2RP2005841//Homo sapiens mRNA for ALEX3, complete cds. //3.50E-52//1091bp//59%/AB039669

C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57). //5.00E-11//155aa//34%/P48837

C-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE). //1.50E-67//388aa//44%/P25500

40 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //1.50E-13//185aa//38%/Q08170

C-NT2RP2006071//Homo sapiens adaptor protein APPL mRNA, complete cds. //5.80E-120//1257bp//64%/AF169797

C-NT2RP2006219//H.sapiens mRNA for DGCR6 protein. //1.10E-214//1026bp//97%/X96484

C-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds. //0//1669bp//88%/U49055

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C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAINLC1].//2.00E-59//388aa//32%/P46821

C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, c complete cds.//2.80E-274//1236bp//99%/AF035262

C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEBOX PROTEIN (RATHKE POUCH HOMEBOX).//3.40E-07//50aa//50%/Q61658

C-NT2RP2006456//Homo sapiens leucine-rich glioma-inactivated protein precursor (LGI1) mRNA, complete cds.//1.30E-37//484bp//65%/AF055636

C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%/AJ006266

C-NT2RP2006534//5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN (EC 2.7.1.-) (AMPK ALPHA-1 CHAIN) (FRAGMENT).//3.20E-11//32aa//96%/Q13131

C-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//3.10E-272//1220bp//95%/AF038966

C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.20E-134//486aa//50%/P24461

C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%/P09543

C-NT2RP2006598//Homo sapiens retinoid x receptor interacting protein mRNA, complete cds.//3.10E-295//1193bp//99%/AF113538

C-NT2RP3000031//HISTONE DEACETYLASE HDA1.//1.10E-71//350aa//42%/P53973

C-NT2RP3000046//MITOCHONDRIAL GTPASE MSS1 PRECURSOR.//4.60E-78//421aa//37%/P32559

C-NT2RP3000047//NPL4 PROTEIN.//1.10E-85//526aa//36%/P33755

C-NT2RP3000050//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.20E-150//490aa//53%/Q05481

C-NT2RP3000068//SON OF SEVENLESS PROTEIN HOMOLOG 1 (SOS-1) (MSOS-1).//2.20E-06//165aa//27%/Q62245

C-NT2RP3000085//ACETYL-/PROPIONYL-COENZYME A CARBOXYLASE ALPHA CHAIN [CONTAINS: BIOTIN CARBOXYLASE (EC 6.3.4.14); BIOTIN CARBOXYL CARRIER PROTEIN (BCP)].//1.90E-123//436aa//50%/P46401

C-NT2RP3000109//P54 PROTEIN PRECURSOR.//0.0000065//358aa//22%/P13692

C-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//2.90E-11//721aa//23%/P08640

C-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN

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N).//9.30E-84//453aa//42%/Q04652

C-NT2RP3000252//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2388bp//99%/AF120334

C-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//0//2730bp//82%/D29766

C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//100%/AJ242978

C-NT2RP3000333//Rattus norvegicus db83 mRNA, complete cds.//2.90E-191//1094bp//85%/AB006135

C-NT2RP3000341//Homo sapiens mitochondrial inner membrane preprotein translocase Tim17a mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.50E-246//1124bp//99%/AF106622

C-NT2RP3000350//Homo sapiens GTP-binding protein NGB mRNA, complete cds.//0//2392bp//99%/AF120334

C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2.00E-111//226aa//92%/P08760

C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%/AB019219

C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.10E-107//206aa//99%/P35293

C-NT2RP3000393//Rattus norvegicus DNA-binding protein PREB (Preb) mRNA, complete cds.//5.80E-266//1373bp//86%/AF061817

C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOXPROTEIN 13)//1.70E-139//679aa//41%/O43143

C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%/AF071185

C-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-CRPE INTERGENIC REGION.//2.90E-15//319aa//26%/P37908

C-NT2RP3000441//Homo sapiens squamous cell carcinoma antigen recognized by T cell (SART-2) mRNA, complete cds.//3.40E-42//645bp//67%/AF098066

C-NT2RP3000512//Human HOX2C mRNA from the Hox2 locus.//0//1934bp//99%/X16667

C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.80E-28//536aa//27%/P28160

C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.90E-12//192aa//30%/P15151

C-NT2RP3000562//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//2165bp//99%/AF093097

C-NT2RP3000578//HES1 PROTEIN.//1.30E-22//229aa//27%/P35843

4437

C-NT2RP3000590//UVS-2 PROTEIN.//1.30E-22//458aa//24%/P33288
 C-NT2RP3000596//TRICHOHYALIN.//2.50E-17//304aa//28%/Q07283
 C-NT2RP3000603//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.70E-11//90aa//42%/Q13562
 C-NT2RP3000605//Mus musculus mRNA for wizL, complete cds.//0//2232bp//82%/AB012265
 C-NT2RP3000624//Rattus norvegicus mRNA for SECIS binding protein 2 (sbp2gene).//5.80E-234//1562bp//81%/AJ251245
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.00E-140//499aa//46%/P51523
 C-NT2RP3000739//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//1.40E-24//155aa//37%/Q10149
 C-NT2RP3000742//1-PHOSPHATIDYLYNOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT).//4.10E-165//371aa//49%/P10895
 C-NT2RP3000753//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.00E-10//565aa//24%/P12036
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7.00E-28//176aa//34%/Q94650
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.50E-36//417aa//31%/Q61982
 C-NT2RP3000826//Homo sapiens mRNA for seven transmembrane protein TM7SF3, complete cds.//0//2522bp//99%/AB032470
 C-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//8.30E-108//331aa//50%/P27448
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.90E-69//1611bp//61%/U53445
 C-NT2RP3000869//Drosophila melanogaster AAA family protein Bor (bor) mRNA, complete cds.//2.60E-138//1673bp//67%/AF227209
 C-NT2RP3000875//MEVALONATE KINASE (EC 2.7.1.36) (MK).//7.70E-87//175aa//98%/Q03426
 C-NT2RP3000917//DHP1 PROTEIN.//1.00E-193//428aa//55%/P40848
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.70E-185//585bp//88%/AF015264
 C-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//1.90E-46//73aa//98%/P39027C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159

4438

C-NT2RP3001055//Drosophila melanogaster separation anxiety protein (san)mRNA, complete cds.//3.80E-38//462bp//70%/AF225902
 C-NT2RP3001057//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//9.00E-201//584aa//54%/Q05481
 C-NT2RP3001081//Homo sapiens RCC1-like G exchangein g factor RLG mRNA, complete cds.//7.10E-47//537bp//74%/AF060219
 C-NT2RP3001096//Rattus norvegicus leprecan (lepre1) mRNA, complete cds.//1.70E-94//787bp//66%/AF087433
 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3.00E-44//260aa//40%/P55201
 C-NT2RP3001111//Homo sapiens TRF-proximal protein mRNA, complete cds.//1.50E-149//731bp//97%/AF097725
 C-NT2RP3001113//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//2.90E-11//631aa//23%/P25386
 C-NT2RP3001120//ZINC FINGER PROTEIN 136.//7.80E-170//512aa//58%/P52737
 C-NT2RP3001140//F-SPONDIN PRECURSOR.//9.90E-238//419aa//96%/P35446
 C-NT2RP3001150//TRANSCRIPTION TERMINATION FACTOR RHO.//0.00000031//207aa//29%/P52154
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MADI-SCY1 INTERGENIC REGION.//1.70E-10//196aa//27%/P53154
 C-NT2RP3001216//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.0000023//137aa//33%/P35663
 C-NT2RP3001221//GAMMA-BUTYROBETAINE, 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAINE HYDROXYLASE).//1.90E-31//353aa//30%/P80193
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.20E-166//395aa//51%/P14873
 C-NT2RP3001253//NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//1.70E-10//540aa//23%/P32380
 C-NT2RP3001268//Homo sapiens zinc finger protein ZNF228 (ZNF228) mRNA, complete cds.//0//3606bp//99%/AF198358
 C-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//1.30E-99//669bp//83%/Y18101
 C-NT2RP3001307//Gallus gallus RPE65 mRNA, complete cds.//4.20E-29//530bp//63%/AB017594
 C-NT2RP3001338//ZINC FINGER PROTEIN 81 (FRAGMENT).

4439

//2.40E-16//175aa//28%/P51508
 C-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN P
 RECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICAR
 BOXYLATE CARRIER PROTEIN).//3.60E-25//129aa//34%/P
 32089
 C-NT2RP3001383//Mus musculus ARL-6 interacting pro
 tein-6 (Aip-6) mRNA, partial cds.//3.40E-40//355bp
 //79%/AF133913
 C-NT2RP3001384//Homo sapiens mRNA for LA95 protei
 n.//0//1214bp//99%/AJ243467
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//
 1.30E-61//374aa//36%/P49711
 C-NT2RP3001399//SSU72 PROTEIN.//1.30E-16//84aa//52
 %//P53538
 C-NT2RP3001407//SCY1 PROTEIN.//0.00000033//143aa//
 25%/P53009
 C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1.00E-16
 //77aa//46%/033529
 C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//
 2.70E-10//159aa//33%/009053
 C-NT2RP3001428//NUCLEOPROTEIN TPR.//1.40E-128//152
 aa//99%/P12270
 C-NT2RP3001453//ANTIGEN PEPTIDE TRANSPORTER 2 (APT
 2) (HISTOCOMPATIBILITYANTIGEN MODIFIER 2).//3.20E-
 90//157aa//59%/P36371
 C-NT2RP3001457//Drosophila melanogaster Melted (me
 lt) mRNA, partial cds.//4.60E-20//792bp//59%/AF20
 5831
 C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.
 //9.10E-13//87aa//43%/P11632
 C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRN
 A, complete cds.//0//1475bp//99%/U13395
 C-NT2RP3001497//Homo sapiens multiple membrane spa
 nning receptor TRC8 (TRC8) mRNA, complete cds.//0/
 //2295bp//99%/AF064801
 C-NT2RP3001527//Human Sp140 protein (Sp140) mRNA,
 complete cds.//4.30E-290//793bp//93%/U63420
 C-NT2RP3001529//SP00B-ASSOCIATED GTP-BINDING PROTE
 IN.//1.00E-61//345aa//42%/P20964
 C-NT2RP3001538//HYPOTHETICAL 39.0 KD PROTEIN T28D
 9.3 IN CHROMOSOME II.//9.10E-10//158aa//31%/Q1002
 2
 C-NT2RP3001554//MICROTUBULE-ASSOCIATED PROTEIN 1B
 [CONTAINS: LIGHT CHAINLC1].//1.40E-76//388aa//32%/P
 46821
 C-NT2RP3001580//Mus musculus strain C57BL/J germ c
 ell-less protein (Gcl)mRNA, complete cds.//0//1730
 bp//85%/AF163665
 C-NT2RP3001587//Human anthracycline-associated res
 istance ARX mRNA, complete cds.//0//2617bp//99%/U

4440

35832
 C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.
 80E-18//91aa//38%/Q92609
 C-NT2RP3001646//WD-40 REPEAT PROTEIN MSI2.//8.80E-
 09//132aa//31%/022468
 C-NT2RP3001671//Homo sapiens mRNA for NS1-binding
 protein (NS1-BP).//0//1557bp//98%/AJ012449
 C-NT2RP3001672//Homo sapiens Sex comb on midleg ho
 molog 1 isoform 2 (SCMH1) mRNA, complete cds.//0//
 2836bp//99%/AF149046
 C-NT2RP3001679//Homo sapiens rec mRNA, complete cd
 s.//0//2495bp//99%/AB023584
 C-NT2RP3001688//Homo sapiens DNA binding protein p
 96PIF mRNA, complete cds.//0//1869bp//99%/AF17386
 8
 C-NT2RP3001690//INTRACELLULAR PROTEIN TRANSPORT PR
 OTEIN US01.//0.00000024//481aa//21%/P25386
 C-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECU
 RSOR.//3.40E-33//161aa//32%/P54356
 C-NT2RP3001712//Homo sapiens HP1-BP74 protein mRN
 A, complete cds.//0//1788bp//99%/AF113534
 C-NT2RP3001723//Homo sapiens cell recognition mole
 cule Caspr2 (CASPR2) mRNA, complete cds.//1.40E-58
 //1138bp//63%/AF193613
 C-NT2RP3001724//Homo sapiens chromodomain-helicase
 -DNA-binding protein mRNA, complete cds.//1.10E-24
 0//902bp//99%/AF054177
 C-NT2RP3001727//Rattus norvegicus implantation-ass
 ociated protein (IAG2)mRNA, partial cds.//6.90E-13
 2//774bp//88%/AF008554
 C-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//7.10
 E-132//294aa//84%/Q14141
 C-NT2RP3001739//HYPOTHETICAL 72.5 KD PROTEIN C2F7.
 10 IN CHROMOSOME I.//1.40E-15//190aa//32%/Q09701
 C-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPR
 OTEIN M (HNRNP M).//1.80E-117//462aa//55%/P52272
 C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCL
 E.//1.60E-11//348aa//27%/P24733
 C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEI
 N).//7.40E-18//249aa//30%/Q04652
 C-NT2RP3001854//Homo sapiens novel retinal pigment
 epithelial cell protein (NORPEG) mRNA, complete c
 ds.//0//2742bp//99%/AF155135
 C-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX
 PROTEIN PREP-1).//8.10E-125//302aa//60%/P55347
 C-NT2RP3001857//VEGETATIBLE INCOMPATIBILITY PROTEI
 N HET-E-1.//1.20E-14//242aa//24%/Q00808
 C-NT2RP3001898//Homo sapiens mRNA for UDP-N-acetyl
 glucosamine: alpha-1,3-D-mannoside beta-1,4-N-acet
 ylglucosaminyltransferase IV, complete cds.//0//15

4441

87bp//100%/AB000624
 C-NT2RP3001931//Rattus norvegicus clone C48 CDK5 a
 ctivator-binding protein mRNA, complete cds.//4.30
 E-91//656bp//81%/AF177478
 C-NT2RP3001938//SPORULATION-SPECIFIC PROTEIN 1 (EC
 2.7.1.-).//1.30E-22//227aa//33%/P08458
 C-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C1
 0.5 IN CHROMOSOME III.//3.10E-92//314aa//51%/Q092
 51
 C-NT2RP3001969//TRICHOHYALIN.//2.70E-11//442aa//23 10
 %//P37709
 C-NT2RP3002004//H.sapiens mRNA for FAST kinase.//
 1.50E-192//475bp//94%/X86779
 C-NT2RP3002007//SAP1 PROTEIN.//1.10E-68//474aa//32
 %//P39955
 C-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C09F
 5.2 IN CHROMOSOME III.//5.30E-25//139aa//48%/Q092
 32
 C-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY
 PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD CO 20
 ATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR H
 A2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.00E-299//397aa
 //94%/P18484
 C-NT2RP3002056//RETINOBLASTOMA BINDING PROTEIN 1
 (RBBP-1).//2.00E-48//475aa//35%/P29374
 C-NT2RP3002062//Homo sapiens BAG-family molecular
 chaperone regulator-5mRNA, complete cds.//0//3764b
 p//99%/AF095195
 C-NT2RP3002081//Xenopus laevis chromosome condensa
 tion protein XCAP-G mRNA, complete cds.//4.10E-233 30
 //1896bp//69%/AF111423
 C-NT2RP3002108//DEC1 PROTEIN (MDM20 PROTEIN).//7.9
 0E-09//181aa//22%/Q12387
 C-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1
 HOMOLOG (GTP-BINDINGPROTEIN GST1-HS).//2.80E-253/
 //474aa//93%/P15170
 C-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN
 HCNGP.//1.90E-151//223aa//91%/Q02614
 C-NT2RP3002273//SCD6 PROTEIN.//1.30E-09//295aa//28
 %//P45978
 C-NT2RP3002303//PROBABLE UNDECAPRENYL PYROPHOSPHAT
 E SYNTHETASE (EC 2.5.1.31) (UPP SYNTHETASE) (DI-TR
 ANS-POLY-CIS-DECAPRENYLCISTRANSFERASE).//8.60E-49/
 //243aa//43%/Q58767
 C-NT2RP3002330//Homo sapiens eRFS mRNA, complete c
 ds.//0//2443bp//99%/U87791
 C-NT2RP3002351//Human mRNA for NAD-dependent methy
 lene tetrahydrofolatedehydrogenase cyclohydrolase
 (EC 1.5.1.15).//4.20E-70//590bp//76%/X16396
 C-NT2RP3002399//DNA REPLICATION LICENSING FACTOR M 50

4442

CM4 (CDC21 HOMOLOG) (P1-CDC21).//8.60E-79//416aa//
 34%/P33991
 C-NT2RP3002501//THREONINE DEHYDRATASE CATABOLIC (E
 C 4.2.1.16) (THREONINEDEAMINASE).//3.70E-43//318aa
 //37%/P05792
 C-NT2RP3002529//VACUOLAR PROTEIN SORTING-ASSOCIATE
 D PROTEIN VPS45.//8.90E-95//542aa//38%/P38932
 C-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C
 3.4 IN CHROMOSOME III.//5.80E-40//161aa//52%/Q100
 10
 C-NT2RP3002602//PROBABLE PROTEIN DISULFIDE ISOMERA
 SE ER-60 PRECURSOR (EC5.3.4.1) (ERP60) (58 KD MICR
 OSOMAL PROTEIN) (P58) (HIP-70) (Q-2).//2.90E-19//1
 73aa//28%/P11598
 C-NT2RP3002628//PROBABLE PROTEIN DISULFIDE ISOMERA
 SE P5 PRECURSOR (EC 5.3.4.1).//2.50E-26//90aa//42%
 //P38660
 C-NT2RP3002631//Homo sapiens Ran binding protein 1
 1 mRNA, complete cds.//0//1703bp//99%/AF111109
 C-NT2RP3002650//Mus musculus growth suppressor 1L
 (Gros1) mRNA, completecds.//0//2109bp//87%/AF1651
 63
 C-NT2RP3002663//Homo sapiens putative glycolipid t
 ransfer protein mRNA,complete cds.//8.10E-263//124
 3bp//97%/AF103731
 C-NT2RP3002671//ELONGATION FACTOR 2 (EF-2).//2.50E
 -73//179aa//36%/P13060
 C-NT2RP3002682//Homo sapi
 ens CGI-145 protein mRNA,
 complete cds.//0//1596bp
 //98%/AF151903
 C-NT2RP3002688//Mouse mRN
 A for kinesin-like protei
 n (Kif1b), complete cds.//
 //1.10E-93//1205bp//69%/D
 17577
 C-NT2RP3002770//MYELOID D
 IFFERENTIATION PRIMARY RE
 SPONSE PROTEIN MYD116.//
 1.00E-07//70aa//41%/P175
 64
 C-NT2RP3002785//LETHAL (2)
 DENTICLELESS PROTEIN (DTL
 83 PROTEIN).//2.50E-55//1
 87aa//39%/Q24371
 C-NT2RP3002810//HISTIDINE
 -RICH PROTEIN KE4.//2.20E
 -10//260aa//26%/Q31125
 C-NT2RP3002818//INSERTION
 ELEMENT IS2A HYPOTHETICA

4443

4444

- L 48.2 KD PROTEIN. //5.70E-226//303aa//97%//P51026
 C-NT2RP3002869//Mus musculus semaphorin V1a mRNA, complete cds. //2.50E-232//1282bp//85%//AF030430
 C-NT2RP3002876//Drosophila melanogaster eyelid (elid) mRNA, complete cds. //1.30E-29//805bp//61%//AF053091
 C-NT2RP3002909//P53-BINDING PROTEIN 2 (53BP2) (BCL2-BINDING PROTEIN) (BBP). //1.50E-125//512aa//47%//Q13625
 C-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN). //2.00E-111//551aa//42%//Q04652
 C-NT2RP3002953//Homo sapiens protocadherin beta 5 (PCDH-beta5) mRNA, complete cds. //0//2388bp//99%//AF152498
 C-NT2RP3002969//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds. //0//2722bp//99%//D89053
 C-NT2RP3002972//Halocynthia roretzi mRNA for HrPET-1, complete cds. //3.90E-52//899bp//64%//AB029333
 C-NT2RP3002988//Homo sapiens Ikb kinase-b (IKK-beta) mRNA, complete cds. //1.80E-292//1325bp//99%//AF080158
 C-NT2RP3003032//Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds. //0//2656bp//99%//AF084555
 C-NT2RP3003059//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds. //3.80E-152//1007bp//82%//U78090
 C-NT2RP3003061//ANKYRIN. //1.40E-20//200aa//37%//Q02357
 C-NT2RP3003071//NEUROGENIC PROTEIN BIG BRAIN. //1.10E-05//258aa//24%//P23645
 C-NT2RP3003078//Rattus norvegicus mRNA for ischemia related factor NYW-1, complete cds. //2.60E-112// 50 633bp//88%//AB027149
 C-NT2RP3003101//Mouse mRNA for tetracycline transporter-like protein, complete cds. //3.60E-83//807bp//72%//D88315
 C-NT2RP3003133//Homo sapiens ZK1 mRNA for Kruppel-type zinc finger protein, complete cds. //0//1998bp//91%//AB011414
 C-NT2RP3003138//Homo sapiens kinesin superfamily motor KIF4 mRNA, complete cds. //0//2159bp//98%//AF071592
 C-NT2RP3003145//Mus musculus metallopeptidase CPX-1 mRNA, complete cds. //0//2251bp//81%//AF077738
 C-NT2RP3003185//TROPOMYOSIN 1, FUSION PROTEIN 33. //2.80E-06//402aa//23%//P49455
 C-NT2RP3003193//ZINC FINGER PROTEIN 135. //7.30E-98//269aa//62%//P52742
 C-NT2RP3003197//HYPOTHETICAL 33.8 KD PROTEIN C5H1 0.01 IN CHROMOSOME I. //5.70E-09//169aa//31%//Q0967 20 4
 C-NT2RP3003203//Rattus norvegicus golgi stacking protein homolog GRASP55mRNA, complete cds. //2.00E-210//1851bp//76%//AF110267
 C-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAP1C) mRNA, complete cds. //4.30E-187//1750bp//75%//U20286
 C-NT2RP3003230//Homo sapiens mRNA for hCRNN4, complete cds. //0//2350bp//99%//AB030656
 C-NT2RP3003242//Homo sapiens stanniocalcin-related 30 protein mRNA, complete cds. //0//2366bp//99%//AF098462
 C-NT2RP3003251//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //4.20E-86//366aa//48%//P19474
 C-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds. //0//2596bp//98%//L36983
 C-NT2RP3003290//Mus musculus mRNA for Ndr1 related protein Ndr3, complete cds. //1.5e-310//1468bp//82%//AB033922
 C-NT2RP3003301//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-). //1.10E-170//585aa//54%//064948
 C-NT2RP3003313//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP80 mRNA A, complete cds. //0//2476bp//99%//AF117657
 C-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (R052). //1.30E-35//178aa//44%//Q62191
 C-NT2RP3003353//HYPOTHETICAL 26.2 KD PROTEIN IN GD 50 I1-COX15 INTERGENIC REGION. //2.80E-07//161aa//28%//

4445

/P40084

C-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//0//2133bp//85%/U09874

C-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//9.20E-45//782bp//65%/U90653

C-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//6.30E-270//743bp//90%/AF071317

C-NT2RP3003490//Homo sapiens mRNA for putative phospholipase, complete cds.//4.50E-81//649bp//67%/AB019435

C-NT2RP3003491//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//5.60E-36//842bp//62%/AF091624

C-NT2RP3003500//SCY1 PROTEIN.//9.20E-27//601aa//23%/P53009

C-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//4.50E-30//191aa//40%/P40529

C-NT2RP3003589//Homo sapiens ras-related GTP-binding protein mRNA, complete cds.//0//3131bp//94%/AF106681

C-NT2RP3003659//HES1 PROTEIN.//5.90E-22//229aa//27%/P35843

C-NT2RP3003665//Homo sapiens mRNA for beta-ureidopropionase, complete cds.//0//1690bp//99%/AB013885

C-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7).//2.20E-13//146aa//42%/P14209

C-NT2RP3003701//F-SPONDIN PRECURSOR.//1.80E-17//324aa//26%/P35446

C-NT2RP3003716//SLIT PROTEIN PRECURSOR.//6.60E-10//150aa//34%/P24014

C-NT2RP3003726//Homo sapiens spermatogenesis associated PD1 mRNA, complete cds.//0//2568bp//99%/U28164

C-NT2RP3003799//Rattus norvegicus Srg1 (Sytr1) mRNA, complete cds.//9.00E-238//1529bp//84%/U71294

C-NT2RP3003800//Rattus norvegicus tyrosine protein kinase pp60-c-src mRNA, complete cds.//1.90E-163//924bp//89%/AF130457

C-NT2RP3003809//SAV PROTEIN.//1.10E-131//576aa//41%/Q07590

C-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP).//9.60E-19//174aa//31%/P02720

C-NT2RP3003831//Homo sapiens ENDOGL-1 (alias ENGL-a) mRNA for endonuclease G-like protein-1, complete cds.//2.2e-316//1436bp//99%/AB020523

C-NT2RP3003846//Homo sapiens mRNA for putative pho

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spholipase, complete cds.//4.80E-277//1255bp//99%/AB019435

C-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//4.50E-147//874bp//87%/U19181

C-NT2RP3003914//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//2.20E-20//76aa//64%/Q09332

C-NT2RP3003918//Homo sapiens VAMP-associated protein B (VAP-B) mRNA, complete cds.//0//2191bp//99%/AF086628

C-NT2RP3004013//M. musculus Spnr mRNA for RNA binding protein.//6.50E-240//1215bp//94%/X84692

C-NT2RP3004016//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.50E-17//226aa//26%/Q13263

C-NT2RP3004078//H. sapiens HRFX2 mRNA.//0//1806bp//99%/X76091

C-NT2RP3004125//Mus musculus zinc finger protein splice variant FIZ1-B (Fiz1) mRNA, complete cds.//4.60E-229//1560bp//78%/AF126747

C-NT2RP3004148//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//7.90E-05//271aa//22%/P08640

C-NT2RP3004155//Homo sapiens COQ7 protein mRNA, complete cds.//1.10E-179//823bp//100%/AF098948

C-NT2RP3004189//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%/Q00808

C-NT2RP3004206//CROOKED NECK PROTEIN.//1.40E-220//567aa//67%/P17886

C-NT2RP3004207//Homo sapiens mRNA for type I transmembrane receptor (psk-1 gene).//0//2445bp//100%/AJ245820

C-NT2RP3004209//Homo sapiens ubiquitin processing protease (Ubp-M) mRNA, complete cds.//0//2320bp//99%/AF126736

C-NT2RP3004242//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//4.70E-13//118aa//33%/P52734

C-NT2RP3004258//Homo sapiens ZIS1 mRNA, complete cds.//0//1861bp//99%/AF065391

C-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//2.40E-248//1126bp//100%/AF088982

C-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//5.10E-24//597bp//61%/AF007871

C-NT2RP3004348//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.10E-185//1130bp//82%/X67877

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C-NT2RP3004378//Drosophila melanogaster separation anxiety protein (san)mRNA, complete cds.//3.90E-38//462bp//70%/AF225902

C-NT2RP3004424//Homo sapiens mRNA for stromal antigen 3 (STAG3 gene).//1.00E-66//364bp//93%/AJ007798

C-NT2RP3004428//CHROMODOMAIN HELICASE-DNA-BINDING PROTEIN 4 (CHD-4) (MI-2 AUTOANTIGEN 218 KD PROTEIN) (MI-2-BETA).//5.20E-09//212aa//25%/Q14839

C-NT2RP3004472//GERM CELL-LESS PROTEIN.//1.60E-61//170aa//40%/Q01820

C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATE D PROTEIN VPS35.//3.30E-113//466aa//42%/P34110

C-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//4.00E-303//1385bp//99%/AB012851

C-NT2RP3004498//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//2.00E-249//1777bp//80%/U83176

C-NT2RP3004504//M.musculus mRNA for CPEB protein.//1.90E-295//893bp//92%/Y08260

C-NT2RP3004507//MOB1 PROTEIN (MPS1 BINDER 1).//3.70E-37//190aa//39%/P40484

C-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//0//2075bp//87%/L11316

C-NT2RP3004544//THYROID RECEPTOR INTERACTING PROTEIN 10 (TRIP10) (FRAGMENT).//1.00E-22//1.3aa//53%/Q15642

C-NT2RP3004566//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.20E-95//434aa//43%/P51523

C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//3.80E-08//150aa//28%/Q01484

C-NT2RP3004572//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds.//0//1853bp//99%/AF040701

C-NT2RP3004578//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//5.50E-12//396aa//23%/P39922

C-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//0//1807bp//99%/AJ006266

C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.20E-75//464aa//35%/Q02084

C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds.//0//3972bp//98%/AF093097

C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.70E-72//254aa//45%/P54352

C-NT2RP3004670//Homo sapiens GN6ST mRNA for N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds.//0//2393bp//99%/AB014679

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C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//2.60E-98//239aa//64%/P35526

C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.90E-51//335aa//37%/Q64375

C-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//2160bp//99%/AJ012449

C-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds.//0//2161bp//99%/AB011538

C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%/Q10568

C-NT2RP4000129//Xenopus laevis F-box protein 28 (Fbx28) mRNA, partial cds.//1.40E-28//296bp//75%/AF176667

C-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//4.30E-188//1543bp//78%/U35776

C-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.00E-71//396aa//36%/P22579

20 C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.90E-15//104aa//40%/P15287

C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%/AJ006470

C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.70E-84//208aa//76%/Q03173

C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.50E-29//153aa//43%/O23968

C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I.//3.50E-297//1024aa//55%/P87115

C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//1.50E-26//237aa//28%/Q01631

C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//3.00E-07//101aa//32%/P26372

C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%/AF044195

40 C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.60E-77//262aa//54%/O75570

C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%/AJ238243

C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.90E-110//435aa//50%/P52738

C-NT2RP4000415//Drosophila melanogaster fumble (fumble) mRNA, complete cds.//6.20E-19//902bp//57%/AF221546

50 C-NT2RP4000417//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2

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-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT). //2.60E-51//438aa//33%/P45701
 C-NT2RP4000449//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds. //0//3143bp//99%/AF083106
 C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO. //3.00E-07//175aa//27%/P09309
 C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15). //2.50E-37//291aa//38%/P50101
 C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4). //1.90E-67//721aa//29%/Q09475
 C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1). //8.80E-50//214aa//50%/P40484
 C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1. //1.50E-106//495aa//45%/P45818
 C-NT2RP4000524//Mus musculus Sec8 mRNA, complete cds. //0//3131bp//87%/AF022962
 C-NT2RP4000528//NPLA PROTEIN. //9.80E-86//515aa//37%/P33755
 C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN). //7.40E-14//233aa//31%/P40319
 C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds. //2.90E-188//863bp//99%/AF067730
 C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO. //3.70E-07//175aa//27%/P09309
 C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPSE. //1.10E-32//350aa//30%/P39625
 C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X. //1.10E-13//295aa//27%/Q11073
 C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN. //3.20E-191//199aa//78%/P10267
 C-NT2RP4000737//Mus musculus F-box protein FBL10 mRNA, partial cds. //4.60E-250//1462bp//84%/AF176524
 C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CP T1-SPC98 INTERGENIC REGION. //0.00000032//67aa//31%/P53915
 C-NT2RP4000817//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //9.80E-11//503aa//23%/P08640
 C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1. //4.30E-94//810bp//65%/Y18265
 C-NT2RP4000839//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //8.50E-21//271aa//28%/Q00808
 C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (AR

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GINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B). //5.70E-82//324aa//48%/Q09175
 C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT). //4.10E-85//174aa//55%/P16415
 C-NT2RP4000878//MYELOID UPREGULATED PROTEIN. //6.20E-91//173aa//87%/Q35682
 C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN). //9.60E-96//513aa//42%/P22314
 C-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds. //0//2127bp//86%/D45913
 C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN). //2.60E-26//227aa//36%/Q06828
 C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1). //1.50E-76//346aa//43%/Q61068
 C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein. //0//2487bp//99%/Y16521
 C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505. //1.40E-07//185aa//25%/Q58900
 C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). //1.40E-26//90aa//42%/P38660
 C-NT2RP4000979//Homo sapiens putative HIV-1 infection related protein mRNA, partial cds. //2.30E-81//389bp//100%/AF094583
 C-NT2RP4000989//UNC-47 PROTEIN. //8.20E-06//173aa//25%/P34579
 C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135). //0//838aa//87%/P70700
 C-NT2RP4001004//VACUOLAR PROTEIN 8. //3.70E-16//401aa//26%/P39968
 C-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds. //3.50E-257//1377bp//91%/U67140
 C-NT2RP4001029//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds. //0//2002bp//98%/AF198487
 C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) //1.50E-92//443aa//44%/Q09996
 C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65. //6.70E-51//335aa//37%/Q64375
 C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (COLGIC2+-ATPASE). //1.30E-123//563aa//

- 46%/P13586
C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439bp//99%/AB023967
C-NT2RP4001086//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//2.30E-07//474aa//22%/P12036
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.60E-17//121aa//36%/P51400
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.90E-115//224aa//100%/P38378
C-NT2RP4001122//TIPD PROTEIN.//1.40E-65//253aa//41%/O15736
C-NT2RP4001126//TRICHOHYALIN.//2.90E-18//380aa//26%/Q07283
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLA SE (EC 3.5.1.18) (SDAP).//2.10E-07//93aa//33%/P44514
C-NT2RP4001148//SOF1 PROTEIN.//1.30E-104//236aa//52%/P33750
C-NT2RP4001149//Homo sapiens cleft lip and palate transmembrane protein1 (CLPTM1) mRNA, complete cds.//4.40E-187//731bp//100%/AF037339
C-NT2RP4001150//NC-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NR-CAM) (BRAVO).//3.40E-29//385aa//29%/P35331
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//4.70E-29//227aa//35%/P52178
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.//4.40E-104//1460bp//65%/U95760
C-NT2RP4001207//Homo sapiens Ran binding protein 1 mRNA, complete cds.//0//2940bp//99%/AF111109
C-NT2RP4001213//ZINC FINGER PROTEIN 184 (FRAGMENT).//5.70E-141//511aa//43%/Q99676
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%/P38660
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.80E-103//508aa//43%/Q04652
C-NT2RP4001256//Homo sapiens mRNA for gamma tubulin ring complex protein(76p gene).//0//2006bp//100%/AJ249677
C-NT2RP4001260//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//0//1866bp//100%/AF174601
C-NT2RP4001274//Human transporter protein (gl7) mRNA, complete cds.//4.40E-58//1196bp//61%/U49082
C-NT2RP4001276//TRICHOHYALIN.//7.90E-09//126aa//32
%/Q07283
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.90E-17//296aa//29%/P24391
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.50E-213//1129bp//92%/AJ001119
C-NT2RP4001336//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN.//0.000016//186aa//29%/O24076
C-NT2RP4001339//Homo sapiens mRNA for AMMERCI protein.//9.20E-160//736bp//99%/AJ007014
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%/AB017494
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//1.40E-58//2425bp//59%/U53445
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREC PROTEIN).//1.60E-19//222aa//30%/Q08180
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.20E-17//146aa//35%/P18160
C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOME I.//2.00E-53//436aa//30%/Q10085
C-NT2RP4001389//KES1 PROTEIN.//1.70E-31//342aa//34%/P35844
C-NT2RP4001407//TRICHOHYALIN.//1.90E-05//298aa//21%/P22793
C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.70E-190//422aa//82%/Q14141
C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.20E-138//419aa//54%/Q99676
C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.70E-66//738bp//71%/AF129131
C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78%/Q02218
C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1.00E-27//374aa//29%/P39010
C-NT2RP4001529//Homo sapiens transcription factor LBP-1b (LBP-1) mRNA, complete cds.//0//2002bp//98%/AF198487
C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NO T1/CDC39-HMR INTERGENIC REGION.//5.70E-54//242aa//38%/P25656

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C-NT2RP4001551//Homo sapiens chromatin-specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds. //0//3202bp//99%/AF152961
 C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-). //4.70E-09//216aa//24%/P96902
 C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN N. //5.40E-07//213aa//26%/Q02453
 C-NT2RP4001568//ZINC FINGER PROTEIN GCS1. //1.80E-10//109aa//36%/P35197
 C-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP). //0//874aa//96%/P53620
 C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein. //0//1087bp//87%/AJ223830
 C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNALIGASE) (ILERS). //1.70E-14//373aa//47%/P73505
 C-NT2RP4001634//CENTROMERIC PROTEIN E (CENP-E PROTEIN). //2.80E-14//652aa//22%/Q02224
 C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN M ET18/MMS19. //5.10E-46//234aa//32%/P40469
 C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK). //6.40E-19//111aa//45%/P25323
 C-NT2RP4001656//VACUOLAR BIOGENESIS PROTEIN END1 (PEP5 PROTEIN). //1.10E-45//310aa//27%/P12868
 C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT). //4.00E-10//243aa//25%/Q10568
 C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT. //3.00E-10//128aa//32%/Q10282
 C-NT2RP4001730//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT). //6.40E-170//1168aa//33%/Q09332
 C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2). //3.90E-236//665aa//58%/P51523
 C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN). //4.10E-16//263aa//27%/P98174
 C-NT2RP4001790//Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds. //0//3053bp//99%/AF170025
 C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). //1.20E-30//241aa//30%/Q35566
 C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4. //1.10E-19//77aa//54%/P55083
 C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complete cds. //6.30E-99//555bp//73%/AF155595
 C-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1. //1.40E-85//489aa//43%/P55194

4454

C-NT2RP4001861//TRICHOHYALIN. //1.00E-35//307aa//34%/P37709
 C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //1.40E-08//345aa//25%/Q00808
 C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM 1. //1.30E-38//258aa//32%/Q12024
 C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF. //9.80E-60//303aa//38%/P49711
 C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PINT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE). //1.50E-13//211aa//28%/Q43209
 C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR. //1.20E-13//356aa//27%/P13816
 C-NT2RP4001966//Mus musculus ODZ3 (Odz3) mRNA, partial cds. //0//3203bp//87%/AF195418
 C-NT2RP4001975//Homo sapiens golgi membrane protein GP73 mRNA, complete cds. //0//3024bp//99%/AF23605
 C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN). //6.90E-24//370aa//27%/Q04652
 C-NT2RP4002047//GTP-BINDING PROTEIN LEPA. //1.50E-168//601aa//52%/Q067618
 C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOXPROTEIN 13) //1.00E-137//679aa//40%/Q43143
 C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //3.00E-150//722aa//39%/Q05481
 C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNIT S) (TFIIA-42) (TFIIAL). //6.70E-06//250aa//31%/P52655
 C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-). //1.50E-63//159aa//53%/P38938
 C-NT2RP4002791//NUCLEOPROTEIN TPR. //6.50E-05//659aa//23%/P12270
 C-NT2RP5003461//RLR1 PROTEIN. //9.70E-22//177aa//27%/P53552
 C-NT2RP5003477//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1. //5.50E-15//280aa//27%/Q00808
 C-NT2RP5003500//Mus musculus mRNA for heparan sulfate 6-sulfotransferase2, complete cds. //1.30E-237//820bp//87%/AB024565
 C-NT2RP5003506//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds. //0//2289bp//99%/AF095448
 C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR). //3.30E-23//219aa//40%/P37116

4455

C-OVARC1000001//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//7.00E-217//683bp//99%//AB029290

C-OVARC1000006//HISTONE H2A.1.//1.10E-55//117aa//99%//P02262

C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//4.20E-06//102aa//32%//014727

C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.60E-295//1393bp//97%//AF058922

C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.27.1) (RNASE LE).//3.20E-07//60aa//45%//P80022

C-OVARC1000071//Homo sapiens NTF2-related export protein NXT1 (NXT1) mRNA, complete cds.//1.50E-47//727bp//67%//AF156957

C-OVARC1000085//Human mRNA for proteasome subunit HC5.//1.00E-151//699bp//100%//D00761

C-OVARC1000087//HISTONE MACRO-H2A.1.//1.60E-12//174aa//26%//Q02874

C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF).//8.40E-14//259aa//30%//P51610

C-OVARC1000106//TROPOMYOSIN 1, FUSION PROTEIN 33.//0.000032//165aa//27%//P49455

C-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//2.70E-12//120aa//32%//Q13107

C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Sp1.//2.50E-95//461bp//98%//AJ242975

C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.80E-32//511bp//65%//AF068332

C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA).//8.20E-120//351aa//54%//Q16665

C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III) (AMINOPEPTIDASE YSCI).//5.40E-53//384aa//30%//P14904

C-OVARC1000304//PROTEIN MOV-10.//1.10E-249//519aa//87%//P23249

C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.70E-40//154aa//38%//P29363

C-OVARC1000326//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//9.20E-148//787bp//76%//U19614

4456

C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.90E-14//200aa//27%//P40004

C-OVARC1000437//TENSIN.//7.90E-181//340aa//84%//Q04205

C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.20E-25//227aa//25%//P11075

C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.10E-10//125aa//35%//P51452

C-OVARC1000479//Rattus norvegicus mRNA for TIP120, complete cds.//0//1872bp//89%//D87671

C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.20E-157//892bp//91%//AF051850

C-OVARC1000556//RIBOSOMAL PROTEIN S6 KINASE II ALPHA 2 (EC 2.7.1.-) (S6KII-ALPHA 2) (P90-RSK 2) (RIBOSOMAL S6 KINASE 3) (RSK3) (PP90RSK3).//3.30E-67//132aa//95%//Q15349

C-OVARC1000564//Homo sapiens sorting nexin 5 (SNX5) mRNA, complete cds.//1.0E-310//1440bp//98%//AF121855

C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%//D43772

C-OVARC1000679//Homo sapiens myosin-IXa mRNA, complete cds.//0//808bp//99%//AF117888

C-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.10E-209//293aa//95%//P39098

C-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//0//759bp//98%//AF038661

C-OVARC1000746//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000017//78aa//48%//P25159

C-OVARC1000751//PROBABLE PROTEIN PHOSPHATASE 2C T2 3F11.1 (EC 3.1.3.16) (PP2C).//5.60E-11//74aa//37%//P49596

C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.10E-46//121aa//79%//P08886C-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (75 KD GLUCOSEREGULATED PROTEIN) (GRP 75).//3.90E-46//78aa//98%//035501

C-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//2.80E-258//1183bp//99%//Y17711

C-OVARC1000846//NUCLEOLIN (PROTEIN C23).//0.0000097//109aa//30%//P08199

C-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//0//2095bp//99%//AF045584

4457

C-OVARC1000862//*M. musculus* mRNA for FT1. //5.90E-22
6//1498bp//81%/Z67963
C-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1). //2.2
0E-50//206aa//52%/P40484
C-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-). //1.30E-32//170aa//34%/P37440
C-OVARC1000915//*Homo sapiens* histone deacetylase 5
mRNA, complete cds. //1.60E-121//591bp//97%/AF132
608
C-OVARC1000936//COAT PROTEIN GP37 (ENV PROTEIN GP3 10
7). //0.0000054//135aa//28%/P03398
C-OVARC1000937//S-PHASE ENTRY CYCLIN 6. //4.90E-10/
/61aap//49%/P32943
C-OVARC1000945//*Rattus norvegicus* mRNA for atypica
l PKC specific bindingprotein, complete cds. //0//1
961bp//82%/AB005549
C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933. //1.20
E-17//127aa//33%/Q58343
C-OVARC1000999//ANKYRIN HOMOLOG PRECURSOR. //4.10E-
11//189aa//32%/Q06527
C-OVARC1001034//*Mus musculus* Fn54 mRNA, partial cd
s. //1.50E-178//1113bp//86%/AF001533
C-OVARC1001038//*Homo sapiens* mRNA for Ariadne-2 pr
oteIn. //0//1172bp//97%/AJ130978
C-OVARC1001051//EPIDERMAL GROWTH FACTOR RECEPTOR S
UBSTRATE SUBSTRATE 15(PROTEIN EPS15) (AF-1P PROTEI
N). //1.10E-08//216aa//23%/P42566
C-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECUR
SOR. //1.90E-35//76aa//98%/P43490
C-OVARC1001065//*Homo sapiens* CGI-12 protein mRNA,
complete cds. //1.00E-215//1027bp//98%/AF132946
C-OVARC1001068//*Homo sapiens* Era GTPase A protein
(HERA-A) mRNA, partialcds. //0//1819bp//99%/AF0826
57
C-OVARC1001092//*Homo sapiens* mRNA for JM5 protein,
complete CDS (clone IMAGE 53337, LLNLc110F1857Q7
(RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)). //2.00E-214//769bp//97%/AJ005897
C-OVARC1001107//*Homo sapiens* protein methyltransfe
rase (JBP1) mRNA, complete cds. //6.10E-276//594bp/
/98%/AF167572
C-OVARC1001113//*Homo sapiens* diaphanous 1 (HDIA1)
mRNA, complete cds. //5.1e-310//1588bp//93%/AF0517
82
C-OVARC1001154//*Homo sapiens* clone 24720 epithelin
1 and 2 mRNA, complete cds. //2.30E-296//1561bp//9
3%/AF055008
C-OVARC1001171//*Homo sapiens* translation initiatio
n factor 3 47 kDa subunit mRNA, complete cds. //5.7
0E-151//436bp//92%/U94855

4458

C-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2. //1.10
E-11//221aa//25%/P48510
C-OVARC1001200//*Mus musculus* mRNA for HS1 binding
protein 3. //5.80E-88//658bp//80%/AJ132192
C-OVARC1001232//CLEAVAGE AND POLYADENYLATION SPECI
FICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNI
T). //5.10E-22//83aa//37%/Q10568
C-OVARC1001244//*H. sapiens* mRNA for *Drosophila* fema
le sterile homeotic (FSH) homologue. //0//1467bp//9
9%/X62083
C-OVARC1001271//NUCLEOLAR TRANSCRIPTION FACTOR 1
(UPSTREAM BINDING FACTOR 1) (UBF-1). //0.0000014//2
24aa//26%/P25976
C-OVARC1001306//N-MYC PROTO-ONCOGENE PROTEIN. //0.0
0000073//247aa//27%/P18444
C-OVARC1001342//40S RIBOSOMAL PROTEIN S8. //1.40E-1
10//207aa//99%/P09058C-OVARC1001372//*Homo sapiens*
liprin-alpha4 mRNA, partial cds. //2.00E-252//1146
bp//99%/AF034801
20 C-OVARC1001381//*Homo sapiens* mRNA for candidate tu
mor suppressor involved in B-CLL. //6.00E-148//683b
p//99%/AJ224819
C-OVARC1001417//*Homo sapiens* thyroid hormone recep
tor-associated proteincomplex component TRAP170 mR
NA, complete cds. //0//1715bp//99%/AF135802
C-OVARC1001419//*Homo sapiens* GOK (STIM1) mRNA, com
plete cds. //4.90E-48//586bp//69%/U52426
C-OVARC1001436//ENL PROTEIN. //0.00000009//81aa//39
%/Q03111
30 C-OVARC1001476//*Mus musculus* YGR163w mRNA homology
e, complete cds. //1.80E-187//510bp//89%/AB017616
C-OVARC1001496//*Homo sapiens* C-terminal binding pr
oteIn 2 mRNA, completecds. //0//1876bp//98%/AF0165
07
C-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DO
MINANT POLYCYSTIC KIDNEY DISEASE PROTEIN 1). //0//7
77aa//91%/P98161
C-OVARC1001555//NGG1-INTERACTING FACTOR 3. //4.40E-
19//130aa//40%/P53081
40 C-OVARC1001577//*Homo sapiens* SRp46 splicing factor
transcribed retroseudogene. //0//1167bp//100%/AF
031165
C-OVARC1001610//*Homo sapiens* choline/ethanolaminep
hosphotransferase (CEPT1) mRNA, complete cds. //0//
1870bp//99%/AF068302
C-OVARC1001703//*Mus musculus* ARL-6 interacting pro
tein-2 (Aip-2) mRNA, complete cds. //3.50E-16//399b
p//61%/AF133670
C-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PRO
TEIN 1B) (SPR1B) (SPR1B). //2.80E-10//106aa//38%/Q

62267

C-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//4.40E-40//195aa//41%/P07106

C-OVARC1001726//APICAL-LIKE PROTEIN (APXL PROTEIN).//4.30E-16//116aa//43%/Q13796

C-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, FIBROBLAST ISOFORM F2.//4.00E-122//282aa//85%/P08942

C-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1).//6.40E-85//514aa//34%/P12945

C-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//0//963bp//99%/U97670

C-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//2.70E-190//1624bp//76%/AF068748

C-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1).//3.10E-81//497aa//35%/P12945

C-OVARC1001943//Mus musculus DEB-91 mRNA, complete cds.//0//2035bp//87%/AF143859

C-OVARC1001987//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds.//0//1083bp//99%/AF203687

C-OVARC1002050//Homo sapiens mRNA for actin binding protein ABP620, complete cds.//0//1019bp//99%/AB029290

C-OVARC1002112//HISTONE MACRO-H2A.1.//3.00E-174//371aa//90%/Q02874

C-OVARC1002127//SODIUM-INDEPENDENT ORGANIC ANION TRANSPORTER 2 (BRAIN DIGOXIN CARRIER PROTEIN) (BRAIN-SPECIFIC ORGANIC ANION TRANSPORTER) (OATP-B1).//5.40E-52//306aa//35%/O35913

C-OVARC1002138//SAP1 PROTEIN.//7.60E-60//128aa//59%/P39955

C-OVARC1002156//Danio rerio uridine kinase mRNA, complete cds.//6.00E-16//262bp//64%/AF195851

C-OVARC1002165//3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 2 (EC 1.3.99.5) (STEROID 5-ALPHA-REDUCTASE 2) (SR TYPE 2).//7.60E-08//114aa//37%/P31213

C-OVARC1002182//BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN) (BTRCP).//1.70E-09//207aa//30%/Q91854

C-PLACE1000004//Homo sapiens IDN3-B mRNA, complete cds.//0//2365bp//99%/AB019602

C-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.60E-81//212aa//70

%//P34547

C-PLACE1000040//TRANSFORMING PROTEIN P21/K-RAS 2B.//1.40E-17//185aa//32%/P08643

C-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//7.90E-54//190bp//94%/L22154

C-PLACE1000066//SSU72 PROTEIN.//1.10E-39//206aa//43%/P53538

C-PLACE1000081//Human SEC7 homolog Tic (TIC) mRNA, complete cds.//0//2077bp//99%/U63127

10 C-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3).//1.80E-62//158aa//81%/P20290

C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CROTONASE).//2.80E-29//134aa//43%/P52046

C-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.30E-305//1417bp//98%/AF058291

20 C-PLACE1000185//Homo sapiens mRNA for N-Acetylglucosamine kinase.//4.90E-258//1183bp//99%/AJ242910

C-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%/P08640

C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99%/AJ224979

C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.70E-30//352aa//31%/P15151

30 C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.20E-132//334aa//72%/P23246

C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//2.80E-06//134aa//29%/P53368

C-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//2041bp//87%/U35245

C-PLACE1000547//Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB) mRNA, complete cds.//3.70E-241//1124bp//98%/AF135421

40 C-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.60E-47//207aa//46%/P51522

C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINENUCLEOTIDE-BINDING PROTEIN 1).//1.60E-270//437aa//86%/P32455

C-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//0//1540bp//99%/AJ012449

C-PLACE1000610//MSN5 PROTEIN.//0.0000026//136aa//26%/P52918

50 C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.00E-55//779bp//6

4461

4462

7%/AF044201

C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.20E-3
9//261aa//27%/Q08891C-PLACE1000653//Homo sapiens N-acetylglucosamine-p
hosphate mutase mRNA, complete cds.//0//1992bp//99%
//AF180371C-PLACE1000656//Homo sapiens mRNA for JM4 protein,
complete CDS (clone IMAGE 546750 and LLNLc110F185
7Q7 (RZPD Berlin)).//2.10E-27//1260bp//99%/AJ005
896C-PLACE1000706//Homo sapiens transcriptional inter
mediary factor 1 gamma mRNA, complete cds.//0//1366
bp//99%/AF119043C-PLACE1000755//Homo sapiens mRNA for Helicase-MO
I, complete cds.//4.60E-250//1189bp//97%/AB028449C-PLACE1000769//Homo sapiens CGI-18 protein mRNA,
complete cds.//0//1985bp//98%/AF132952C-PLACE1000786//PUTATIVE RHO/RAC GUANINE NUCLEOTID
E EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYS
PLASIA PROTEIN HOMOLOG).//7.10E-09//59aa//47%/P527
34C-PLACE1000793//NEUROGENIC PROTEIN BIG BRAIN.//1.7
0E-07//251aa//24%/P23645C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOM
AL PROTEIN YHR148W.//2.50E-49//181aa//54%/P32899C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN
AKR1.//2.60E-19//404aa//26%/P39010C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//
4.40E-22//129aa//35%/Q03070C-PLACE1000979//ZINC FINGER PROTEIN 135.//2.50E-15
3//326aa//64%/P52742C-PLACE1000987//Rattus norvegicus late gestation 1
ung 2 protein (Lgl2) mRNA, complete cds.//5.90E-27
8//1476bp//92%/AF110195C-PLACE1001036//Homo sapiens mRNA for alpha integr
in binding protein 63, partial.//0//1988bp//99%/AJ
131721C-PLACE1001054//Homo sapiens mRNA for RuvB-like DN
A helicase TIP49b, complete cds.//4.00E-300//1355b
p//100%/AB024301C-PLACE1001062//Homo sapiens mRNA for lysine-ketog
lutarate reductase/saccharopine dehydrogenase, par
tial CDS.//1.60E-207//742bp//99%/AJ007714C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA,
complete cds.//0//1500bp//99%/AF065485C-PLACE1001104//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZI
PPER PROTEIN) (MYOSINII).//6.80E-18//529aa//23%/Q
99323C-PLACE1001118//ZINC FINGER PROTEIN 135.//5.40E-14
7//443aa//57%/P52742C-PLACE1001171//MYOTUBULARIN.//7.10E-84//198aa//73
%/Q13496C-PLACE1001238//Mouse mRNA for RNA polymerase I as
sociated factor (PAF53), complete cds.//2.00E-202/
/1333bp//80%/D14336C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEI
N).//4.30E-54//257aa//46%/Q04652C-PLACE1001294//Mus musculus XY body protein (Xyb
p) mRNA, complete cds.//6.20E-223//1092bp//78%/AF
120207C-PLACE1001304//Homo sapiens C2H2 (Kruppel-type) z
inc finger protein mRNA, complete cds.//0//2145bp/
/99%/AF159567C-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA,
complete cds.//5.90E-228//827bp//99%/AF009615C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTO
SIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3.00E-
33//138aa//42%/Q61103C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR K
INASE SUBSTRATE EPS8.//2.30E-61//132aa//46%/Q1292
9C-PLACE1001517//Homo sapiens gene for glycosylphos
phatidylinositol anchor attachment 1 (GPAA1), comp
lete cds.//4.60E-112//392bp//87%/AB002137C-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//
5.70E-130//244aa//99%/Q60809C-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGE
R PROTEIN HPF2).//1.40E-118//429aa//48%/P51523C-PLACE1001672//PROBABLE AMINOTRANSFERASE TO1B11.2
(EC 2.6.1.-).//4.30E-66//174aa//45%/P91408C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOEST
ERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE I
I).//4.00E-81//263aa//56%/P08635C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICAS
E PL10.//3.50E-75//439aa//41%/P16381C-PLACE1001748//Homo sapiens metalloprotease 1 (MP
1) mRNA, complete cds.//0//2602bp//99%/AF061243C-PLACE1001771//Homo sapiens mRNA for transient re
ceptor potential protein TRP6.//0//2900bp//99%/AJ
006276C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.
4.2.8) (PMM).//5.40E-63//427aa//35%/Q57290C-PLACE1001817//Homo sapiens ATP-specific succinyl
-CoA synthetase beta subunit (SCS) mRNA, partial c
ds.//0//1995bp//99%/AF058953C-PLACE1001845//Mus musculus cyclin ania-6a mRNA,
complete cds.//3.30E-31//925bp//62%/AF159159C-PLACE1001869//L-RIBULOXINASE (EC 2.7.1.16).//2.0
0E-27//270aa//31%/P94524

50 C-PLACE1001920//Homo sapiens WDC-3.13 isoform 2 mR

4463

NA, complete cds.//0//1729bp//99%/AF099935
 C-PLACE1001983//HYPOTHETICAL 46.4 KD PROTEIN IN FF
 H-GRPE INTERGENIC REGION.//7.50E-16//319aa//26%/P
 37908
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.
 40E-78//496aa//37%/Q49091
 C-PLACE1002046//LIGATIN (FRAGMENT).//1.70E-240//56
 0aa//80%/Q61211
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (AT
 P PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//5.30E-0 10
 7//188aa//29%/P49606
 C-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD
 PROTEIN (SRP72).//6.50E-58//112aa//100%/076094
 C-PLACE1002140//Rattus norvegicus apelin mRNA, com
 plete cds.//1.40E-43//425bp//74%/AF179679
 C-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN S
 WI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTIO
 N FACTOR TYE2).//0.00005//179aa//23%/P32591
 C-PLACE1002395//Mus musculus mRNA for UBE-1c1, UBE
 -1c2, UBE-1c3, complete cds.//7.90E-100//966bp//75 20
 %//AB030505
 C-PLACE1002433//CHROMOSOME ASSEMBLY PROTEIN XCAP-
 E.//5.10E-05//278aa//24%/P50533
 C-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER
 1.//4.50E-76//180aa//83%/P41233
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PRO
 TEIN).//4.20E-06//133aa//29%/Q13105
 C-PLACE1002450//Human zinc finger protein mRNA, co
 mplete cds.//0//2565bp//99%/U69274
 C-PLACE1002474//Mus musculus matrilin-2 precursor 30
 mRNA, complete cds.//0//2092bp//84%/U69262
 C-PLACE1002493//Homo sapiens signal transducing ad
 aptor molecule 2A (STAM2) mRNA, complete cds.//1.7
 0E-113//545bp//98%/AF042273
 C-PLACE1002500//Rattus norvegicus zinc transporter
 (ZnT-2) mRNA, complete cds.//2.90E-58//465bp//80%
 //U50927
 C-PLACE1002532//HOMEODOMAIN PROTEIN DLX-5.//1.20E-152
 //289aa//96%/P70396
 C-PLACE1002571//ACTIN-LIKE PROTEIN 13E.//5.00E-99/ 40
 //386aa//48%/P45890
 C-PLACE1002583//GLUTAMATE RECEPTOR, IONOTROPIC KAI
 NATE 2 PRECURSOR (GLUTAMATE RECEPTOR 6) (GLUR-6)
 (GLUTAMATE RECEPTOR BETA-2) (GLUR BETA-2) (FRAGMEN
 T).//5.60E-34//76aa//98%/P39087
 C-PLACE1002591//CORONIN-LIKE PROTEIN P57.//4.40E-7
 0//208aa//66%/P31146
 C-PLACE1002598//OLIGORIBONUCLEASE (EC 3.1.-.-).//
 5.50E-17//76aa//56%/P45340
 C-PLACE1002655//ADSEVERIN (SCINDERIN) (SC).//2.50E 50

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-278//543aa//92%/Q28046
 C-PLACE1002665//Mus musculus enhancer of polycomb
 (Epc1) mRNA, completecds.//0//2462bp//89%/AF07976
 5
 C-PLACE1002685//Homo sapiens B cell linker protein
 BLNK mRNA, alternatively spliced, complete cds.//
 0//1750bp//99%/AF068180
 C-PLACE1002714//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZI
 PPER PROTEIN) (MYOSINII).//9.40E-13//500aa//21%/Q
 99323
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTO
 R KIAA0001.//9.00E-45//305aa//33%/Q15391
 C-PLACE1002775//PEREGRIN (BR140 PROTEIN).//3.80E-1
 3//272aa//28%/P55201
 C-PLACE1002782//Rattus norvegicus zinc transporter
 (ZnT-2) mRNA, complete cds.//3.80E-43//385bp//77%
 //U50927
 C-PLACE1002816//HISTONE DEACETYLASE HDA1.//2.20E-4
 8//217aa//46%/P53973
 C-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGE
 R PROTEIN HPF1).//5.50E-203//396aa//86%/P51522
 C-PLACE1002908//Homo sapiens XGalT-1 mRNA for gala
 ctosyltransferase I, complete cds.//0//1654bp//99%
 //AB028600
 C-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//1.
 40E-78//496aa//37%/Q49091
 C-PLACE1003030//Homo sapiens snRNA activating prot
 ein complex 190kD subunit (SNAP190) mRNA, complete
 cds.//8.50E-44//225bp//100%/AF032387
 C-PLACE1003045//POLYCYSTIN 2 (AUTOSOMAL DOMINANT P
 OLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYC
 S TWIN) (R48321).//1.70E-05//150aa//24%/Q13563
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.60E-
 79//253aa//60%/Q13268
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18
 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBI
 QUITIN CARRIER PROTEIN) (PM42).//3.80E-37//143aa//
 51%/P42743
 C-PLACE1003176//Homo sapiens clone pHN1868 tyrosyl
 -DNA phosphodiesteraseprotein (TDP1) mRNA, partial
 cds.//1.70E-148//687bp//99%/AF182003
 C-PLACE1003190//SOF1 PROTEIN.//1.90E-110//325aa//4
 8%/P33750
 C-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTO
 R KIAA0001.//4.90E-76//309aa//47%/Q15391
 C-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEI
 N.//7.90E-22//70aa//47%/P21541
 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGE
 R PROTEIN HPF1).//6.90E-206//396aa//86%/P51522
 C-PLACE1003353//Homo sapiens breast cancer antitest

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rogen resistance 3 protein (BCAR3) mRNA, complete cds. //0//2435bp//99%/U92715
 C-PLACE1003366//Homo sapiens otoferlin (OTOF) mRNA, complete cds. //1.40E-78//542bp//67%/AF107403
 C-PLACE1003394//Homo sapiens RAB14 protein (RAB14) mRNA, complete cds. //2.60E-139//648bp//99%/AF152463
 C-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER YIL006W. //1.30E-40//278aa//36%/P40556
 C-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR. //1.70E-23//322aa//26%/Q13201
 C-PLACE1003519//H. sapiens hnRNP-E2 mRNA. //5.10E-218//905bp//99%/X78136
 C-PLACE1003521//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III. //0.0000011//101aa//32%/Q09475
 C-PLACE1003537//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACT OR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT). //7.70E-68//404aa//33%/P32802
 C-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG. //2.60E-93//270aa//66%/P46975
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta. //5.90E-278//1275bp//99%/D83200
 C-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR. //0.00000023//82aa//35%/Q02516
 C-PLACE1003611//Homo sapiens anaphase-promoting complex subunit 4 (APC4) mRNA, complete cds. //6.20E-169//683bp//99%/AF191338
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN. //3.20E-10//380aa//25%/P18824
 C-PLACE1003669//TRICHOHYALIN. //5.60E-09//219aa//30%/P22793
 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //8.00E-19//209aa//34%/Q08170
 C-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds. //6.20E-282//1316bp//98%/AF053305
 C-PLACE1003738//ZINC FINGER PROTEIN 135. //9.60E-118//350aa//46%/P52742
 C-PLACE1003760//Homo sapiens tetraspanin TM4-A mRNA, complete cds. //5.20E-289//1313bp//97%/AF133423
 C-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLYLTRANSFERASE). //3.70E-222//651aa//66%/P25500
 C-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) (FRAGMENT). //6.70E-113//501aa//46%/P10895
 C-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AM

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MONIA LIGASE) (CTP SYNTHETASE). //1.40E-243//584aa//74%/P17812
 C-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS). //2.40E-108//581aa//40%/Q05506
 C-PLACE1003923//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds. //0//1670bp//99%/AF033120
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN). //2.40E-124//326aa//73%/P80385
 C-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds. //0//2384bp//86%/AF032666
 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4). //6.10E-181//340aa//96%/P29387
 C-PLACE1004149//Rattus norvegicus GERp95 mRNA, complete cds. //3.30E-41//452bp//65%/AF195534
 C-PLACE1004183//Homo sapiens for TOM1-like protein. //0//1279bp//97%/AJ010071
 C-PLACE1004197//BUTYROPHILIN PRECURSOR (BT). //4.50E-10//208aa//27%/Q62556
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds. //0//1882bp//99%/AF069493
 C-PLACE1004256//Mus musculus short coiled coil protein SCOC0 (Scoc) mRNA, complete cds. //2.00E-93//960bp//76%/AF115778
 C-PLACE1004258//Homo sapiens vanilloid receptor-like protein 1 (VRL-1) mRNA. //0//1144bp//98%/AF129112
 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-). //9.70E-36//389aa//31%/O15393
 C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds. //0//1498bp//99%/AF084830
 C-PLACE1004302//SOF1 PROTEIN. //1.90E-110//325aa//48%/P33750
 C-PLACE1004316//H. sapiens mRNA for apoptosis specific protein. //0//1767bp//99%/Y11588
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds. //0//2512bp//99%/AF100153
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-). //1.20E-39//385aa//33%/Q63448
 C-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds. //0//985bp//99%/U49283
 C-PLACE1004460//MATERNAL TUDOR PROTEIN. //0.0000002

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//218aa//23%/P25823
 C-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1). //2.90E-56//276aa//41%/P51522
 C-PLACE1004506//Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds. //2.10E-16//402bp//62%/U90878
 C-PLACE1004510//Homo sapiens TATA binding protein associated factor (TAFII150) mRNA, complete cds. //3.40E-227//1037bp//99%/AF040701
 C-PLACE1004550//Homo sapiens CGI-20 protein mRNA, complete cds. //3.50E-274//1305bp//97%/AF132954
 C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT). //0//525aa//99%/Q10568
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR. //7.70E-18//264aa//32%/Q13438
 C-PLACE1004646//B.taurus mRNA for retinal pigment epithelial membrane receptor p63. //4.40E-42//985bp//59%/X66277
 C-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds. //1.30E-195//982bp//96%/AF035606
 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-RECOGNIN). //4.40E-35//578aa//27%/O60152
 C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3GalVI, complete cds. //7.10E-224//790bp//98%/AB022918
 C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN). //1.90E-32//259aa//32%/P30337
 C-PLACE1004793//RETROVIRUS-RELATED ENV POLYPROTEIN. //5.20E-47//577aa//25%/P10267
 C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE). //4.70E-65//695aa//29%/Q01631
 C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //5.90E-19//196aa//36%/Q08170
 C-PLACE1004868//MALE STERILITY PROTEIN 2. //3.90E-39//261aa//27%/Q08891
 C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C. //9.30E-11//94aa//47%/O42643
 C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A). //4.90E-48//198aa//44%/P06151
 C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds. //0//1853bp//98%/AF099936
 C-PLACE1004937//SEL-10 PROTEIN. //6.30E-125//357aa//58%/Q93794

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C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B041 6.5 IN CHROMOSOME X. //2.00E-14//205aa//26%/Q11073
 C-PLACE1005052//Homo sapiens CGI-16 protein mRNA, complete cds. //6.6E-313//1413bp//99%/AF132950
 C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN). //2.60E-56//565aa//30%/Q04652
 C-PLACE1005176//Homo sapiens hypothalamus protein HT001 mRNA, complete cds. //3.90E-212//1040bp//96%/AF113539
 C-PLACE1005187//APAG PROTEIN. //3.80E-13//122aa//36%/P05636
 C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-). //1.30E-27//349aa//32%/Q01577
 C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP). //2.30E-13//269aa//28%/P53352
 C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3). //2.00E-111//226aa//92%/P08760
 C-PLACE1005331//Homo sapiens 7h3 protein mRNA, partial cds. //1.20E-226//748bp//95%/AF209931
 C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACILHYDROLYASE). //8.60E-09//194aa//27%/O33335
 C-PLACE1005467//PENICILLIN-BINDING PROTEIN 4* (PBP 4*) (PBP 4A). //1.10E-09//93aa//31%/P32959
 C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6. //0//1649bp//99%/AJ006276
 C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C1 0.5 IN CHROMOSOME III. //5.60E-52//173aa//57%/Q09251
 C-PLACE1005549//Homo sapiens mRNA for Rho guanine nucleotide-exchange factor, splice variant NET1A. //7.60E-97//1287bp//67%/AJ010046
 C-PLACE1005557//60S RIBOSOMAL PROTEIN L27. //1.90E-11//60aa//48%/P46288
 C-PLACE1005584//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2.9/ER2.6). //6.80E-09//267aa//30%/P29128
 C-PLACE1005611//Mus musculus mRNA for mDj10, complete cds. //2.00E-33//379bp//66%/AB028860
 C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds. //0//2130bp//99%/AF083255
 C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE). //2.10E-148//321aa//83%/P31350
 C-PLACE1005727//Homo sapiens STRIN protein (STRIN) mRNA, complete cds. //2.00E-118//378bp//98%/AF162

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C-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11. //1.30E-237//585aa//72%/Q60710

C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3:1.2.14) (THIOESTERASE I). //2.50E-79//209aa//53%/P08635

C-PLACE1005803//Homo sapiens mRNA for transcription factor (SMIF gene). //0//1985bp//99%/AJ275986

C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds. //1.10E-217//994bp//99%/AF 10 027156

C-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //0//2040bp//99%/AF065482

C-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KDSUBUNIT (CPSF 100 KD SUBUNIT). //0//730aa//99%/Q10568

C-PLACE1005890//BEM46 PROTEIN (FRAGMENT). //9.90E-42//224aa//43%/P54069C-PLACE1005921//AIG1 PROTEIN. //3.00E-31//284aa//31%/P54120

C-PLACE1005951//Homo sapiens prolactin regulatory element-binding protein (PREB) mRNA, complete cds. //1.10E-264//661bp//99%/AF203687

C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-). //6.70E-30//198aa//37%/P43636

C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE) //5.40E-54//455aa//32%/P14904

C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TF IID 90 KD SUBUNIT (TAFII-90). //1.40E-07//254aa//25%/P38129

C-PLACE1006003//Homo sapiens CGI-94 protein mRNA, complete cds. //2.40E-177//829bp//99%/AF151852

C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2. //0//1564bp//99%/AJ236876

C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine. //4.70E-161//744bp//99%/X99906

C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds. //1.50E-148//681bp//99%/AF03 9023

C-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E). //2.00E-28//236aa//30%/P98110

C-PLACE1006167//PAF1 PROTEIN. //7.30E-15//437aa//24%/P38351

C-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR H A2/AP2 ADAPTIN ALPHA C SUBUNIT). //1.70E-169//373aa//88%/P17427

C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06. //2.70E-116//496aa//48%/Q09747

C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN). //2.00E-16//244aa//31%/P28675

C-PLACE1006288//VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 1 (VDAC1) (PLASMALEMMAL PORIN) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN) (PORIN 31HL) (PORIN 31HM). //4.60E-117//147aa//80%/P21796

C-PLACE1006318//Mus musculus skm-BOP2 (Bop) mRNA, complete cds. //3.00E-07//376bp//59%/U76374

C-PLACE1006335//Homo sapiens NY-REN-50 antigen mRNA A, partial cds. //0//1649bp//99%/AF155112

C-PLACE1006368//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR). //1.30E-18//460aa//24%/Q00547

C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds. //0//1168bp//99%/AF062085

C-PLACE1006438//ZINC FINGER PROTEIN 165. //2.50E-45//122aa//43%/P49910

20 C-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME). //1.20E-83//313aa//49%/P27550

C-PLACE1006482//TRANSCRIPTION FACTOR MAFF. //7.70E-55//142aa//85%/Q90595

C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68). //1.10E-229//367aa//96%/Q00004

C-PLACE1006492//Homo sapiens transmembrane protein 2 (TMEM2) mRNA, complete cds. //0//2618bp//99%/AF 137030

30 C-PLACE1006506//Homo sapiens anaphase-promoting complex subunit 4 (APC4)mRNA, complete cds. //0//2170 bp//99%/AF191338

C-PLACE1006531//Homo sapiens putative RNA-binding protein Q99 mRNA, complete cds. //0//1967bp//99%/AF093097

C-PLACE1006534//POLYPEPTIDE N-ACETYLGALACTOSAMINYL TRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1). //8.30 E-08//100aa//41%/Q10472

C-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT). //1.20E-09//426aa//21%/P39922

C-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds. //0//1464bp//99%/U97670

C-PLACE1006626//Homo sapiens mRNA for Helicase-WO I, complete cds. //0//1760bp//99%/AB028449

50 C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, completecds, clone:HP10328. //5.80E-24//734bp//62%/AB015630

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C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (F
LAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2)
(FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.90E-
13//177aa//33%/Q59263
C-PLACE1006754//BILIARY GLYCOPROTEIN 1 PRECURSOR
(BGP-1) (ANTIGEN CD66) (CD66A ANTIGEN).//6.20E-63//
191aa//43%/P13688
C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOL
OG.//9.80E-213//232aa//80%/P08547
C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROL
ASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (U
BIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQU
ITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//
2.00E-15//188aa//29%/P35123
C-PLACE1006878//TRNA-SPLICING ENDONUCLEASE SUBUNIT
SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDONUCLEASE).//
1.90E-08//122aa//36%/P16658
C-PLACE1006917//HSH49 PROTEIN.//5.50E-12//97aa//35
%/Q99181
C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.
6 IN CHROMOSOME III.//6.70E-48//278aa//41%/Q10000
C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.30
E-86//522aa//36%/P97998
C-PLACE1006958//Homo sapiens mRNA for heat shock p
rotein apg-1, completecds.//0//1770bp//99%/AB0234
21
C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DEL
AYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.20E-35
//180aa//33%/Q14542
C-PLACE1007105//Homo sapiens muskellin (MKLN1) mRN
A, complete cds.//0//2449bp//98%/AF047489
C-PLACE1007140//TRICHOHYALIN.//1.30E-25//816aa//22
%/P37709
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROP
ORPHYRINOGEN III OXIDASE (EC 1.-.-) (COPROPORPHY
RINOGENASE) (COPROGEN OXIDASE).//1.00E-42//370aa//
31%/P54304
C-PLACE1007239//Homo sapiens mRNA for transcriptio
n elongation factor S-II, hS-II-T1, complete cds.//
6.50E-216//1068bp//96%/D50495
C-PLACE1007243//UNC-47 PROTEIN.//1.70E-07//211aa//
27%/P34579
C-PLACE1007257//Homo sapiens mRNA for dia-12c prot
ein.//0//2052bp//99%/Y15908
C-PLACE1007317//Drosophila melanogaster Adrift (ad
rift) mRNA, complete cds.//4.10E-17//1037bp//56%/AF117649
C-PLACE1007346//Homo sapiens estrogen-responsive B
box protein (EBBP) mRNA, complete cds.//0//2366bp
//99%/AF096870

4472

C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDI
NG PROTEIN UNC-13.//0.00000044//127aa//30%/P27715
C-PLACE1007409//WHITE PROTEIN.//1.10E-64//428aa//3
2%/Q17320
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.1
4.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP
103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (A
DABP).//8.80E-25//140aa//35%/P27487
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTID
E EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSP
LASIA PROTEIN HOMOLOG).//5.40E-53//426aa//33%/P52
734
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (C
YTOKERATIN 19) (K19) (CK 19).//1.40E-85//385aa//45
%/P08728
C-PLACE1007537//Homo sapiens ankyrin repeat-contai
ning protein ASB-2 mRNA, complete cds.//8.9e-316//
1485bp//98%/AF159164
C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D
3.4 IN CHROMOSOME III.//1.00E-49//361aa//36%/P345
37
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMEN
T).//1.60E-143//666aa//44%/Q99676
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//1.
00E-07//228aa//31%/P32506
C-PLACE1007649//GLUCOAMYLASE S1/S2 PRECURSOR (EC
3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA
-D-GLUCAN GLUCOHYDROLASE).//4.50E-05//197aa//26%/P08640
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOP
ROTEIN) (LA AUTOANTIGEN HOMOLOG).//8.70E-09//279aa
//28%/Q26457
C-PLACE1007697//GCN20 PROTEIN.//7.60E-119//717aa//
38%/P43535
C-PLACE1007705//Mus musculus mRNA for Ndr1 related
protein Ndr3, complete cds.//1.10E-184//1096bp//8
2%/AB033922
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP
1) mRNA, complete cds.//0//3431bp//99%/AF061243
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.
4.23.-).//1.50E-44//231aa//42%/P10265
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete
cds.//0//1836bp//99%/AB019602
C-PLACE1007897//Homo sapiens FLASH mRNA, complete
cds.//0//2145bp//99%/AF154415
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZI
PPER PROTEIN) (MYOSINII).//2.60E-14//370aa//25%/Q
99323
C-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FI
G1-GIP1 INTERGENIC REGION.//6.70E-13//168aa//31%/

- P38226
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//0//2252bp//99%//AF084530
C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//0//2300bp//99%//AF079529
C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.10E-36//202aa//48%//P52272
C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.10E-14//128aa//39%//Q63622
C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6E-318//613aa//94%//P52590
C-PLACE1008080//Homo sapiens mRNA for HEXIM1 protein, complete cds.//0//2152bp//99%//AB021179
C-PLACE1008111//PROBABLE OXIDOREDUCTASE (EC 1.-.-).//3.00E-25//208aa//37%//Q03326
C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III.//1.30E-24//395aa//31%//Q09531
C-PLACE1008177//TRICHOHYALIN.//2.30E-29//487aa//26%//P37709
C-PLACE1008201//Rattus rattus zinc finger protein, complete cds.//0//2265bp//83%//L23077
C-PLACE1008244//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//9.50E-21//148aa//38%//Q00808
C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.30E-283//671aa//77%//P53620
C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.30E-18//162aa//37%//P12689
C-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//5.20E-137//672bp//77%//AF078779
C-PLACE1008330//EOSINOPHIL LYSOPHOSPHOLIPASE (EC 3.1.1.5) (CHARCOT-LEYDEN CRYSTAL PROTEIN) (LYSOLECITHIN ACYLHYDROLASE) (CLC) (GALACTIN-10).//2.20E-23//94aa//47%//Q05315
C-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (ME5) mRNA, partial cds.//1.90E-170//780bp//100%//AF036144
C-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN).//5.30E-26//309aa//30%//Q04652
C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.30E-114//243aa//87%//P05432
C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%//P41541
C-PLACE1008426//RESTIN (CYTOPLASMIC LINKER PROTEIN -170) (CLIP-170).//1.80E-11//365aa//25%//Q42184
C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.10E-11//189aa//32%//Q06527
C-PLACE1008465//Homo sapiens mRNA for rapa-1 (rapa gene).//6.60E-243//1102bp//99%//AJ277275
C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.10E-09//62aa//48%//P22620
C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.80E-236//453aa//96%//P37199
C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//1850bp//99%//AJ006591
C-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2).//5.20E-90//483aa//38%//Q02668
C-PLACE1008650//PRL1/PRL2-LIKE PROTEIN.//2.00E-127//354aa//62%//Q13615
C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%//AF038406
C-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//0//1670bp//99%//AF060543
C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1A.//2.30E-269//1225bp//99%//AJ004974
C-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//8.80E-268//1171bp//90%//AF032668
C-PLACE1009020//NIFS PROTEIN.//3.90E-55//279aa//41%//P12623
C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%//AJ003112
C-PLACE1009060//BR01 PROTEIN.//6.70E-19//567aa//24%//P48582
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.90E-44//480aa//30%//P30432
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.10E-179//452aa//67%//P51814
C-PLACE1009113//Homo sapiens X-ray repair cross-complementing protein 3(XRCC3) mRNA, complete cds.//0//2529bp//99%//AF035586
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2.00E-68//181aa//43%//Q05086
C-PLACE1009158//Mus musculus mRNA for death inducer-obliterator-1 (Dio-1).//5.40E-200//1790bp//75%//AJ238332

4475

C-PLACE1009186//Homo sapiens small zinc finger-like protein (TIM9b) mRNA, complete cds.//9.60E-255//1179bp//98%/AF150105
 C-PLACE1009246//POLLEN SPECIFIC PROTEIN SF3.//4.40E-16//82aa//43%/P29675
 C-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//2.00E-78//262aa//43%/P34110
 C-PLACE1009308//GLUCOSE REPRESSION MEDIATOR PROTEIN.//4.00E-06//439aa//23%/P14922
 C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.10E-132//1229bp//75%/AF107295
 C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.50E-10//151aa//29%/Q12067
 C-PLACE1009398//ZINC FINGER PROTEIN 135.//6.20E-97//361aa//51%/P52742
 C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME I.//4.70E-08//165aa//33%/Q09820
 C-PLACE1009443//Mus musculus F-box protein FBL8 mRNA, complete cds.//1.00E-173//1367bp//77%/AF176523
 C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.80E-71//82aa//89%/P42356
 C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.10E-289//550aa//93%/P54319
 C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//3.90E-40//179aa//37%/P34580
 C-PLACE1009477//Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2) mRNA, complete cds.//6.60E-147//592bp//99%/AF043117
 C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.10E-99//228aa//75%/Q99418
 C-PLACE1009571//Homo sapiens PTD002 mRNA, complete cds.//5.90E-185//857bp//99%/AF078857
 C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.10E-54//291aa//40%/Q00808
 C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.30E-60//209aa//41%/P25159
 C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.50E-285//538aa//99%/P55161
 C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%/AF062534
 C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME I.//7.00E-33//166aa//43%/Q09876

4476

C-PLACE1009721//MSF1 PROTEIN.//1.70E-22//176aa//33%/P35200
 C-PLACE1009731//AIG1 PROTEIN.//1.60E-22//274aa//28%/P54120
 C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds.//4.30E-294//1329bp//100%/AB012190
 C-PLACE1009798//RLR1 PROTEIN.//1.60E-18//270aa//23%/P53552
 C-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.30E-59//405aa//33%/P38968
 C-PLACE1009861//CATHEPSIN B-LIKE CYSTEINE PROTEINASE 6 PRECURSOR (EC 3.4.22.-).//6.50E-28//209aa//38%/P43510
 C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION.//1.90E-108//277aa//43%/P53145
 C-PLACE1009925//Homo sapiens RNA helicase (RIG-I) mRNA, complete cds.//0//1730bp//99%/AF038963
 C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.60E-59//450aa//34%/P28175
 C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.20E-70//736bp//73%/U48288
 C-PLACE1010053//M. musculus Spnr mRNA for RNA binding protein.//6.00E-279//1402bp//94%/X84692
 C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%/AF065482
 C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.40E-268//506aa//98%/Q62671
 C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.30E-114//537aa//44%/Q04652
 C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.70E-20//156aa//42%/P22082
 C-PLACE1010148//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//4.60E-07//431aa//23%/P35662
 C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.80E-11//95aa//49%/Q01130
 C-PLACE1010231//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).//5.10E-27//371aa//28%/Q14246
 C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.60E-77//214aa//62%/P25722
 C-PLACE1010310//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//1.20E-18//467aa//30%/P46804
 C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE

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TRANSLOCATOR PRECURSOR (CTPT). //1.10E-09//350aa//
22%/P52178
C-PLACE1010362//1-PHOSPHATIDYLYNOSITOL PHOSPHODI-
TERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLYNOSIT-
OL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC). //2.00E-09//
126aa//29%/P34024
C-PLACE1010481//Bos taurus C5-glucuronyl epimerase
mRNA, partial cds. //0//2082bp//91%/AF003927
C-PLACE1010522//Homo sapiens mRNA for DEPP (decidu-
al protein induced by progesterone), complete cds. //10
/0//1981bp//99%/AB022718
C-PLACE1010529//Homo sapiens TANK binding kinase T-
BK1 (TBK1) mRNA, complete cds. //0//1750bp//99%/AF-
191838
C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PR-
OTEIN USO1. //1.20E-07//616aa//24%/P25386
C-PLACE1010579//Homo sapiens CED-6 protein (CED-6)
mRNA, complete cds. //8.80E-300//1359bp//99%/AF19-
1771
C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxi-
somal membrane anchor protein, complete cds. //0//19-
04bp//99%/AB017546
C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORM-
S (TNTC). //0.00000016//120aa//28%/P02642
C-PLACE1010628//Homo sapiens S164 gene, partial cd-
s; PS1 and hypothetical protein genes, complete cd-
s; and S171 gene, partial cds. //7.50E-08//324bp//6-
4%/AF109907
C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13. //5.
70E-75//423aa//39%/Q01755
C-PLACE1010662//UDP-GLUCOSE: GLYCOPROTEIN GLUCOSYL-
TRANSFERASE PRECURSOR (EC 2.4.1.-) (DUCT). //1.80E-2-
22//808aa//52%/Q09332
C-PLACE1010702//ZINC FINGER PROTEIN 43 (ZINC PROTE-
IN HTF6). //5.20E-151//427aa//55%/P28160
C-PLACE1010720//Homo sapiens mRNA for chromosome-a-
ssociated polypeptide-C, complete cds. //4.00E-299//
1091bp//99%/AB019987
C-PLACE1010743//Homo sapiens myosin-IXb splice var-
iant (Myo9b) mRNA, partial cds. //8.90E-91//668bp//40
82%/AF020267
C-PLACE1010761//Homo sapiens mRNA for cisplatin re-
sistance-associated overexpressed protein, complet-
e cds. //0//1448bp//99%/AB034205
C-PLACE1010771//M. musculus HCNGP mRNA. //7.40E-168//
966bp//89%/X68061
C-PLACE1010811//Rattus norvegicus mRNA for protein
encoded by bdeight gene, partial. //1.60E-217//858-
bp//87%/AJ010392
C-PLACE1010833//CALTRACTIN (CENTRIN). //0.0000001// 50

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154aa//28%/P41209
C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGE-
R PROTEIN HTF10) (HPF7). //1.30E-143//407aa//58%/Q-
05481
C-PLACE1010896//NUF1 PROTEIN (SPINDLE POLY BODY SP-
ACER PROTEIN SPC110). //1.50E-25//583aa//23%/P3558-
0
C-PLACE1010926//HYPOTHETICAL 72.2 KD PROTEIN C12C-
2.05C IN CHROMOSOME II. //7.60E-23//103aa//53%/Q09-
746
C-PLACE1010942//Homo sapiens intersectin long isof-
orm (ITSN) mRNA, complete cds. //0//1440bp//99%/AF-
114487
C-PLACE1010960//ACTIN-LIKE PROTEIN 13E. //5.30E-98//
297aa//48%/P45890
C-PLACE1011041//Homo sapiens mRNA for BAP2-alpha p-
rotein, complete cds. //0//1701bp//97%/AB015019
C-PLACE1011046//1-PHOSPHATIDYLYNOSITOL-4, 5-BISPHOS-
PHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-
BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-I) (PLC-15-
4). //0//646aa//97%/P10894
C-PLACE1011056//HISTONE H1, CONADAL. //6.80E-13//15-
4aa//37%/P02256
C-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL-
PRECURSOR (MEF-G). //1.50E-22//63aa//88%/Q07803
C-PLACE1011114//PROBABLE ATP-DEPENDENT RNA HELICAS-
E HAS1. //2.90E-71//190aa//44%/Q03532
C-PLACE1011160//Homo sapiens HFB30 mRNA, complete
cds. //0//1691bp//99%/AB022663
30 C-PLACE1011185//INSERTION ELEMENT IS1 PROTEIN INS-
B. //1.30E-89//167aa//100%/P03830
C-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).
//3.20E-12//212aa//29%/Q03326
C-PLACE1011229//Homo sapiens ubiquitin-specific pr-
otease homolog (UPH) mRNA, complete cds. //2.30E-15-
2//701bp//99%/AF153604
C-PLACE1011310//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH
MUSCLE. //3.50E-20//496aa//25%/P10587
C-PLACE1011332//Homo sapiens N-acetylglucosamine-p-
hosphate mutase mRNA, complete cds. //7.20E-151//697-
bp//99%/AF102265
C-PLACE1011340//Homo sapiens IDN3-B mRNA, complete
cds. //1.20E-74//380bp//97%/AB019602
C-PLACE1011371//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY
CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2). //1.70E-78//
383aa//39%/Q61703
C-PLACE1011399//Homo sapiens CGI-72 protein mRNA,
complete cds. //3.20E-90//427bp//99%/AF151830
C-PLACE1011433//TRANSCRIPTION FACTOR IIIA (FACTOR
A) (TFIIIA). //3.00E-10//236aa//25%/P34695

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C-PLACE1011477//Homo sapiens sorting nexin 2 (SNX 2) mRNA, complete cds. //0//2040bp//99%//AF065482
 C-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT). //4.90E-11//147aa//32%//P52178
 C-PLACE1011576//Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds. //0//1791bp//82%//L11672
 C-PLACE1011586//Rattus norvegicus clone C53 CDK5 activator-binding protein mRNA, complete cds. //4.10E-259//1538bp//87%//AF177476
 C-PLACE1011635//Homo sapiens heparan sulfate D-glucosaminyl 3-O-sulfotransferase-3B (3OST3B1) mRNA, complete cds. //0//1559bp//99%//AF105377
 C-PLACE1011664//CROOKED NECK PROTEIN. //1.60E-187//505aa//64%//P17886
 C-PLACE1011858//Homo sapiens BAG-family molecular chaperone regulator-2mRNA, complete cds. //1.30E-255//1179bp//99%//AF095192
 C-PLACE1011896//Mus musculus Wnt10a mRNA, complete cds. //2.60E-287//1820bp//85%//U61969
 C-PLACE1011922//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B). //1.30E-15//409aa//27%//P35580
 C-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds. //0//2782bp//99%//AF059617
 C-PLACE1012031//Homo sapiens sorting nexin 13 (SNX 13) mRNA, partial cds. //0//1701bp//100%//AF121862
 C-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III. //2.60E-42//104aa//49%//Q09475
 C-PLACE2000015//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15(PROTEIN EPS15) (AF-1P PROTEIN). //1.10E-116//364aa//45%//P42566
 C-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA, complete cds. //2.70E-107//981bp//74%//AF082556
 C-PLACE2000034//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48). //2.20E-29//212aa//35%//P10586
 C-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C). //6.10E-293//388aa//99%//P38650
 C-PLACE2000062//Homo sapiens mRNA for type II membrane protein similar to HIV gp120-binding C-type l

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ectin, complete cds, clone: HP01347. //6.30E-166//656bp//94%//AB015629
 C-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds. //0//3174bp//99%//AF027219
 C-PLACE2000164//TIPD PROTEIN. //2.10E-59//481aa//33%//O15736
 C-PLACE2000216//SPECTRIN BETA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID BETACHAIN) (FODRIN BETA CHAIN) (SPTBN1). //6.60E-115//226aa//99%//Q01082
 C-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN). //6.00E-57//239aa//34%//Q04652
 C-PLACE2000274//DYNEIN BETA CHAIN, CILIARY. //2.20E-167//880aa//37%//P23098
 C-PLACE2000341//Homo sapiens sodium-dependent multivitamin transporter (SMVT) mRNA, complete cds. //0//1554bp//99%//AF069307
 C-PLACE2000371//TENSIN. //2.90E-78//561aa//37%//Q04205
 C-PLACE2000373//F-SPONDIN PRECURSOR. //8.60E-16//371aa//28%//P35446
 C-PLACE2000398//LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48). //6.30E-37//90aa//98%//P10586
 C-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (12E7). //1.60E-14//180aa//39%//P14209
 C-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS). //9.90E-229//821aa//54%//Q09996

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C-PLACE2000411//Homo sapiens epsin 2b mRNA, complete cds. //3.80E-271//642bp //99%//AF062085
 C-PLACE2000427//PROBABLE HELICASE MOT1. //1.20E-26//200aa//27%//P32333
 C-PLACE2000438//POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N-ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1). //2.10E-86//348aa//41%//Q10472
 C-PLACE2000458//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN). //2.50E-25//165aa//40%//P33450
 C-PLACE2000477//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds. //6.70E-127//671bp//94%//AF072733
 C-PLACE3000009//DNA-DIRECTED RNA POLYMERASE II LARGE SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT). //3.50E-30//400aa//30%//P11414
 C-PLACE3000020//Homo sapiens type III adenylyl cyclase (AC-III) mRNA, complete cds. //0//2253bp//99%//AF033861
 C-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme. //0//1979bp//90%//Y17267
 C-PLACE3000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15. //1.90E-08//281aa//22%//P22224
 C-PLACE3000145//TENSIN. //1.00E-108//277aa//75%//Q04205
 C-PLACE3000147//Homo sapiens metalloproteinase with thrombospondin type1 motifs ADAMTS1 (ADAMTS1) mRNA, complete cds. //0//2043bp//99%//AF170084
 C-PLACE3000169//ZINC FINGER PROTEIN 135. //2.50E-90//358aa//47%//P52742
 C-PLACE3000218//Homo sapiens putative protein O-mannosyltransferase (POMT2) mRNA, complete cds. //0//1862bp//98%//AF105020
 C-PLACE3000242//Human trophinin mRNA, complete cds. //0//2290bp//99%//U04811
 C-PLACE3000244//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR). //0//1435aa//92%//P53995
 C-PLACE3000254//Homo sapiens transcriptional activator SRCAP (SRCAP) mRNA, complete cds. //0//4583bp//83%//AF143946
 C-PLACE3000339//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //9.60E-08//359aa//23%//P08640
 C-PLACE3000350//SERINE/THREONINE-PROTEIN KINASE SULKU (EC 2.7.1.-). //1.00E-54//418aa//38%//P46549

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C-PLACE3000416//Homo sapiens mRNA for actin binding protein ABP620, complete cds. //1.80E-141//565bp//98%//AB029290
 C-PLACE3000477//Homo sapiens phosphoprotein pp75 mRNA, partial cds. //0//3012bp//98%//AF153085
 C-PLACE4000009//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B). //2.90E-54//626aa//29%//P35580
 C-PLACE4000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP). //3.10E-111//348aa//41%//P46100
 C-PLACE4000052//Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds. //0//4661bp//99%//AF165281
 C-PLACE4000063//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //1.70E-15//740aa//23%//P08640
 C-PLACE4000100//Homo sapiens hydroxypyruvate reductase (GRHPR) gene, complete cds. //0//4199bp//97%//AF146689
 C-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds. //1.60E-86//190aabb//88%//AF091234
 C-PLACE4000156//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //1.40E-235//516aa//51%//Q05481
 C-PLACE4000192//ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654). //7.00E-22//369aa//25%//P52746
 C-PLACE4000211//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zincfinger domain 2A, complete cds. //0//5709bp//96%//AB032254
 C-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds. //0//2567bp//88%//AF030430
 C-PLACE4000259//H. sapiens gene for U5 snRNP-specific 200kd protein. //0//5143bp//90%//Z70200
 C-PLACE4000261//PEREGRIN (BR140 PROTEIN). //9.50E-10//128aa//34%//P55201
 C-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds. //0//2034bp//89%//AF032667
 C-PLACE4000326//NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1). //8.10E-24//319aa//31%//P30771
 C-PLACE4000369//Homo sapiens thyroid hormone receptor-associated protein complex component TRAP240 mRNA, complete cds. //1.40E-185//1135bp//67%//AF117754
 C-PLACE4000401//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME). //7.20E-22//54aa//62%//Q01576

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C-PLACE4000431//H.sapiens gene for U5 snRNP-specific 200kd protein.//0//5142bp//90%/Z70200

C-PLACE4000450//Homo sapiens BAZ2A mRNA for bromodomain adjacent to zincfinger domain 2A, complete cds.//0//5709bp//96%/AB032254

C-PLACE4000489//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-1 BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//5.70E-60//254aa//44%/P13002

C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCHPROTEIN).//2.40E-191//828aa//48%/P21783

C-PLACE4000548//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.70E-13//784aa//21%/P08640

C-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS PROTEIN).//1.50E-26//252aa//35%/P55824

C-PLACE4000581//FIBROPELLEIN I PRECURSOR (EPIDERMAL GROWTH FACTOR-RELATED PROTEIN 1) (UEGF-1).//9.30E-70//226aa//52%/P10079

C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.90E-17//201aa//34%/P49816

C-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//0//6340bp//87%/Y17267

C-SKNMC1000011//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//5.50E-35//431aa//29%/O60100

C-SKNMC1000013//Homo sapiens ATP-binding cassette protein M-ABC1 mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//2384bp//99%/AF047690

C-SKNMC1000046//Homo sapiens liprin-alpha3 mRNA, partial cds.//1.90E-162//749bp//99%/AF034800

C-SKNMC1000050//CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CANP) (M-TYPE).//3.20E-41//87aa//98%/P17655

C-SKNMC1000091//Homo sapiens mRNA for leucine-zipper protein, complete cds.//6.10E-190//872bp//99%/AB021663

C-THYR01000034//TRICHOHYALIN.//9.40E-10//176aa//30%/P37709

C-THYR01000072//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//3.40E-16//201aa//29%/P11799

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C-THYR01000085//PAIRED BOX PROTEIN PAX-8, ISOFORMS 8A/8B.//2.00E-72//155aa//92%/Q06710

C-THYR01000121//Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds.//0//1737bp//87%/U49055

C-THYR01000132//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.10E-159//824bp//95%/U97018

C-THYR01000173//Homo sapiens AP-mu chain family member mu1B (HSMU1B) mRNA, complete cds.//0//1713bp//99%/AF020797

C-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//0//2362bp//99%/AJ005698

C-THYR01000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.00E-118//239aa//66%/P51523

C-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2161bp//99%/AB016068

C-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//0//1567bp//99%/AF124145

C-THYR01000343//ATROPHIN-1 (DENTATORUBRAL-PALLIDOL UYSIAN ATROPHY PROTEIN).//4.90E-06//280aa//31%/P54259

C-THYR01000358//SELENIUM-BINDING LIVER PROTEIN.//2.30E-229//237aa//79%/P17563

C-THYR01000394//Homo sapiens peroxisomal membrane protein PMP 24 mRNA, complete cds.//1.20E-299//1325bp//99%/AF072864

C-THYR01000395//Homo sapiens actin-binding protein (IPP) mRNA, complete cds.//0//2092bp//99%/AF156857

C-THYR01000401//Human Tcd37 homolog (HTcd37) mRNA, partial cds.//1.10E-90//430bp//99%/U67085

C-THYR01000488//Homo sapiens HFB30 mRNA, complete cds.//0//2254bp//100%/AB022663

C-THYR01000501//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//4.20E-98//408aa//42%/P19474

C-THYR01000569//Mus musculus hematopoietic zinc finger protein mRNA, complete cds.//0//1557bp//91%/AF118566

C-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds.//0//1901bp//99%/AF075587

C-THYR01000605//Homo sapiens histone acetyltransferase (HBOa) mRNA, complete cds.//0//3080bp//99%/AF140360

C-THYR01000662//Homo sapiens XPV mRNA for DNA polymerase eta, complete cds.//0//2341bp//99%/AB02431

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C-THYRO1000666//Mus musculus mRNA for kinesin like protein 9.//0//2001bp//86%/AJ132889
 C-THYRO1000684//Homo sapiens BAG-family molecular chaperone regulator-5mRNA, complete cds.//0//3347bp//99%/AF095195
 C-THYRO1000748//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//3.30E-96//335aa//52%/P98171
 C-THYRO1000756//ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (EC 2.4.99.-) (ST6GALNACII1) (STY).//1.80E-55//243aa//42%/Q64686
 C-THYRO1000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//2.40E-157//1656bp//70%/U37373
 C-THYRO1000852//Human branched-chain amino acid aminotransferase (ECA40)mRNA, complete cds.//1.40E-137//689bp//96%/U62739
 C-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B)mRNA, partial cds.//0//2387bp//99%/AF079529
 C-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE).//7.50E-57//315aa//43%/P32322
 C-THYRO1000951//DIHYDROXYACETONE KINASE 2 (EC 2.7.1.29) (GLYCERONE KINASE).//5.00E-83//566aa//37%/P43550
 C-THYRO1000983//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B).//6.30E-17//143aa//39%/P35132
 C-THYRO1001003//UBIQUITIN-CONJUGATING ENZYME E2-2 1.2 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//5.90E-14//84aa//41%/P52491
 C-THYRO1001033//TRANSFORMATION-SENSITIVE PROTEIN I EF SSP 3521.//8.40E-12//167aa//29%/P31948
 C-THYRO1001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//1.20E-67//245aa//62%/P98168
 C-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds.//1.30E-110//1947bp//65%/AF053700
 C-THYRO1001134//Homo sapiens CGI-78 protein mRNA, complete cds.//0//1898bp//99%/AF151835
 C-THYRO1001189//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-200//546aa//62%/Q05481
 C-THYRO1001204//Homo sapiens cathepsin Z precursor (CTS2) gene, exons 4,5, and 6 and complete cds; and TH1 gene partial sequence.//3.80E-100//478bp//99%/AF136276
 C-THYRO1001287//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSID

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ASE) (FRAGMENT).//3.40E-51//429aa//33%/P45701
 C-THYRO1001313//Homo sapiens sorting nexin 11 (SNX11) mRNA, complete cds.//0//2330bp//94%/AF121861
 C-THYRO1001347//Homo sapiens RAN binding protein 16 mRNA, complete cds.//2.00E-263//3101bp//68%/AF064729
 C-THYRO1001374//CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE (EC 3.1.2.2) (LONG CHAIN ACYL-COA THIOESTER HYDROLASE) (CTE-II).//1.80E-13//361aa//22%/000154
 C-THYRO1001405//PLECTIN.//6.90E-19//450aa//27%/P30427
 C-THYRO1001406//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//1.10E-131//219aa//81%/070503
 C-THYRO1001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//2.70E-171//559aa//59%/P35580
 C-THYRO1001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//0//1784bp//99%/AJ002190
 C-THYRO1001656//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//4.10E-273//1947bp//82%/AF175968
 C-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59kDa isoform.//0//1820bp//99%/AJ225089
 C-THYRO1001703//NIFR3-LIKE PROTEIN.//2.90E-32//282aa//32%/P45672
 C-THYRO1001721//RING CANAL PROTEIN (KELCH PROTEIN).//9.30E-34//220aa//38%/Q04652
 C-THYRO1001738//TUBULIN--TYROSINE LIGASE (EC 6.3.2.25) (TTL).//2.40E-20//217aa//30%/P38584
 C-THYRO1001809//MYOCYTE NUCLEAR FACTOR (MNF).//1.40E-74//158aa//89%/P42128
 C-Y79AA1000013//Mus musculus RING finger protein A07 mRNA, complete cds.//8.90E-205//1435bp//81%/AF171060
 C-Y79AA1000033//Homo sapiens CARD4 mRNA, complete cds.//0//2929bp//96%/AF126484
 C-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//2.40E-30//80aa//60%/P25916
 C-Y79AA1000059//Homo sapiens aryl-hydrocarbon interacting protein-like 1(AIPL1) gene, complete cds.//0//980bp//96%/AF180472
 C-Y79AA1000181//Homo sapiens CGI-01 protein mRNA, complete cds.//0//1858bp//99%/AF132936
 C-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA, complete cds.//7.10E-71//345bp//100%/AF081192
 C-Y79AA1000231//Homo sapiens nucleolar protein NOP

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5/NOP58 mRNA, complete cds. //0//1515bp//99%/AF123534
 C-Y79AA1000268//Mus musculus Nip2l mRNA, complete cds. //2.10E-50//648bp//64%/AF035207
 C-Y79AA1000313//CALPHOTIN. //0.000011//336aa//23%/Q02910
 C-Y79AA1000328//SEL-10 PROTEIN. //0.00000067//219aa//25%/Q93794
 C-Y79AA1000342//Homo sapiens Cizl mRNA, complete cds. //0//2644bp//81%/AB030835
 C-Y79AA1000346//Homo sapiens nonclathrin coat protein gamma2-COP mRNA, complete cds. //0//2520bp//99%/AF157833
 C-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein. //0//2048bp//93%/X84692
 C-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161. //4.00E-20//261aa//27%/P25343
 C-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds. //8.30E-252//1207bp//85%/U41736
 C-Y79AA1000540//CELL POLARITY PROTEIN TEA1. //2.10E-12//211aa//33%/P87061
 C-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT). //0//652aa//98%/P17427
 C-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION. //2.40E-27//216aa//34%/P28320
 C-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds. //2.00E-287//2031bp//82%/AF060503
 C-Y79AA1000705//M.musculus mRNA of enhancer-trap-1 locus 1. //5.80E-254//1477bp//84%/X69942
 C-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds. //0//1594bp//99%/AF093670
 C-Y79AA1000748//Rattus norvegicus clone C42 CDK5 activator-binding protein mRNA, complete cds. //6.60E-286//1832bp//84%/AF177477
 C-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP). //4.90E-91//200aa//64%/Q61990
 C-Y79AA1000782//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5). //3.00E-37//469aa//27%/P49902
 C-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds. //1.10E-236//1076bp//99%/AF098799
 C-Y79AA1000794//Homo sapiens actin-associated protein 2E4/kaptin (2E4) mRNA, 2E4-1 allele, complete cds. //0//1610bp//99%/AF105369

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C-Y79AA1000800//Homo sapiens putative secreted protein (ZSIG11) mRNA, complete cds. //1.60E-284//1288bp//99%/AF072733
 C-Y79AA1000833//TUBULIN ALPHA-1 CHAIN. //5.00E-173//220aa//79%/P05209
 C-Y79AA1000962//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSINII). //4.20E-17//430aa//27%/Q99323
 C-Y79AA1000966//Homo sapiens COP9 complex subunit 4 mRNA, complete cds. //0//1586bp//99%/AF100757
 C-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit(eIF-2B gamma) mRNA, complete cds. //3.90E-248//1468bp//87%/U38253
 C-Y79AA1000985//Human centrosomal protein kendrin mRNA, complete cds. //4.70E-151//985bp//87%/U52962
 C-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD). //3.10E-138//583aa//47%/P45953
 C-Y79AA1001211//Homo sapiens origin recognition complex subunit 6 (ORC6)mRNA, complete cds. //0//1435bp//99%/AF139658
 C-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1). //7.70E-50//228aa//42%/P51657
 C-Y79AA1001236//Homo sapiens cell division protein mRNA, complete cds. //0//1612bp//99%/AF063015
 C-Y79AA1001299//Homo sapiens mRNA for integrase interactor 1b protein (INI1B). //0//996bp//99%/AJ011738
 C-Y79AA1001312//ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46). //0.00000023//193aa//30%/Q03309
 C-Y79AA1001323//Mus musculus mRNA for GSG1, complete cds. //3.30E-172//1171bp//83%/D87325
 C-Y79AA1001384//Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds. //0//4708bp//99%/AF055084
 C-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-1J). //1.20E-58//178aa//66%/P31271
 C-Y79AA1001394//CELL DIVISION PROTEIN FTSH HOMOLOG (EC 3.4.24.-). //1.20E-13//230aa//32%/D83746
 C-Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen(MA4) mRNA, partial cds. //8.50E-65//784bp//62%/AF083115
 C-Y79AA1001493//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B). //3.80E-18//151aa//38%/P35132
 C-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds. //4.50E-193/

- /1333bp//80%/D14336
 C-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.50E-76//85aa//90%/P42356
 C-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COALIGASE) (ACYL- ACTIVATING ENZYME).//1.90E-40//482aa//27%/P27550
 C-Y79AA1001594//HYALURONAN-MEDIATED MOTILITY RECEPTOR (HYALURONIC ACID RECEPTOR).//2.50E-14//410aa//24%/Q00547
 C-Y79AA1001603//POLYPEPTIDE N-ACETYLGALACTOSAMINYL TRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP ACETYLGALACTOSAMINYLTRANSFERASE) (UDP-GALNAC: POLYPEPTIDE, N-ACETYLGALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%/Q07537
 C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%/P52740
 C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA A, complete cds.//3.4e-310//1430bp//98%/AF077049
 C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gcl)mRNA, complete cds.//1.40E-78//227aa//40%/Q01820
 C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-47//626bp//68%/AF033120
 C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Rho) mRNA, complete cds.//1.20E-258//1185bp//99%/J04137
 C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase2 (IP6K2) mRNA, complete cds.//0//1689bp//98%/AF177145
 C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%/AF192913
 C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%/P43489
 C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%/P51149
 C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%/AF174602
 C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.00E-10//94aa//47%/042643
 C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%/P42743
 C-Y79AA1002083//H. sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%/X86018
 C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%/P16415
 C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%/Q24133
 C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%/Q13329
 C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%/Q02357
 C-Y79AA1002209//TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-72//437aa//39%/P00952
 C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa//25%/Q13829
 C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%/016264
 C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PS02 /SNM1.//7.10E-17//213aa//31%/P30620
 C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%/000445
 C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%/AB013384
 C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%/AF116574
 C-Y79AA1002311//R. norvegicus mRNA for cytosolic resinsiferatoxin-bindingprotein.//2.90E-186//1130bp//82%/X67877
 C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%/Y18208
 C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%/X91879
 C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPH) mRNA, complete cds.//3.9e-317//1902bp//86%/U49385
 C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESC2).//9.80E-62//318aa//35%/Q04725
 C-Y79AA1002433//Homo sapiens chromatin-specific transcription elongationfactor FACT 140 kDa subunit mRNA, complete cds.//0//1545bp//96%/AF152961
 C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//49%/Q05481
 C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%/Q05481
 C-Y79AA1002487//Homo sapiens chromosome 5 F-box pr

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otein Fbx4 (FBX4) mRNA, complete cds. //7.3e-311//1
444bp//98%//AF129534

【1136】

【配列表】

配列表は公開・登録公報長大データCD-ROM「14
(2002)-001(002)」を参照

【図面の簡単な説明】

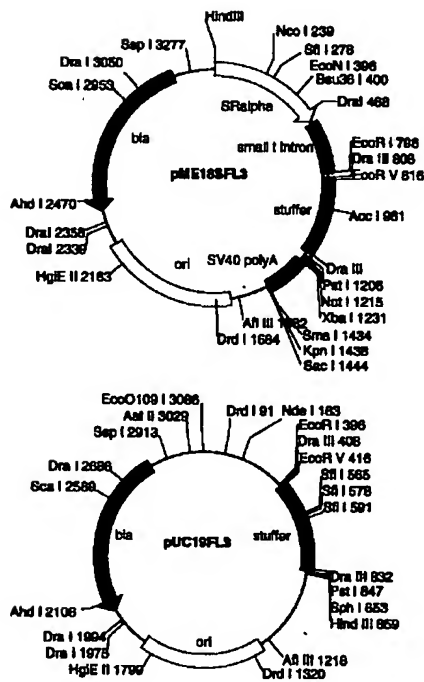
4492

* 【図1】 pME18SFL3とpUC19FL3のベクターのマップ

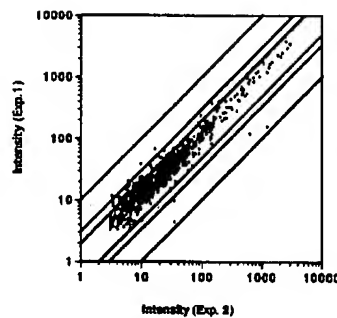
【図2】 遺伝子発現解析の再現性を示すグラフ。縦軸と横軸はそれぞれ異なる実験によって得られた発現強度を示している。

【図3】 遺伝子発現解析における検出感度を示すグラフ。縦軸は発現強度を、横軸はプローブの濃度 ($\mu\text{g}/\text{m}$) を示す。

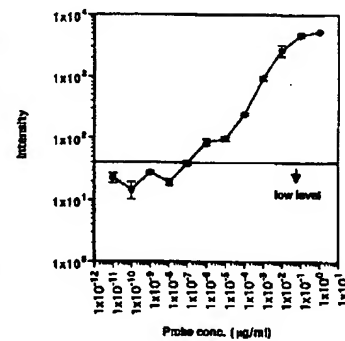
【図1】



【図2】



【図3】



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